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Evaluation of Variance Components and Genetic Parameters in F1 Progenies of *Coffea canephora* Pierre x *C. congensis* Froehner

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Authors' contributions

This work was carried out in collaboration among all authors. Authors KMO, KZJ, NASP and OMP, designed and wrote the study protocol. Author KMO conducted the documentary research, wrote the 1st draft and the revisions to the manuscript. The authors NASP, KZJ and YAA participated in the elaboration of the 1st draft, the statistical analysis and made a major contribution to the elaboration of the final document. The authors ADS and LNH took part in the interpretation of the results and contributed to the development of the final document. All authors read and approved the final manuscript.

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ABSTRACT

The diploid species *Coffea congensis* is of interest in improving the organoleptic quality of *C. canephora.* F1 crosses of *C. canephora* x *C. congensis* named Congusta in 3 x 5 factorial design have been carried out. The work aimed to assess the genetic parameters in the hybrids in order to integrate them into the selection schemes under way in Côte d'Ivoire. The experimental design was a randomized complete block design. Each cross was represented by a minimum of 29 plants and a maximum of 55 plants. The spacing used was 3 x 1.5 m. Male genotypes *C. congensis* brought little

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improvement in offspring regardless of their insignificant additive gene effect in the hybrids. Low heritabilities were found for vegetative vigor traits DICO, GAT and NPLA ranging from 0.13 to 0.23 in the narrow sense and from 0.18 to 0.32 in the broad sense. For production, the narrow sense heritabilities were stable during the first three years of harvest with values between 0.23 and 0.25 whereas the broad sense heritability was irregular. The estimation GCA and SCA showed that all the traits except RCAR had ratio between both effects above 1. The study of correlations between traits showed insignificant correlations between production and vegetative traits, with coefficients below 0.30. However, The selection of 83 high-producing trees from 14 out of 15 studied families make it possible to create good vegetative trees linked to high yield.

Keywords: Congusta hybrid; quantitative genetic; organoleptic; Côte d'Ivoire.

1. INTRODUCTION

Coffee is the second most important commercial product that is exported by developing countries [1]. Commercial coffee production is based on only two main species among the 139 species of the Coffea genus: *C. arabica* Linné which accounts for 65% and *C. canephora* Pierre ex Froehner which accounts for the remaining 35% [2]. In Côte d' Ivoire, this plant cultivation, essentially made up of the *C. canephora* species, is made up of small farms characterized by their reduced size ranging between 0.5 and 3 ha and low annual yields, of the order of 250 Kg/ha of merchant coffee [3]. With an average annual production of about 271,000 tons of green coffee, Côte d'Ivoire was ranked third in the world and first African coffee-producing country until the end of the 1980s [4]. Since then, its production has steadily declined to just under 90,000 tons in 2018, ranking it fifteenth in the world.

This drop in production is due to the combined effect of several factors, including economic constraints with the collapse of world prices for Robusta coffee due to its unattractive cup quality [5]. To face these constraints, and in its desire to make Ivorian coffee more competitive on the international market and promote a sustainable coffee economy, the State of Côte d'Ivoire has initiated since 1960, extensive programs to improve its coffee through research. The work carried out for this purpose has exploited the intraspecific diversity of *C. canephora*, first through clonal selection since 1960 [6] and then reciprocal recurrent selection from 1990 until now [7,8]. Although the results obtained showed a significant increase in productivity, organoleptic quality was not improved. For example, the caffeine content remained above 2.5% dry content [9]. One of the recommended ways of improving organoleptic quality is interspecific h2ybridization, which exploits the specific diversity of the large Ivorian coffee collection [10]. In the program, the Coffea canephora species was crossed with diploid species. Among these, *C. congensis* is known for its low caffeine content, which varies from 0 to 1.9 % dry content [11]. However, the genetic parameters conditioning the success of such hybridization have been little studied in contrast to the intraspecific hybrids *C. canephora*.

The present work aims to improve of productivity and organoleptic quality of coffee-beverage in Côte d'Ivoire by accessing the heritability, combining ability and correlations between traits in 15 F1 families of the cross between *C. canephora* and *C. congensis*, called Congusta.

