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Research Note

Correlation and path-coefficent analysis in half sib families of globe artichoke (*Cynara cardunculus var. Scolymus* (l.) Fiori)

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Abstract:
The yield is a complex trait and indirect selection through correlated, less complex and easy measurement traits would be an advisable strategy to increase yield. To assess artichoke genetic variation for different agronomic traits, the phenotypic and genotypic correlation coefficients among these traits and the direct and indirect effects of these traits on the total yield, 10 half-sib families were used. Total yield recorded positive genotypic correlation with number of heads and the length, diameter and weight of heads. Number of head and their weight had direct positive contribution towards total yield per plant. Indirect effect of plant diameter and length and weight of head, on number of heads plant height, are shown. These results allow us to select materials with high yields by choosing those with a large diameter of plant and upper length of main head.

Key words:
Genetic correlation; Agronomic traits; Path analysis; Half-sibs, *Cynara*

Globe artichoke (*Cynara cardunculus var. scolymus* (L.) Fiori) is a diploid (2n = 2x = 34) ~~an~~ allogamous and entomophilous plant of the *Asteraceae* family. It is originated in the Mediterranean Basin and mostly cultivated for its edible immature flower heads eaten as a fresh, frozen or canned delicacy (Bianco, 2005). Worldwide, globe artichoke is mainly vegetatively propagated by rooted offshoots in a dormant or active growing state or by rooted basal stem portions. A large number of varietal types or ecotypes are present in Mediterranean countries (Sonnante *et al*. 2007). In Argentine, vegetatively propagated varietal types are used in a great proportion of the planted area (Cravero *et al*. 2010). These varietal types are used as semi-perennial crops, which can remain in production for 7–10 years. Presently, seed propagated varieties of good quality and uniformity are scarce in the market; therefore, the production of seeds of high yielding varieties is an important objective for artichoke breeding programs.

Traditionally, plant breeders have optimized yield largely by empirical selection, however, selection of high yielding cultivars via specific traits requires knowledge not only of final yield but also of the many yield components. The yield is a quantitative trait which is affected by many genetic and environmental factors (Martin, *et al*. 2010). Since yield is a complex trait, indirect selection through correlated, less complex and easy measurement traits would be an advisable strategy to increase the grain yield. Indirect selection depends on high correlations between yield and target yield components.

In agriculture, correlation coefficients in general show associations among characteristics and the degree of linear relation between these characteristics. It is not sufficient to describe this relationship when the causal association among characteristics is needed (Toker and Cagirgan, 2004). If there is genetic correlation between traits direct selection of one trait can cause change in the other trait. When more than two variables are involved, the correlations *per se* do not give the complete picture of their interrelationships (Fakorede and Opeke, 1985). The path analysis has been widely used by plant breeders (Indu Rani *et al*., 2008 in tomato, Togay *et al*., 2008 in pea and Ali *et al*, 2009 in chickpea) to assist in identifying traits that are useful as selection criteria to improve crop yield because it identifies the causes and measures the relative importance of the association and is used to determine the amount of direct and indirect effect of the causal components on the effect component (Dewey and Lu, 1959).

The objectives of this study were: (i) to assess artichoke genetic variation in germplasm for different agronomic traits, (ii) to assess the phenotypic and genotypic correlation coefficients among agronomic traits and seed yield, and (iii) to characterize the germplasm for use as parents in a breeding program.

The present investigation for correlation and path analysis studies of morphological traits of globe artichoke was conducted at the research station of the Faculty of Agriculture of Rosario University, Argentina (33° 1´ S and 60° 53' W) during 2008. The experimental material consisted of 10 half-sib families of globe artichoke originating by open pollination between experimental clones from our breeding program. The station has a temperate climate, loamy soil, an average annual rainfall of 950 mm and is representative of the major production area of globe artichoke in Argentina. A randomized complete block design with 3 replications of 20 plants was used. Planting was done with a spacing of 140 cm between rows and 80 cm within rows during the fall period. Fertilization was conducted prior to planting by incorporating urea at a 150 kg ha^{-1} dose. Typical loamy soil of the Argentine pampas are rich in phosphorus and potassium, hence no other macro-element were applied. Herbicides linuron at a 600 g ai ha^{-1} and haloxyfop-R-methyl ester at a 30gai ha^{-1} were applied at 30 days and 180 days after plantation respectively. *Aphiscide pirimicarb* at a 210 g ai ha^{-1} and insecticide clorpirifos at a 200 g ai ha^{-1} were also applied 2 and 4 months after plantation, respectively.

