Genotypic correlations, phenotypic, environmental and path analysis in tree tomato (*Cyphomandra betacea* Cav. Sendt.)

Correlaciones genotípicas, fenotípicas y ambientales, y análisis de sendero en tomate de árbol (*Cyphomandra betacea* Cav. Sendt.)

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Abstract

In this study different production components were evaluated and phenotypic, genetic and environmental correlations were estimated, considering nine characters related to the size and quality of tomato tree fruit (*Cyphomandra betacea* Cav Sendt.), it also established the direct and indirect effects of the component variables of quality on fruit weight. To effect the existing data of 81 hybrids (72 interpopulation hybrids and nine controls) arranged in three replications, in the Department of Nariño, Colombia conditions were used. The results indicated that genotypic correlations were higher than the phenotypic and environmental ones. The fruit weight (FW) presented the highest genetic correlation with seed weight per fruit (rG = 0.97) and with seed pulp plus seed weight (rG = 0.92). Path analysis based on genotypic correlations showed that pulp plus seed weight was the variable that had the most direct effect on the FW (1.353). This shows that selection of the fruit weight results in an increase in weight of pulp plus seed. Given the phenotypic correlations, this analysis established that the direct effects of fruit seed weight (FSW) and pulp plus seed weight (P + S) (1.166 and 0.743, respectively) are the largest contributors to FW.

Key words: *Cyphomandra betacea*, environmental correlation, genetic correlation, phenotypic correlation, path analysis.

Resumen

En el estudio se evaluaron diferentes componentes de producción y se estimaron las correlaciones fenotípicas, genéticas y ambientales, considerando nueve variables relacionadas con el tamaño y la calidad del fruto de tomate de árbol (*Cyphomandra betacea* Cav. Sendt.); igualmente se establecieron los efectos directos e indirectos de las variables componentes de calidad sobre el peso del fruto. Para el efecto se utilizaron los datos existentes de 81 híbridos (72 híbridos interpoblacionales y nueve testigos) dispuestos en tres repeticiones, en condiciones del departamento de Nariño, Colombia. Los resultados obtenidos indicaron que las correlaciones genotípicas fueron superiores a las fenotípicas y ambientales. El peso de fruto (PF) presentó las mayores correlaciones genéticas con el peso de semilla por fruto (rG =

0.97) y con el peso de pulpa más semilla (rG = 0.92). El análisis de sendero con base en correlaciones genotípicas mostró que el peso de pulpa más semilla fue la variable que tuvo el mayor efecto directo sobre el PF (1.353). Esto demuestra que una selección por peso de fruto da como resultado un aumento en peso de pulpa más semilla. Teniendo en cuenta las correlaciones fenotípicas, este análisis permitió establecer que los efectos directos de peso de semilla de fruto (PSF) y peso de pulpa más semilla (P + S) (1.166 y 0.743, respectivamente) son los que más contribuyen al PF.

Palabras clave: Análisis de sendero, correlación ambiental, correlación fenotípica, correlación genética, *Cyphomandra betacea*.

Introduction

In Colombia, tree tomato (*Cyphomandra betacea* Cav. Sendt.) is one of the fruits with high marketing potential due to its nutrient and organoleptic characteristics, besides the fact that it is an economically viable alternative for farmers of the Andean region of Colombia. According to the National Plan for Fruits, nowadays the area devoted to this crop in the country id 9.223 ha, from which the Department of Nariño has 9.08% (760 ha) (Agronet, 2011). For 2014, a growth in grown area in Colombia is projected to be 10.000 ha, that will generate 7.823 direct jobs (Tafur, 2006). Its potential as fruit crop is determined by its adaptation to tropical conditions; however, this potential is affected by the semi-wild condition of the crop and lack of technological support, because its development is fundamentally based on empirical knowledge, as results of the farmers´ efforts. This is reflected on the poor offer of breeding genotypes that can supply the producer demands and help solving the phytosanitary problems of the crop at the Andean region of the Department of Nariño (Lagos, 2008).