2. MATERIAL AND METHODS

2.1 Presentation of the Study Site

The work was carried out at the research station of the Centre National de Recherche Agronomique (CNRA) of Divo in Côte d'Ivoire. This station is located 17 km from the town and about 200 km north-west of Abidjan. The geographical coordinates are 5°46' North latitude and 5°17' west longitude. The average altitude of the study site is 197 m above sea level (GPS Data).

The climatic data of this station correspond to the norms indicated by [12] for coffee cultivation. Rainfall has a bimodal distribution, with two rainy periods from March to June and from September to November, alternating with two dry seasons, from December to February and from July to August. The values of the rainfall data produced by the meteorological service of the research station were between 738 and 1600 mm/year from 1986 to 2015. Temperatures averaged between 24.1 and 26.9 °c per year during the same period. Humidity is relatively high, sometimes exceeding 80%. The soils in the study area are deep, dark brown, sandy-clayey

or humus-bearing depending on the type of relief, with an average altitude of 197 m above sea level. The percentage of potassium in these soils is low and the pH is acidic, between 6 and 5.2 for a depth of 1 m.

2.2 Plant Material

The plant material is composed of F1 hybrids derived from the cross between *C. canephora* and *C. congensis*. The *C. canephora* (female sires) was composed of 3 clones which are representative of the known diversity of the species [13]. These are one clone from the Guinean pool coded G, one from the Congolese pool coded C and one hybrid (H) between the two pools. The *C. congensis* (male sires) were made up of 5 genotypes (301, 302, 303, 304 and 305) selected from the most vigorous and flowering plants in the collection resulting from a survey in Cameroon. The F1 hybrids resulting from these crosses following a complete factorial plan (3x5) numbering 956 trees were divided into 15 families of 29 to 55 trees per family (Table 1). Congusta hybrids (Cg1 and Cg2) and Canephora clones (T1, T2 and H) were used as controls in the trial.

2.3 Methods

2.3.1 Obtaining hybrids

Hybrids are obtained by manual pollination. This technique consisted of collecting anthers from male coffee trees before pollen dehiscence (Fig. 1-A) and storing them in the laboratory. These anthers were dried in sieve bags. Once the anthesis was complete, the ripe pollen was removed from the stamen (Fig. 1-B), sieved and then stored in a test tube in the freezer. At the same time, flowering branches from the mother trees were selected. The flowers of these branches were emasculated by removing their stamens (Fig. 1-C) to protect them from contamination by illegitimate pollen and isolated in tissue sleeves (Fig. 1-D). From the beginning of the receptive period of the female flowers, the emasculated flowers were smeared with pollen (Fig. 1-E). The pollen smearing was repeated 3 to 4 times during the receptivity period, which is a maximum of two days, in ordre to maximise the chances of pollination. The resulting seeds are deseeded and then de-pulped and placed in a germinator where they germinate after three weeks. The seedlings (hybrids) are transplanted into polyethylene bags. The seedlings of each offspring are raised in the nursery for eight months before being planted in the field. Approximately eighteen months elapse between pollination and field cultivation.

2.3.2 Cultivation in the field

All the trees of the progeny analyzed were planted following a completely randomized system. This device is adapted to shrubby plants such as cocoa and coffee trees because it allows a better control of soil micro-homogeneities.

Coffee trees were planted at a density of 2222 trees per hectare, with 3 m between contiguous lines, and 1.5 m between trees on the same line. They were left to grow freely, with two stems per plant after arching. The previous crops were abandoned coffee plantations, felled one year before the site was prepared for the experimental plots. Land preparation was carried out between January and May of the year of planting, and consisted of burning, swathing, staking and pruning.

2.3.3 Data collection

The analysis covered 7 traits including:

- 3 on vegetative vigor (stem diameter (DICO) in mm, number of plagiotropic branches (NPLA), general appearance of the tree (GAT))
- 1 on yield (production of fresh cherries from each tree 3, 4, 5, 6, 7 years after planting; and the average annual production of fresh cherries. (Pr03, Pr04, Pr05, Pr06, Pr07 and PCUM in hg)
- 3 on the granulometry (weight of one hundred beans (W100 in g); yield in merchant coffee (RCMA in p.c) rate of caracolis (RCAR in p.c).