In the spring of 2009, the following traits were evaluated: plant height (PH) (cm) and plant diameter (PD) (cm), number of head per plant (NH), weight of the main head (WH) (g), total yield (TY) (g/pl), marketable yield (MY) (g/pl) per plant as TY multiplied by the quality of the head. The quality was evaluated according Asprelli *et al*. (2001), by visual inspection using a scale ranging from 0.2 (poor quality) to 1 (best quality), considering spineless bracts, tightness, color and general aspect of main head. The length (LH) (cm) and diameter (DH) (cm) of main head were also evaluated to obtain the length-diameter ratio (R). Bottom weight of the first bud (BW) (g), bottom diameter (BD) (cm) and bottom height of the first bud (BH) (cm) were also recorded.

The normal distribution of traits was tested according to Shapiro and Wilk (1965). The mean values of the traits were compared by ANOVA and Duncan's multiple range test was used to determine statistical differences among treatments (Sokal and Rohlf, 1969). Genetic correlations between traits were determined according to the method of Kwon and Torrie (1964): $r_g = Covg_{ij/} \sigma^2 g_{i*} \sigma^2 g_j$ where $Covg_{ij,}$ $\sigma^2 g_i$ and $\sigma^2 g_j$ are the estimates of covariance and variance for traits i and j respectively. Phenotypic and genetic correlations and hereditability values were obtained by the GENES software (Cruz, 2001) and path analysis by InfoGen software (Balzarini and Di Renzo, 2003).

Significant differences were found among half-sib families for most of the traits evaluated except plant diameter, thus reflecting extensive genetic variation in this species. The mean values and standard errors for each morphological trait for the different half-sibs families are shown in Table 1.

Heritability values for total yield and artichoke number were higher than those obtained for weight of the heads. Highest heritability values were expressed by head shape (h^2= 0.78 for HD and h^2= 0.80 for LH) (Table 1). Among the bottom quality characters plant diameter and plant length presented the highest values of heritability (0.54 and 0.62 respectively).

These families therefore, constitute a germplasm pool of adequate variability which is essential for plant breeding (Dudley & Moll, 1969). The analysis of variance components and the heritability values indicate that it could be possible to increase yield and associated characters (Mishra and Roy, 2003; Marker and Joshi, 2005, Shikano, 2008).

Correlation studies between characters have great value in determination of the most effective procedures for selection of superior genotypes. The results clearly indicate the different pattern of association between the characters measured (Table 2). In general, it was observed that estimates of genotypic correlations were in most cases higher than their corresponding phenotypic correlations. This agrees with the findings of Akbar *et al* (2007) in mustard, Crippa *et al* (2009) in lentil and Espósito *et al*. (2010) in pea. More significant genotypic association between the different pairs of character than the phenotypic correlation indicated that the characters are more related genotypically than phenotypically. Plant length as weight of the main head and those traits related with shape head are more related genotypically than phenotypically with total yield. Total yield per plant recorded positive genotypic correlation with number of heads per plant (r=0.85) and the length, the diameter and weight of heads (r= 0.67; r=0.91 and r=0.75, respectively). This fact indicating that total yield may be improved through the selection of any of these characters.

In some instances, simple correlation coefficients can lead to errors regarding the true relation between two variables, constituting an inadequate and unreal measurement of cause and effect. High or low correlation coefficient between two variables can therefore be the effect of a third variable or group of variables (Cruz *et al*., 2004). According to these authors, a coefficient of partial correlation, calculated removing the effects of other variables on the association studied is a more representative estimate on the relation between variables. Path analysis is a type of multiple regression analysis and allows the study of direct and indirect effects of certain traits on a basic variable; calculations are performed through regression equations. In cases where path analysis considers a unique causal model, it is simply a standardized analysis of partial regression, being useful when correlation coefficients are partitioned in direct and indirect effects (Uzzo *et al*., 2004).