In Colombia and Ecuador, which are the main producers of this fruit, there are not commercial varieties but, local populations that have been multiplied and selected traditionally by the farmers. In consequence, this crop is characterized by high heterogeneity in shape and size of the fruit between and within the same crop, as results of hybridations and mixes of genetic material through the time (Lobo, 2000).

This species is still under domestication processes and the existing cultivars have been product of the empiric selection done by the farmers. The populations of these cultivars have high degree of vulnerability to phytosanitary problems due to their natural co-evolution with the pathogens, to the selection level that have had and, to the seeds sown by the farmers which are from unknown sources (Lagos, 2008).

The plant breeder role identifying the individuals or crops that simultaneously meet the desirable traits is not easy, because several of these traits are positive or negatively associated. The associations between the traits of interest in plant breeding are evaluated by means of phenotypic, genotypic and environmental correlations. Phenotypic correlations are directly estimated from the mean phenotypic values in the field, being, therefore, the result of genetic and environmental causes. The genotypic correlation, contrastingly, corresponds to the genetic part of the phenotypic correlation and is used to guide breeding programs because of its inheritable nature (Cruz, 2001; Cruz and Regazzi, 1997; Falconer and Makay, 1996; Vencovsky and Barriga, 1992; Mariotti, 1986; Hallauer and Miranda, 1981). However, the correlation coefficients, nonetheless their high utility in the quantification of the size and direction of factors´ effects in the determination of complex characters, offer only a relative importance of the direct and indirect effects of these factors. The

solution raised for this limitation is to perform a path analysis, because it unfolds the estimated correlations into direct and indirect effects (Falconer and Mackay, 1996; Cruz and Regazzi, 1997).

According to the above, this research aim to the identification of the variables that affect the most the tree tomato fruit quality and yield, to be used as selection criteria in breeding programs of this species, this, in order to meet the demands of the producers and the agroindustry sector. By variables such as: fruit weight (FW), pulp plus seeds weight (P + S), juice content (JC), pH, brix° (BX), titratable acidity (TA), maturity index (MI), fruit seed weight (FSW) and total number of seeds (TNS) the phenotypic, genotypic and environmental correlations were unfolded by path analysis.

Materials and methods

Location

This research was carried on at three locations considered as replicates to fulfill the experimental design. The first one, in the town of Pasto, village Pradera, at 01° 19' 33.3" N and 77° 19' 18.9" W, with average temperature of 18 °C and at 1980 MASL; the second in the town Ipiales, village Yanalá, at 0° 52' 23" N and 77° 33' 3.8" W, with average temperature of 12 °C and at 2730 MASL; and the third one in the town Tangua, village El Placer, at 1° 8' 10.08" N and 77° 26' 3.41" W, with average temperature of 16 °C and at 2000 MASL.

Experimental design

The experimental design used was in completely randomized blocks, with three replicates (places of fruit collection) and 81 treatments that corresponded to 72 interpopulation hybrids and nine controls (Table 1). The experimental plot consisted of six plants, with 2.5 m of distance between them, with 2.5 m of distance between experimental plots and useful plot with four central plants that occupied 25 m^2.

Evaluated variables

Fruits, once collected, were taken to the lab of Biotechnology of the Universidad de Nariño for the corresponding analysis, detailed as follows.

Fruit weight (FW). It was measured in six fruits per experimental plot.

Pulp plus seed weight (P + S). For this measurement the weight (g) of the pulp including the seeds of each fruit of the experimental plot was taken.

Juice content (JC). Using a blender, the pulp juice was extracted from each one of the fruits and its volume was measured in ml.

pH. It was determined with a pH meter Inolab-WTW series pH 720".

Total soluble solids (°brix). They were determined with a pocket refractometer Atago PAL-1". The read was corrected using the citric acid percentage (A.C.) by means of the equation $bx = 0.19 \times A.C. + T.S.S.$, where *T.S.S.* are the total soluble solids.