2.3.4 Statistical analysis

All, the studied traits were subjected to an analysis of variance using the REML procedure of SAS software version 9.4 (2018). The data collected have a Poisson distribution, characterized by the equality between the variance and the mean, thus inducing coefficients of variation that are too high. A square root transformation X_{trans}= sqrt (x + 0.5) that is best suited to these conditions was applied. The model applied to the analysis of genetic parameters is a two-factor, male and female, interacting model. The mathematical form of the individual performance of the coffee trees is as follows according to [14]:

$$Yijk = \mu + Mi + Fj + Iij + \varepsilon ijk$$

Where:
Yijk: the observed performance of individual k, resulting from the crossing of male i and female j; μ: the family average; Mi: the part of the performance due to the male i effect; (p levels), Fj: the part of the performance due to the female j effect; (m levels); Iij: the part of the performance due to the interaction male i x female j effect; εijk: the residual part.

The equality between the statistical model and the genetic model made it possible to determine the different genetic variances [15]:

$$\sigma^2_{Am} = 4(MS_M - MS_I) / nf$$
$$\sigma^2_{Af} = 4(MS_F - MS_I) / nm$$
$$\sigma^2_{D} = 4(MS_I - MS_E) / n$$

Where
σ^2_{Am} =male additive variance; σ^2_{Af} =female additive variance, σ^2_{D} = dominance variance
MS_M, MS_F, MS_I, MS_E: mean square of male M, female F, interaction (M x F) and residual
n: number of repetitions for each crossing
f: number of female sires
m: number of male sires,

In the previous formulas, MS_M-MS_I is assimilated to the male variance (σ^2_m), MS_F- MS_I to the female variance (σ^2_f) and MS_I-MS_E to the male x female interaction variance (σ^2_{mxf}).

The narrow sense heritability (h^2) and the broad sense heritability (H^2) were calculated according to the following formulas used by [16].

$$h^2 = (1/2[\sigma^2 A_m + \sigma^2_{Af}]) / (\sigma^2_{Am} + \sigma^2_{Af} + \sigma^2_D + \sigma^2_E)$$

$$H^2 = (1/2(\sigma^2_{Am} + \sigma^2_{Af}) + \sigma^2_D)) / (\sigma^2_{Am} + \sigma^2_{Af} + \sigma^2_D + \sigma^2_E)$$

Where:

h^2= narrow sense heritability; H^2= broad sense heritability.

A heritability less than 0.3 is considered low. On the other hand, it is considered high when it is between 0.3 and 0.5 and very high when it is greater than 0.5 [17].

Methods for estimating General combining ability (GCA) and Specific combining ability (SCA) effects are proposed by [18]. They argue that male (σ^2_m) and female (σ^2_f) main effects, and the male × female interaction (σ^2_{mxf}) effects in a North Caroline (NC II) mating design are equivalent to the GCA (σ^2_g) and the SCA (σ^2_s) effects in a diallele. The estimation of these effects made it possible to show the additive or dominant type of gene effect:

- If σ^2_g / σ^2_s is > to 1, the gene effect is of an additive nature;
- If σ^2_g / σ^2_s is < to 1, the gene effect is of a dominant nature.

The study of correlations makes it possible to develop improvement strategies for two traits simultaneously, knowing the effect that the selection of one will have on the other. They give an idea of which traits can be used as selection criteria. These correlations can be genetic or phenotypic. The genetic correlation coefficient (rG) is a correlation between the genetic values of the same individual for several traits taken in pairs. It is expressed as: r G= (Cov G(x, y))/sqrt ((σ2 G(x)) (σ2 G(y))

Where
Cov G (x, y): genetic covariance of the traits x and y
rG: Genetic correlation coefficient between the two considered traits.

The significance of the correlation coefficients is tested against the values in the r table, with n-2 ddl and the 5% probability threshold. For traits with low correlations, either independent stepwise selection or index selection has been defined in order to achieve optimal genetic progress.