The data (Table 3, Figure 1) also revealed direct and indirect contribution of traits in developing the seed yield. Some of traits (NH and WH) had direct positive contribution towards total yield per plant, so those plants showing a greater number of head and or an average weight of head superior will result in material with a higher performance. However, indirect effect of plant diameter and length and weight of head on number of heads per plant height are shown. A plant with increased stem diameter can withstand a greater number of heads and more weight which will result in higher performance. These results allow us to select material with high yields by choosing those with a large diameter of plant and upper length of main head.

Depending on the values of total yield and marketable yield, the best families would be HS EC_2 and HS EC_4. The selection of plant of these HS families will allow the achievement of superior genotypes for use in a breeding program of this species.

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Table 1: Means, standard errors and heritability values for each morphological trait in the different Half-sibs families (HS)

Families	PH (cm)	PD (cm)	NH	TY (g/pl)	MY (g/pl)	WH (g)	DH (cm)	LH (cm)	R	BD (cm)	BW (g)	BH (cm)
HS EC_1	98.1±3.2	138.2±3.5	3.7^{b}±0.3	669.9^{b}±50.4	411.1^{ab}±43.0	214.5^{a}±11.2	8. 9^{ab}±0.2	9.2^{b}±0.2	1.0^{b}±0.02	5.8^{ab}±0.2	79.2^{ab}±5.8	1.7^{a}±0.1
HS EC_2	96.1±2.2	125.4±5.4	4.8^{ab}±0.3	895.9^{a}± 65.9	498.2^{a}±77.8	242.0^{a}±10.0	9.1^{a}±0.1	10.4^{a}±0.2	1.2^{ab}±0.02	6.1^{a}±0.1	82.2^{a}±4.4	1.8^{a}±0.1
HS EC_3	94.4±2.0	126.6±3.8	4.9^{ab}±0.5	826.6^{b}± 74.5	409.7^{ab}±85.8	194.2^{ab}±8.6	8.6^{ab}±0.1	9.6^{ab}±0.1	1.1^{ab}±0.02	5.5^{ab}±0.1	70.4^{b}±3.8	1.7^{a}±0.1
HS EC_4	95.8±3.4	139.4±4.8	5.7^{a}±0.4	1040.0^{a}±70.8	540.5^{a}± 6.6	240.6^{a}±11.2	9.4^{a}±0.2	10.5^{a}±0.2	1.1^{ab}±0.02	5.5^{ab}±0.2	71.4^{b}±4.5	1.7^{a}±0.1
HS EC_5	86.4±3.1	143.7±4.6	4.5^{ab}±0.6	793.3^{b}±95.5	462.3^{a}±76.5	212.8^{a}±14.7	8.7^{ab}±0.3	9.1^{b}±0.4	1.1^{b}±0.1	6.0^{a}±0.2	73.5^{b}±5.3	1.5^{ab}±0.1
HS EC_6	97.6±2.7	131.6±3.5	3.6^{b}±0.3	568.8^{c}±37.6	199.6^{b}±29.8	182.0^{ab}±10.9	8.2^{b}±0.2	10.1±0.2	1.2^{a}±0.02	5.5^{ab}±0.1	62.6^{bc}±4.7	1.4^{b}±0.1
HS EC_7	103.8±5.0	131.3±7.2	7.0^{a}±0.9	986.8^{a}±82.9	197.4^{b}±24.6	175.3^{b}± 19.2	8.3^{b}±0.3	10.5^{a}±0.7	1.3^{a}±0.1	5.0^{b}±0.2	59.5^{c}±7.3	1.4^{b}±0.2
HS EC_8	92.1±6.0	135.7±6.3	5.7^{a}±0.7	968.2^{a}±87.2	237.2^{b}±31.4	234.5^{a}±15.7	9.0^{a}±0.2	10.6^{a}±0.5	1.2^{ab}±0.04	6.2^{a}±0.3	85.7^{a}±9.9	1.7^{a}±0.1
HS EC_9	82.5±3.6	129.4±4.9	5.1^{b}±0.5	894.6^{a}±92.1	491.0^{a}±92.2	200.1^{a}±12.9	8.8^{ab}±0.2	9.6^{ab}±0.3	1.1^{ab}±0.02	6.0^{a}±0.2	61.9^{bc}±6.3	1.6^{ab}±0.1
HS EC_{10}	110.0±3.6	141.0±6.8	4.8^{b}± 0.7	865.4^{ab}± 77.9	536.9^{a}±75.3	211.9^{a}±17.6	9.2^{a}±0.4	9.1^{b}±0.2	1.0^{b}±0.04	6.5^{a}±0.5	84.0^{a}±10.8	1.6^{ab}±0.1
F	2.9**	1.6^{ns}	3.7***	4.1***	1.9*	3.2**	3.6***	5.1***	5.5***	2.2*	2.0*	3.2***
h^2	0.65		0.73	0.75	0.45	0.69	0.78	0.80	0.81	0.54	0.49	0.62