Titrable acidity (TA). It was determined by the potentiometer titration method and was expressed as A.C. percentage; for calculation the equation used was: $\%.T.A. = (V_1 \times N) / V_2) \times K \times 100$, where: V_1 = volume of-NaOH used (ml); V_2 = volume of the sample (5 ml); K = citric acid equivalent weight (64,04 g) and N = NaOH normality (0.1 meq/ml).

Maturity index (MI). It was calculated by the ratio between the soluble solid content and the total acidity (Galvis, 1992), by the equation: M.I. = (T.S.S.) / (T.A.).

Fruit seed weight (FSW). It was obtained by the extraction of seeds after the juice passed through a sieve, followed by washing, cleaning and drying at room temperature for 7 days.

Table 1. Interpopulational hybrids of tomato tree (*Cyphomandra betacea* Cav. Sendt) evaluated on the experiment.

Crossing	Parent 1	Parent 2	Crossing	Parent 1	Parent 2
1 x 24	CBcon74	CBl79	13 x 36	CBc12	CBb73
1 x 25	CBcon74	CBc039	13 x 37	CBc12	CBf89
1 x 26	CBcon74	CBb75	13 x 38	CBc12	CBu86
2 x 25	CBa09	CBc039	14 x 37	CBp25	CBf89
2 x 26	CBa09	CBb75	14 x 38	CBp25	CBu86
2 x 27	CBa09	CBg70	14 x 39	CBp25	CBsj38
3 x 26	CBb03	CBb75	15 x 38	CBb08	CBu86
3 x 27	CBb03	CBg70	15 x 39	CBb08	CBsj38
3 x 28	CBb03	CBu88	15 x 40	CBb08	CBc046
4 x 27	CBc044	CBg70	16 x 39	CBc93	CBsj38
4 x 28	CBc044	CBu88	16 x 40	CBc93	CBc046
4 x 29	CBc044	CBsj35	16 x 41	CBc93	CBu65
5 x 28	CBi49	CBu88	17 x 40	CBc042	CBco46
5 x 29	CBi49	CBsj35	17 x 41	CBco42	CBu65
5 x 30	CBi49	CBi50	17 x 42	CBc042	CBcon34
6 x 29	CBi51	CBsj35	18 x 41	CBsj36	CBu65
6 x 30	CBi51	CBi50	18 x 42	CBsj36	CBcon34
6 x 31	CBi51	CBl78	18 x 43	CBsj36	CBu87
7 x 30	CBl81	CBi50	19 x 42	CBcon33	CBcon34
7 x 31	CBl81	CBl78	19 x 43	CBcon33	CBu87
7 x 32	CBl81	CBsj37	19 x 44	CBcon33	CBu94
8 x 31	CBunt1305	CBl78	20 x 43	CBp19	CBu87
8 x 32	CBunt1305	CBsj37	20 x 44	CBp19	CBu94
8 x 33	CBunt1305	CBc15	20 x 45	CBp19	CBc95
9 x 32	CBb04	CBsj37	21 x 44	CBc11	CBu94
9 x 33	CBb04	CBc15	21 x 45	CBc11	CBc95
9 x 34	CBb04	CBc040	21 x 46	CBc11	CBl77
10 x 33	CBc14	Cbc15	22 x 45	CBb06	CBc95
10 x 34	CBc14	CBco40	22 x 46	CBb06	CBl77
10 x 35	CBc14	CBu84	22 x 47	CBb06	CBc041
11 x 34	CBb02	CBco40	23 x 46	CBu82	CBl77
11 x 35	CBb02	CBu84	23 x 47	CBu82	CBco41
11 x 36	CBb02	CBb73	23 x 48	CBu82	CBb01
12 x 35	CBl80	CBu84	24 x 47	CBl79	CBco41
12 x 36	CBl80	CBb73	24 x 48	CBl79	CBb01
12 x 37	CBl80	CBf89	25 x 48	CBc039	CBb01

Total number of seeds per fruit (TNS). it is the ratio between FSW and the weight of 100 seeds of each genotype.