Table 1. Factorial grid of the crossing *C. canephora* x C. congensis

C. congensis progenitors (♂) / C. canephora *progenitors* (♀)	301	302	303	304	305
G	G301 (51)	G302 (52)	G303 (49)	G304 (54)	G305 (55)
H	H301 (29)	H302 (54)	H303 (45)	H304 (30)	H305 (49)
C	C301 (47)	C302 (53)	C303 (54)	C304 (48)	C305 (44)

The numbers in brackets indicate the number of trees per progeny

Fig. 1(A-E). The different stages of manual pollination

A*: Harvesting of male flowers, B: Extraction of pollen from the flowers, C: Emasculation of the flowers, D: Sleeving the selected flowering branches, E: Smearing of pollen on the stigmas of the emasculated flowers*

3. RESULTS AND DISCUSSION

3.1 Components of Variance and Heritability

The analysis of variance of the traits showed differences between progenies. It also showed that these differences have a genetic origin due to the female *C. canephora*. Indeed, for most of the traits, the mean squares of the female sires were greater than the mean squares of the male sires with F values between 20.81 and 93.29 for the former, compared to values between 0.36 and 8.01 for the latter (Table 2). The resemblance of the Congusta hybrid to the female canephora sire can be due to the low variability within *C. congensis* genotypes. According to [19], *C. congensis* grows on the banks and periodically flooded banks of watercourses, unlike *C. canephora*. Selection of male genotypes on the basis of their individual performance may bring little improvement in offspring under the coffee growing conditions of Côte d'Ivoire. The results obtained are similar to

those of [20], who showed through the rbcL and matK sequence genes the morphological resemblance of *C. congensis* x *C. canephora* hybrids to *C. canephora* parents although they used Congensis as the female parent. If there is variability in the populations of *C. congensis* species, as indicated by [21,11,22], it can be demonstrated after a more extensive evaluation of the three populations in the collection, of Congolese, Cameroonian and Central African origin.

Estimation of the variance components showed that female additive variances prevailed over male additive variances. In many cases, male additive variances are even insignificant. Only female heritabilities are considered for these traits. For vegetative vigor trait, the number of plagiotropic branches (NPLA) had a narrow sense heritability of 0.23 and a broad sense heritability of 0.32. On the other hand, low heritabilities were noted for the Stem diameter (DICO) and general appearance of the tree (GAT) with a narrow sense heritability of 0.13 each and broad sense heritability of 0.24 and 0.18 respectively (Table 3). The low heritability of vegetative vigor traits therefore indicate important environmental effects in the phenotypic expression of these traits. These results are similar to those of [17,23], who estimated heritabilities between 0.13 and 0.22 for the former and between 0.11 and 0.14 for the latter, for all vegetative vigor traits in *C. canephora*. Bikila et al. [24] also found similar results for *C. canephora*. At the level of the technological traits, notably the yield of merchant coffee (RCMA) and the rate of caracolis (RCAR), the heritabilities were of the order of 0.20 each in the strict sense and 0.50 in the broad sense. These two characteristics are therefore strongly influenced by the environment whereas results reported by [17] revealed heritabilities that were insignificant for the same traits in the strict and broad sense. Estimate heritabilities for yield had not varied considerably in the narrow sense from three first years production ranging from 0.23 to 0.25. But, irregular broad sense heritability were observed with values of 0.37, 0.29, 0.37, 0.45 and 0.41 respectively from first year (Pr03) to fifth year (Pr07).The higher heritability were established at the forth year with value of 0.39 in the narrow sense and 0.45 in the broad sense. Regardless of these results, six years old plants could be considered as favorable to selection. Such conclusion had been expressed by [25] after finding same results whereas [26] estimated heritability near 0.79 both in *C. canephora*.