Values followed by a same letter do not differ according Duncan´s test (P < 0.01).
*** p<0.001; ** p<0.01; * p<0.05; ns non significant

Table 2: Estimates of genotypic (above diagonal) and phenotypic correlation coefficients (below diagonal) for different quantitative traits in HS families of globe artichoke

	PH	PD	WH	TY	NH	MY	DH	LH	R	BD	BH	BW
PH		-0.18	-0.06	-0.34	-0.25	-0.55	0.03	0.16	0.19	-0.59	0.04	0.35
PD	0.03		0.06	-0.23	-0.27	-0.05	0.43	-0.66	-0.93	-0.35	-0.52	-0.02
WH	0.07	0.18		0.75	0.49	0.96	0.93	0.52	-0.22	0.17	0.94	0.64
TY	0.19	0.44	0.45		0.85	0.75	0.91	0.67	-0.04	0.01	0.60	0.12
NH	-0.13	0.01	0.39	0.89		0.39	0.66	0.72	0.20	-0.16	0.28	-0.11
MY	-0.19	0.18	0.69	0.58	0.38		0.89	0.09	-0.88	0.38	0.81	0.41
DH	0.11	0.32	0.90	0.76	0.51	0.81		0.37	-0.40	0.01	0.96	0.47
LH	0.18	-0.31	0.49	0.36	0.60	0.05	0.38		0.71	-0.37	0.32	-0.10
R	0.14	-0.53	-0.24	-0.001	0.18	-0.60	-0.41	0.69		-0.43	-0.45	-0.50
BD	-0.24	-0.06	0.38	0.18	-0.12	0.35	0.24	-0.20	-0.42		0.43	0.49
BH	0.07	-0.19	0.78	0.27	0.22	0.62	0.74	0.26	-0.35	0.40		0.68
BW	0.33	0.11	0.70	0.26	-0.05	0.36	0.55	0.006	-0.44	0.61	0.74	

Table 3 The direct and indirect contribution of different traits to yield in HS families of globe artichoke

	Indirect effects											
	PH	PD	NH	WH	MY	LH	DH	R	BW	BD	BH	Correlation value with Yield
PH	**0.01**	0.01	0.07	0.06	0.03	0.02	-0.01	-0.0004	-0.01	0.01	-0.001	0.19^{**}
PD	-0.003	**0.04**	0.27	0.06	0.05	0.01	-0.01	0.01	-0.01	0.01	-0.001	0.44^{***}
NH	0.001	0.01	**0.77**	0.03	0.07	0.03	-0.004	-0.01	-0.0008	-0.002	-0.001	0.89^{***}
WH	0.004	0.01	0.14	**0.18**	0.07	0.04	-0.02	0.02	-0.02	0.02	-0.005	0.45^{***}
MY	0.002	0.01	0.32	0.08	**0.16**	0.0005	-0.01	0.02	-0.01	0.01	-0.005	0.58^{***}
LH	0.003	0.005	0.24	0.08	0.0008	**0.10**	-0.01	-0.05	-0.01	0.003	-0.002	0.36^{**}
DH	0.003	0.01	0.14	0.15	0.05	0.04	**-0.02**	0.04	-0.02	0.02	-0.004	0.41^{***}
R	0.00006	-0.003	0.11	-0.05	-0.04	0.06	0.01	**-0.08**	0.01	-0.01	0.002	-0.001
BW	0.004	0.01	0.02	0.15	0.05	0.02	-0.01	0.03	**-0.03**	0.02	-0.004	0.26^{**}
BD	0.003	0.01	-0.05	0.13	0.05	0.01	-0.01	0.04	-0.02	**0.03**	-0.004	0.18^{*}
BH	0.001	0.005	0.10	0.09	0.07	0.02	-0.01	0.01	-0.01	0.01	**-0.01**	0.27^{**}

Figure 1: Path diagram showing causal relationships between the response variable.