Detection of QTLs for Yield in Globe Artichoke





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Cynara cardunclus L. (allogamous Asteraceae) includes two domesticated taxa, globe artichoke and cultivated cardoon, as well as the wild cardoon, commonly considered to be the wild ancestor of both domesticated forms. Globe artichoke is an important horticultural crop in Argentina and the United States. The edible part are the heads (capitulum) consumed as fresh or canned, which are important sources of antioxidants due to the high content of phenolic compounds.

Materials & Methods

The aim of this work was to identify QTLs controlling the genetics basis of yield-related traits in globe artichoke as a first step to MAS.

Plant Material. 115 F_1 progeny derived from an inter-botanical variety cross and both parents were grown at the Experimental Field Station of the Universidad Nacional de Rosario in 2014 (*Figure 1*).

Morphological Analysis. Seven agronomic traits were evaluated (*Table 1*). The normal distribution of the traits was verified by a Shapiro-Wilks test. The t-Student test was performed to compare the means values between parents. The correlation between traits was determined by the Pearson's coefficient.

Molecular Analysis & QTLs association. A total of 247 SSRs were used to evaluate the genotypes. The markers were tested for an expected Mendelian segregation in the F_1 by a $\chi 2$ test. Only SSRs showing a fully consistent with monogenic segregation ($\chi 2 \le \chi 2_{\alpha=0.1}$) were used for QTLs association. Association between SSR locus and traits was determined by a one-way ANOVA ($p \le 0.05$). The proportion of total phenotypic variance explained by each QTL was estimated by R^2 values.

Morphological Traits	
Head per plant	NHF
Fresh weight of main head (g)	WN
Diameter of main head (cm)	DM
Length of main head (cm)	LMH
Fresh weight of 2 nd heads (g)	W2I

Table 1: Morphological traits evaluated

Table 4: SSR-QTL association and R² values.

Diameter of 2nd heads (cm)

Length of 2nd heads (cm)

Results

All the morphological traits showed normal distribution (W > 0.94) and both parental genotypes were significantly different (*Figure 2, Table 2*). The correlation analysis revealed that diameter and length of the main and secondary heads were the most important factors influencing fresh weigh (*Table 3*). A total of 70 SSRs showed Mendelian segregation and were used for QTLs association. SSR markers linked to QTL and % of total phenotypic variation explained by each QTLs (R^2) are shown in *Table 4*.



Wild Cardoon

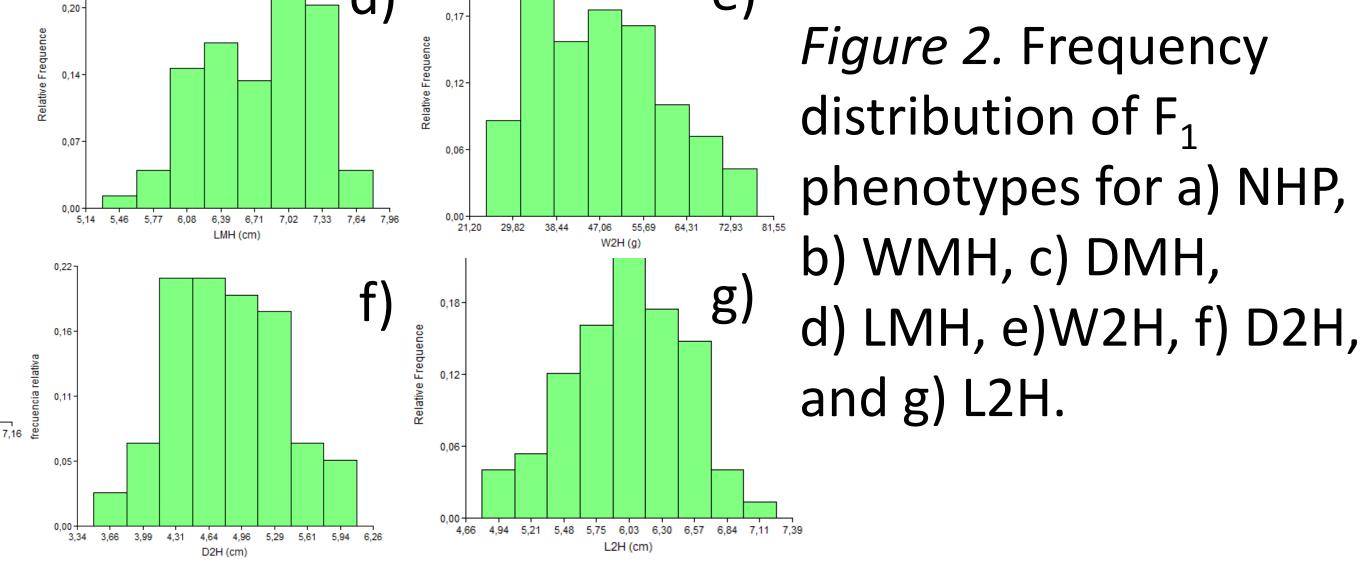


Estrella del Sur



F₁ progeny Figure 1. Inter-botanical variety cross and its progeny.