3.2 General and Specific Combining Abilities

The estimated values of the general combining ability effects (σ^2g) and specific combining ability effect (σ^2s) were used to calculate their ratios (Table 5). The most important ratios were observed for $W100_G$ with values of 31.25. NPLA and GAT had σ^2g 5 times higher than σ^2s. For RCMA, the GCA was quite close to the SCA with a rate of 1.04. For the rate of caracolis (RCAR), the situation where SCA is predominant over GCA was observed with σ^2g/σ^2s between 0.56. The predominance of additive effects (GCA) over dominance effects (SCA) for a given trait would reflect the use of poorly selected sires [27]. Indeed, several authors consider that despite generations of selection, coffee tree populations remain little changed, notably due to the strict allogamy of species [28,29] proposed, before any other method, that mass selection should first be used to improve populations, by rapidly fixing a significant part of the additive genetic variance. However, this approach faces many difficulties due to the coexistence of SCAs alongside the effects of GCA for some of the trait like RCMA.

3.3 Relations between Traits

In general, strong genetic correlations have been established between the vegetative traits. These correlation ranged from 0.58 to 0.77 (Table 5, below the diagonal). On the other hand, few significant correlations were obtained between the vegetative traits and cumulative production (PCUM) with coefficients of correlation less than 0.40. On the one hand, these results are similar from those of [17] who obtained strong correlations between vigor traits each other and not similar considering strong relation between vigor traits and cumulative production. In terms of correlation between agro-morphological and technological traits, the results also showed overall, not significant correlations. However, high but negative correlations has been established between the pairs of variables NPLA/RCAR, PCUM/W100, and GAT/RCAR with the respective values -0.58, -0.76 and -0.89. Otherwise, vigorous trees provide the formation of two-seeded cherries. But good yield is linked to small seeds. These results encourage index selection where a better compromise will be found in order to have a coffee with a good yield associated to a high technological quality.

The highest genetic correlations correspond to the highest phenotypic correlations. Indeed, the vigor traits have been shown to be the most important, with correlation coefficients ranged from 0.52 and 0.54. (Table 5, above the diagonal). Apart from these correlations, no more strong correlation has been observed. [17] observed similar phenotypic correlations on *C. canephora* species with very low values for correlations between technological and agro-morphological trait ($r<0.3$). Overall, few significant genetic correlations have been showed between vegetative vigor traits and production. The most remarkable correlations are those established on the one hand between the first year production (three years after planting) and the number of plagiotropic branches (NPLA) with a coefficient of 0.51, and on the other hand, the productions every 2 years and the general appearance of the tree (GAT). The significant correlations between yields and GAT alternating every 2 years show that the GAT variable in coffee remains an essential component of yield. This could be explained by a change in its conformation, particularly in the plagiotropic branches. The Congusta hybrid, having more affinity with canephora according to this study, therefore tends to lose its plagiotrope branches along the entire length of the stem like *C. canephora*, a phenomenon observed in a previous study [30].

The low correlations of cumulative production with the morphological traits, and of RCAR with all other traits, make it not possible to select trees with good yields and good morphological and technological qualities at the same time. These results are similar to those of [31] who observed non-significant correlations between production and most morphological traits and even negative correlations between production and leaf area of Congusta hybrids. This situation offers the possibility of improving traits using simple selection methods such as independent level selection.

Each of the five male progenitors of *Coffea congensis* 301, 302, 303, 304 and 305 was used as a tester with the 3 canephora genitors. Sires 302, 303 and 304 produced strong positive correlations between production and the DICO and CONF traits with coefficients between 0.76 and 0.99. These different relationships were rather negative for parent 305 with values from -0.70 to -0.86 (Table 6). Then, the progress made at the level of each genitor does not guarantee the performance level of all offspring. The results obtained show that depending on the male congensis clone, the correlations between traits at the level of half-brother offspring differ especially at the level of the 301 and 305 sires where very strong negative correlations were obtained. Thus, selection for higher production in 301 and 305 will directly select against vegetative vigor. Genotype selection based on those two sires is not reliable strategies.