Statistical analysis

The variables above mentioned were subjected to analysis of phenotypic, genotypic

and environmental correlation according to the proposal of Ceballos (1997). For FW two path analysis were performed (Singh and Chaudhary, 1985), one based on the phenotypic correlations and the other one with the genotypic correlations. Also, groups of the highly correlated variables (r > 0.60) were done and used to select the ones with more importance.

The phenotypic, genotypic, environmental and path correlation coefficients were estimated using the software GENES developed by Cruz (2006). The program applies the classic correlation formulas:

Phenotypic correlation (rF(XY)): rF(XY) = COVF(XY)/ SF(X).SF(Y) genetic correlation (rG(XY)): rG(XY) = COVG(XY)/ SG(X).SG(Y) Environmental correlation (rE(XY)): rE(XY) = COVE(XY)/ SE(X).SE(Y).

where, r(*XY*) and COV(*XY*) = are correlation and covariances for phenotype(rF), genetic (*rG*) and environment (*rE*) between the characters *X* and *Y*, respectively; *S*(*x*) and *S*(*y*) = are the phenotypic, genetic and environmental standard deviations of *X* and *Y*, in its order.

Once the correlation coefficients were estimated the statistical significance was confirmed for each one of them (r), having as nule hypothesis: Ho: r = 0 vs. the alternate hypothesis Ha: r ≠ 0, by doing a 't' test, given by $tc = r\times(n-2)^{1/2}/(1-r_2)^{1/2}$. The calculated 't' (tc) was compared with the 't' of the Table (tt) at a 0.05 significance level and with n = 2 degrees of freedom. The decision rule was: if tc ≥ tt, then the r value is statistically different from 0 (Espitia *et al.*, 2008).

The path analysis consists in unfolding the correlation coefficients (phenotypic, genetic and environmental) into the direct and indirect effects of several characters (causes) on a basic complex variable (effect). Based on the matrices for phenotypic and genotypic correlations, the rF and rG were unfolded to determine the effects that affect the FW. In this case, the FW (effect variable) was in function of the PUS, JC, pH, BX, CA, MI, FSW and TSN (cause variables).

Results and discussion

The phenotypic (rF), genetic (rG) and environmental (rE) correlation coefficients found are shown in Table 2. Without exceptions, the rG were larger in magnitude than the rF. The obtained results indicate a positive and significant rG (P < 0.05) between the FW and P + S (0.92), FW and JC (0.81) and between FW and FSW (0.97) and evidence a common genetic action between these variables, which makes easier the selection since the process will be done using any of them. The rF and rG of FW with P + S (0.71 and 0.97, respectively) and with JC (0.51 and 0.81, respectively) were significant (P < 0.05). The magnitudes of the positive phenotypic genetic correlation suggest that the selection by FW produces an increase in the character previously cited (Table 2).

The rF, rG and rE, between the variables P + S and JC show a smaller phenotypic correlation than the genetic correlation (rF = 0.75 < rG = 0.96), which implies an important environmental correlation (rE = 0.64) and, therefore, there is an effect of the environmental factors and/or of the non-additive factors that negatively affect the level of real association between the characters under study (Espitia *et al.*, 2008). The above also happens between the variables FSW and TNS (rF = 0.98 < rG = 1.02, rE = 0.98).

In the characteristic TSS (°brix) there is a positive and significant genetic and environmental correlation with MI, but, there is not a genetic relation between them, therefore, the phenotype is result of the environment and not of the genotype.

Table 2. Phenotypic (rF), genotypic (rG) and environmental (rE) correlations for the pulp plus seed weigth (P + S), juice content (CJ), pH, soluble solids (ºbrix), titratable acidity (CA), maturity index (IM), seed weight per fruit (FSW) and total number of seeds (TNS).