	0,23							6	a)		0,30							b)		0,247								С)	
	0,17-										0,22-				1						0,18-										
Relative	0,12-							<u> </u>	<u> </u>	Relative Frequence	0,15-			_						Relative	0,12-										
	0,00										0.00								Ц		0.00										
	7	12	1	17	22 N	26 NHP	31	3	36	41	28,4	39,58	50,73	61,88	84,17 H (g)	95,33	106,48	117,63	128,78		3,94	4,26	4,58	4,91	5,23 DI	5,55 MH (cm		6,19	6,52	6,84	7,
																									٥.	(311	.,				



 SSR
 Traits
 R2 (%)
 p-Value
 SSR
 Traits
 R2 (%)
 p-Value

 MS-02
 WMH
 6
 0.045 CyEM_02
 D2H
 6
 0.0355
 Table 3

D2H

L2H

ELMS-02	WMH	6	0.045	CyEM_02	D2H	6	0.0355	Table	<i>3</i> : Co	rr
	W2H	6	0.0499	CELMS-36	D2H	11	0.0119	High positiv		
	D2H	8	0.0164	CyEM_188	DMH	10	0.0075	by arrows.		
ELMS-10	W2H	18	0.0027	CyEM_234	WMH	8	0.0104		NHP	W
	D2H	11	0.0173		DMH	8	0.0151	NHP	1	-
	L2H	8	0.0437		W2H	8	0.008	WMH	0.59)
yEM_244	L2H	6	0.0335		D2H	8	0.0141	DMH	0.49)
yEM_293	W2H	13	0.002		L2H	6	0.0338	LMH	0.60)
	D2H	10	0.0062	CyEM_53	W2H	8	0.0134	W2H	0.38	
ELMS-57	WMH	18	0.0013		D2H	6	0.0341	D2H	0.48	,
	DMH	17	0.002	CyEM_86	D2H	6	0.0333	L2H	0.42	-

Table 3: Correlation analysis.

High positive values indicated by arrows

	•													
	by arrows.													
-		NHP	WMH	DMH	LMH	W2H	D2H	L2H						
-	NHP	1												
	WMH	0.59	1											
•	DMH	0.49	0.89	1										
	LMH	0.60	0.82	0.71	1									
-	W2H	0.38	0.55	0.39	0.5	1,								
-	D2H	0.48	0.56	0.45	0.49	0.93	1							
	L2H	0.42	0.43	0.27	0.57	0.84	0.79	1						

		Genotypes														
			NC		ES				F ₁							
	Traits	Mean	SE	SD	Mean	SE	SD		Mean	SE	min	max	W			
	NHP	17.0	1.08	2.16	4.0	0.41	0.82	*	20.2	0.76	9.0	39.0	0.94			
	WMH (g)	22.9	1.54	3.07	147.3	8.06	16.13	*	73.5	2.05	34.1	123.0	0.97			
	DMH (cm)	4.3	0.09	0.18	7.2	0.09	0.18	*	5.6	0.07	4.1	7.0	0.97			
,	LMH (cm)	4.5	0.10	0.21	8.5	0.83	1.65	*	6.8	0.06	5.3	7.8	0.96			
	W2H (g)	14.3	1.62	3.24	62.3	4.21	8.43	*	47.4	1.53	24.5	78.2	0.95			
	D2H (cm)	3.8	0.18	0.35	5.7	0.21	0.42	*	4.8	0.07	3.5	6.1	0.97			
	L2H (cm)	4.1	0.19	0.39	6.0	0.79	1.57	*	6.0	0.06	4.8	7.3	0.98			

Table 2: Mean values, standard error (SE), and standard deviation(SD) for each trait of Wild Cardoon (WC), Estrella del Sur FCA globe artichoke (ES) and the F_1 . Significant mean differences between parentals are indicated (*p>0.05).

<u>Conclusion</u>

We have detected 22 new QTLs controlling yield-related traits in *Cynara cardunclus* L., providing evidence that there are several loci controlling globe artichoke yield. The SSRs linked to this trait should be used for marker assisted improvement of the species.