Table 2. Mean squares of female, male, "female x male" interaction and F-test of Congusta hybrids after square root transformation

Variables	Female Effect		Male Effect		Female X Male Effect	
	MS	F	MS	F	MS	F
NPLA*	9.93	71.03***	0,14	0.97 ns	0.65	4.66***
DICO	3.02	29.34 ***	0,56	5.45*	0.34	3.28 *
GAT*	1.08	23.32 ***	0,02	0.36 ns	0.12	2.53*
PR03*	155.92	35.90 ***	22,02	5.07*	20.35	4.69***
PR04*	46.58	20.81***	6,11	2.73*	5.27	2.36*
PR05*	400.52	86.18***	37,30	8.02*	22.85	4.92***
PR06*	209.37	38.89***	5,74	1.07 ns	42,31	7.86***
PR07*	224.80	39.35***	34,22	5.99*	46.97	8.22***
PCUM*	792.81	75.50***	84,14	8.01*	119.22	11.35***
RCMA	1296.37	78.95***	118,92	7.24*	137.68	8.38***
W100	329.17	93.29***	59,17	1.68*	14.14	4.01**
RCAR*	29.93	79.25***	13,89	3.68*	6.71	17.76***

****: ns, *, **, ***:..test not significant and significant at 0%, 1%, .01% respectively. F= test F, MS= mean squre, Diameter at collar (DICO), genera appearance of the tree (GAT), number of plagiotropic branches (NPLA), Production of fresh cherries from the Tree n years after planting (Pr0n); Cumulative 5 year harvest (PCUM), Merchantable coffee yield (RCMA), 100 bean weight (W100), Caracolis rate (RCAR), Mean square (MC), SE= Standard error; F= Fishet probabilit*

Table 3. Components of variance and heritabilities of traits

Traits	Components of variance						Heritabilities	
	σ²Af	σ²Am	σ²D	σ²E	σ²G	σ²P	h²	H²
DICO	2.32	0,32	1.24	6.59	2,56	9.15	0.13	0.24
GAT	0.2	0	0.04	0.55	0,14	0.69	0.13	0.18
NPLA	1.52	0	0.28	1.47	1,04	2.51	0.23	**0.32**
Pr03*	5.12	0.44	1.32	4.34	3,92	8.26	0.25	**0.37**
Pr04*	2.32	0.04	0.24	2.24	1,42	3.66	0.24	0.29
Pr05*	5.80	0.08	1.48	4.65	4,60	9.25	0.24	**0.37**
Pr06*	26.40	0	2.08	5.38	15,28	20.66	**0.39**	**0.45**
Pr07*	5.84	0	3.0	5.71	5,92	11.63	0.20	**0.41**
PCUM	30.28	0	8.0	10.50	23.14	33.64	**0.31**	**0.47**
RCMA	20.48	0	19.68	16.45	29.92	46.37	0.18	**0.53**
W100	39.92	1.36	1.2	3.53	21.84	25.37	**0.45**	**0.47**
RCAR	0.36	0.24	0.64	0.38	0.94	1.32	0.19	**0.58**

σ^2Af: female additive variance; σ^2Am: male additive variance; σ^2D: dominance variance; σ^2E: environmental variance; σ^2G: genotypic variance; σ^2P: phenotypic variance; h²: narrow sense heritability; H²: broad sense heritability. Values in bold type indicate heritabilities greater than 0.3

Table 4. Gene effect of general and specific ability for the combination and their ratio

Traits	$\sigma^2_{g\ F}$	$\sigma^2_{g\ M}$	σ^2_s	$\sigma^2_{g\ F} / \sigma^2_s$	$\sigma^2_{g\ M} / \sigma^2_s$
DICO	0.58	0.08	0.31	1.87	0.26
GAT	0.05	0.0	0.01	5.00	ASC
NPLA	0.38	0.01	0.07	5.43	ASC
Pr03	1.28	0.11	0.33	3.88	0.33
Pr04	0.56	0.02	0.06	9.33	0.33
Pr05	1.45	0.0	0.37	3.92	ASC
Pr06	6.6	0.0	0.52	12.69	ASC
Pr07	1.45	0.0	0.75	1.93	ASC
PCUM	7.57	0.02	2.00	7.79	0,35
RCMA	5.12	0.01	4.92	1.04	0,46
$W100_G$	10.0	0.34	0.32	31.25	1,88
RCAR	0.09	0.06	0.16	0.56	0,14