Variable	P + S		JC	pH	Brix	CA	MI	FSW	TNS
FW	rF	0.71*	0.51*	-0.01	0.04	0.23	-0.15	0.31	0.29
	rG	0.92*	0.81*	-0.17	0.01	1.39	999.00	0.97*	1.11
	rE	0.44	0.32	0.05	0.07	0.17	-0.10	-0.04	-0.08
P + S	rF		0.75*	-0.02	0.13	0.18	-0.08	0.27	0.28
	rG		0.96*	0.11	-0.02	1.65	999.00	0.95*	1.31
	rE		0.64*	-0.05	0.20	0.05	0.06	0.02	-0.03
JC	rF			-0.09	0.17	0.14	-0.01	0.26	0.25
	rG			-0.71	-0.03	2.54	999.00	1.27	1.48
	rE			-0.01	0.23	-0.04	0.12	-0.02	-0.03
pH	rF				-0.07	0.07	-0.07	0.02	0.03
	rG				-0.31	4.57	999.00	0.75*	1.16
	rE				-0.04	-0.06	0.06	-0.06	-0.06
Brix	rF					0.17	0.61*	0.04	0.02
	rG					4.06	999.00	0.22	0.21
	rE					-0.03	0.69*	0.00	-0.02
CA	rF						-0.47	0.18	0.21
	rG						999.00	2.01	3.44
	rE						-0.57	0.09	0.07
MI	rF							-0.100	-0.14
	rG							999.00	999.00
	rE							-0.07	-0.07
FSW	rF								0.98*
	rG								1.02
	rE								0.98*

The positive and significant genetic correlations between FSW with P + S (0.95) and pH with FSW (0.75) can be also consider as important, since they suggest that a selection by FSW affects directly the increase or decrease of the P + S (0.95) and pH. It can be assumed that the genetic correlations > 1 (Table 2) are perfect, or that it is recommended to check the variances of each one of the involved variables in the correlation analysis, if one of them shows differences or a significant variance and the other one no, means that this correlation should be discarded (Checa, 2012) as the correlation measures the covariance degree between two variables (Mayo, 1980).

The path analysis that show the decomposition of the phenotypic (rF) and genetic (rG) correlations for FW, are shown on Table 3 and 4. In the path analysis for rF (Table 3) are observed the direct effects of P + S (0.743) and the FSW (1.166) on the correlation coefficient (FW: 0.707 and 0.313, respectively) are positive and larger than the indirect effects of the other variables included in the analysis. These results, both, the direct effects and the correlation coefficients, explain the real relation among both characters, therefore, a direct selection through this characteristic could be effective (Singh and Chaudhary, 1985).

The R^2 coefficient of the path analysis based on the phenotypic correlations was 56% (Table 3), which is considered as low and suggests that the variables on the model do not explain phenotypically the FW. In the analysis of variables with the largest direct effect on the FW were P + S (0.743) and FSW (1.166), whereas on the genetic were P + S (1.35) and FSW (0.874) (Table 4).

Table 3. Path analysis for the phenotypic correlations of fruit weight (FW) in function to the pulp plus seed weigh (P + S), juice content (CJ), pH, soluble solids (ºbrix), titratable acidity (CA), maturity index (IM), seed weight per fruit (FSW) and total number of seeds (TNS) in tomato tree (*C. betacea),* in the town of Pasto - Nariño, Colombia.

Variables	Phenotypic correlations								rG withFW
	P + S	**CJC**	**pH**	**BX**	**CA**	**MI**	**FSW**	**TSN**	
P + S	**0.743**	-0.057	0.000	-0.013	0.027	-0.001	0.313	-0.305	**0.707**
JC	0.554	**-0.077**	0.000	-0.018	0.021	0.000	0.298	-0.267	**0.512**
pH	-0.015	0.007	**-0.004**	0.007	0.011	-0.001	0.018	-0.035	**-0.012**
BX	0.094	-0.013	0.000	**-0.104**	0.026	0.007	0.041	-0.017	**0.036**
C	0.131	-0.010	0.000	-0.018	**0.154**	-0.006	0.209	-0.229	**0.231**
MI	-0.061	0.001	0.000	-0.064	-0.072	**0.012**	-0.118	0.153	**-0.148**
FSW	0.200	-0.020	0.000	-0.004	0.028	-0.001	**1.166**	-1.055	**0.313**
NTS	0.211	-0.019	0.000	-0.002	0.033	-0.002	1.146	**-1.074**	**0.294**

In the diagonal and in bold are the direct effects and outside the diagonal are the indirect ones.