σ^2g F: female variance of general combining ability, σ^2g M: male variance of general combining ability, , σ^2s : variance of specific combining ability. Bold numbers indicate ratios of gene effect (σ^2 g /σ^2s) significatively greater than 1

3.4 Selection Criteria

The efficiency of selection is conditioned by three main factors which are broad sense heritability, phenotypic variance and correlations between traits. Correlation analysis indicated weak associations between production and all the other studied traits. This doesn't mean that selection is not possible, but imply that selection using independent level should be applied to simultaneously improve all the characteristics. So the theoretical genetic gain of these characters was estimated differently depending on the proportion of trees having crossed the threshold of the control clone H, which is the most used clone in coffee research station. Thus, for the production of fresh cherries 83 best trees have crossed the threshold of 43.5 hg of fresh cherries per year. 83 trees also crossed the threshold of 17.5 mm for stem diameter, ie approximately 10% of the trees of the whole test were selected for both traits (Table 7). The selection intensity is therefore 1.76. For Number of plagiotropic branches (NPLA), the selection of heads of clones was made within 3 families, G302, G303 and G304 on a total number of 52 trees which obtained plagiotropic branches greater than or equal to 3.8, ie approximately 5% of the trees under test. Selection intensity is then 2.06. With regard to the general appearance of the tree (GAT), 57 trees had a performance greater than 3, ie 6% of the trees under test. The corresponding selection intensity is equal to 1.99. The calculated genetic gains were therefore 1.49 for DICO, 1.24 for NPLA, 0.33 for GAT and 7.04 for PCUM, i.e. 9.30 %, 43.8%, 10.80% and 46% respectively of the average (Table 8). Similar results had been found by [24] who obtained genetic gains ranged from 15.39% to 6.60% among agronomic traits based on the selection intensity of the best 20% using REML/BLUP.

Table 5. Genetic (below diagonal) and phenotypic (above diagonal) correlations between traits at the F1 *C. canephora* x *C. congensis*

	NPLA	***DICO***	***GAT***	***Pr03***	***Pr04***	***Pr05***	***Pr06***	***Pr07***	***PCUM***	***RCMA***	***W100***	***RCAR***
NPLA		*0.52****	*0.54****	*0.46****	*0.20****	*0.25****	*0.02 ns*	*0.03 ns*	*0.20 ****	*-0.24***	*-0,25***	*0,16 **
DICO	*0.58 **		*0.53 ****	*0.34 ****	*0.14 ****	*0.19 ****	*-0.04ns*	*-0.01ns*	*0.13****	*-0.13**	*-0,10 s*	*0.10 ns*
GAT	*0.77***	*0.72**		*0.48****	*0.33****	*0.30****	*0.04 ns*	*0.08 ns*	*0.29****	*-0.10 ns*	*-0,01 ns*	*0.01 ns*
Pr03	*0.51**	*0.40 ns*	*0,72 **		*0.51****	*0.54 ****	*0.29****	*0.29****	*0.66****	*-0.07 ns*	*-0,13 **	*-0.02 ns*
Pr04	*0.24 ns*	*-0.10 ns*	*0.39 ns*	*0.66 **		*0.47 ****	*0.44****	*0.32****	*0.65 ****	*0.14 **	*0,08 ns*	*-0.19***
Pr05	*0.43 ns*	*0.23 ns*	*0.58 **	*0.83 ****	*0.67 **		*0.38****	*0.47****	*0.77 ****	*-0.05 ns*	*-0,10 ns*	*-0.04 ns*
Pr06	*-0.12 ns*	*-0.36 ns*	*-0.15 ns*	*0.39 ns*	*0.64 **	*0.55 **		*0.40***	*0.72 ****	*0.30***	*0,21***	*-0.21**
Pr07	*0.28 ns*	*-0.02 ns*	*0.44 ns*	*0.74 **	*0.82 ****	*0.92 ****	*0.67 **		*0.76****	*0.10 ns*	*0,04 ns*	*-0.13**
PCUM	*0.26 ns*	*-0.03 ns*	*0.38 ns*	*0.78 ***	*0.84 ***	*0.91 ***	*0.81***	*0.96***		*0.14 **	*0,01 ns*	*-0.17 **
RCMA	*0.25 ns*	*0.46 ns*	*0.74 **	*0.74 **	*-0.33 ns*	*0.46 ns*	*0.31 ns*	*-0.02 ns*	*0.42 ns*		*0,32****	*-0.45***
W100	*0.21ns*	*-0.10 ns*	*0.37 ns*	*0.15 ns*	*-0.78 ***	*-0.72 **	*-0.14 ns*	*-0.73 **	*-0.76 ***	*0.19 ns*		*-0.01 ns*
RCAR	*-0.58 **	*-0.46 ns*	*-0.89 ***	*-0,57 **	*0.05 ns*	*-0.34 ns*	*-0.60 **	*0.24 ns*	*-0.32 ns*	*-0.92 ***	*-0,13 ns*	

*Values in bold indicate correlation coefficients greater than .50. *, **, ***: not different from 0 at the threshold of .05, .01 and .001 respectively. ns: not different from 0 at the threshold of .05*

Table 6. Intra-family half-sib correlations between cumulative production and all the other traits below in F1 hybrids of *C. canephora x C. congensis*

	305	304	303	302	301
NPLA	-0.86 *	0.99	0.16 ns	0.44 ns	-0.80*
DICO	-0.70 *	0.76 *	0.94*	0.90 *	-0.47 ns
GAT	-0.81 *	0.90 *	0.96 *	0.96*	-0.05 ns
RCMA	0.22 *	0.17 ns	0.03 ns	-0.05 ns	0.38 ns
W100	0.14 ns	0.01 ns	0.01 ns	-0.03 ns	0.12 ns
RCAR	-0.23 *	-0.07 ns	-0.06 ns	0.01 ns	-0.39 *

*Values in bold indicate correlation coefficients greater than 0.50 at absolute value. *, **, ***: not different from 0 at the threshold of .05, .01 and .001 respectively. ns: not different from 0 at the threshold of .05*

Table 7. Congusta hybrids selected by progeny with a production similar or higher than that of the control clone H

Progeny	Yield/year (hg)	Number of Selected trees	Selection rate
G301	46,8	1	1,97
H301	59	1	3,45
C301	51,6	8	17,02
G302	57,2	12	23,08
H302	50,6	5	9,26
C302	49,8	2	3,77
G303	61,5	17	34
H303	54,9	2	4,44
C303	54,7	3	5,66
G304	52,8	14	25,92
H304	54,4	1	3,33
G305	50,3	3	5,45
H305	64,0	4	8,16
C305	55,3	10	22,73
		83	10

Table 8. Number of trees selected, selection rate and genetic gain calculated for stem diameter (DICO), general appearance of the tree (GAT) number of plagiotropic branches (NPLA) and cumulative production on five years (PCUM)

Caractères	Number of trees above the mean	Selection rate (%)	Selection intensity	Genetic gain ∆*G/H*
DICO	83	10	1,76	1,49 (9,30)
GAT	57	6	1,99	0,33 (10,84)
NPLA	52	7	1,92	1,24 (43,82)
PCUM	83	10	1,76	7,04 (46,30)

∆G/H: gain compared to the control clone H, with an average of DICO of 17.5 mm, score of 3.5 for GAT, 3.8 plagiotropic branches per plant and 43.5 hg of coffee per year. Figures in brackets indicate genetic gains compared to the population average

4. CONCLUSION

The determination of genetic parameters in *C. canephora* x *C. congensis* gives important information on coffee breeding. Low contribution of Congensis has been found in the interspecific hybrids. Low correlations between vegetative traits and Yield showed that a vigorous coffee tree is not necessarily linked to a productive one. These results give the proof that Congensis trees bring few agro-morphological improvement in *C. canephora*. However the selection of 83 individuals in 14 out of 15 progenies shows the possibility to guarantee improved offspring in vegetative trait linked to high yield and good cup quality. In order to make such results more efficient, further surveys mainly in *C. congensis* species may be carried out in wild coffee

collections with the aim of broadening the genetic base of the male sires as additive gene effect has been observed in most of the traits of the hybrids.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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