Table 4. Path analysis for the genetic correlations of fruit weight (FW) in function to the pulp plus seed weigh (P + S), juice content (CJ), pH, soluble solids (ºbrix), titratable acidity (CA), maturity index (IM), seed weight per fruit (FSW) and total number of seeds (TNS) in tomato tree (*C. betacea),* in the town of Pasto - Nariño, Colombia.

Variables	Genetic correlations								rG with FW
	P + S	**JC**	**pH**	**BX**	**CA**	**MI**	**FSW**	**TSN**	
P + S	**1.353**	-0.461	0.001	-0.005	-0.319	0.560	0.832	-1.041	**0.921**
JC	1.303	**-0.479**	-0.004	-0.007	-0.489	0.560	1.106	-1.182	**0.809**
pH	0.151	0.339	**0.006**	-0.073	-0.882	0.560	0.653	-0.925	**-0.171**
BX	-0.031	0.014	-0.002	**0.235**	-0.783	0.560	0.188	-0.170	**0.012**
CA	2.234	-1.215	0.025	0.953	**-0.193**	0.560	1.758	-2.735	**1.387**
MI	1352.0	-478.39	5.51	234.62	-192.76	**0.00**	872.99	-795.00	**999.00**
FSW	1.289	-0.606	0.004	0.050	-0.388	0.560	**0.874**	-0.815	**0.969**
TSN	1.770	-0.711	0.006	0.050	-0.663	0.560	0.894	**-0.796**	**1.111**
	$R^2 = 1$	h = 0							

In the diagonal and in bold are the direct effects and outside the diagonal are the indirect ones.

The determination coefficient (R^2) in the path analysis for rG indicates that 100% of the FW variability was explained by the variables P + S, JC, PH, BX, CA, MI, FSW and TSN, which is a good fit for the model and shows the importance of the explaining variables in the FW definition (Espitia *et al.*, 2008).

The correlation decomposition (rF = 0.512) between JC and FW (Table 2) is explained in larger proportion by indirect effects of P + S (0.554) than for the direct effects of the JC variable (-0.077); this indicates that the significant and direct correlation between JC and FW is due, in larger proportion, to the indirect influence through P + S. Based on the first path analysis (Table 3) it can be inferred that the selection by larger P + S and JC allows the collection of heavier fruits.

In the case of the path analysis for the rG (Table 4) it is observed that the direct effect of the P + S (1.353) on the correlation coefficient FW = 0.921 is larger than the indirect effects of other variables included in the analysis. As they are positive, both the direct effect and the correlation coefficient, explain the real relation existing between both characters and, indicates that the direct selection through this characteristic is effective (Singh and Chaudhary, 1985). In the same Table 4 is observed that in the path analysis for genetic correlations, the direct effect of the

FSW variable on the FW (0.874) is smaller than the indirect effect of P + S on FW (1.289); in this case, the correlation value (0.969) is attributed to the indirect effect of the P + S variable. In this situation the causal indirect effect is considered for the selection processes (Singh and Chaudhary, 1985).

Conclusions

- In this study, the high values of genetic correlation showed that the variables that affect the most the fruit weight of tomato tree and that can be used as selection criteria are the pulp plus seed weight per fruit and seed weight per fruit.
- In the path analysis for the phenotypic and genetic correlations, the variables with larger direct effect on fruit weight were the seed weight per fruit and the pulp plus seed weight per fruit.

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