Variation of the number of flowering stems and its effect on forage yield in a population of Phalaris aquatica L. in Greece

Dini-Papanastasi O., Goulas C.K.

Systèmes sylvopastoraux. Pour un environnement, une agriculture et une économie durables

Zaragoza : CIHEAM
Cahiers Options Méditerranéennes; n. 12

1995
pages 53-56

Variation of the number of flowering stems and its effect on forage yield in a population of *Phalaris aquatica* L. in Greece.

O. Dini-Papanastasis[1] and C. K. Goulas[2]
1 National Agricultural Research Foundation, Forest Research Institute 570 06 Vassilika Thessaloniki - Greece
2 University of Thessaly, School of Agriculture, Laboratory of Plant Breeding and Genetics 383 34 Volos - Greece

Summary: The relationship between forage yield and number of flowering stems along with their genetic variability was studied in a population of *Phalaris aquatica* L. composed of eighty plants collected from representative regions of Greece. The plants were transplanted and maintained in an isolation field located in Macedonia, Greece. Two trials were established in 1989, one for HS families and another for clone evaluation by using an incomplete block design. Measurements were taken at the end of June 1991 and 1992.
The number of flowering stems per plant varied considerably among HS families and clones in both years. No interaction between families and years was found. The year effect was highly significant, resulting in a 58% reduction in the number of stems per plant for HS families and 79% for the clones in the dry year 1992 as compared to 1991. Variance among HS families was not significant, but highly significant for the clones. The genetic variance component (σ^2_g) was much higher in the favourable year 1991 for both types of progenies, especially for clones. The values of the genetic coefficient of variation (GCV) for HS families and clones were very satisfactory suggesting that genetic variance is present in the population for effective selection. Positive correlation between forage yield and the number of flowering stems was found although the relationship explained only 60% of the variance, indicating that selection for high forage yield with low number of stems should be effective.

Key-words: *Phalaris aquatica* L., flowering stems, variation, breeding, forage yield.

INTRODUCTION

Forage yield in range grasses is a function of leaves and stems with their inflorescences. Flowering stems in general are selected less than leaves by the grazing animals because of their lower nutritive value and palatability (Arnold, 1960). Therefore, in breeding programs aiming to develop cultivars of range grasses for animal use, individuals or populations with more leaves than stems should be selected (Liacos *et al,* accepted for publication). On the other hand, flowering stems are necessary for abundant seed production and increased forage yield. For this reason, genotypes having a good balance between increased foliage and stem number should be a breeding objective in variety development programs.

Phalaris aquatica L. is a very productive and drought resistant forage grass suitable for animal grazing in areas with a dry Mediterranean-type climate and like other range grasses its flowering stems are less nutritious than leaves (Clements *et al.*, 1970). Although several cultivars have been released in Australia (Oram, 1984), they are not equally well adapted in the wide variety of environments encountered in the Mediterranean region and the selection of local varieties is worthwhile.

In an effort to develop cultivars of this interesting grass, a breeding programme was initiated in Greece. So far, satisfactory genetic variance for forage yield was reported (Dini - Papanastasi and Goulas, 1993).

In this paper, the variation of the number of flowering stems and its effect on forage yield is presented and the breeding implications are discussed.

MATERIALS AND METHODS

Eighty plants collected from representative regions of continental Greece, during the period 1965-1969 (Dini - Papanastasi *et al.*, 1989) were used to synthesize the population used in this study. Mother plants were transplanted and maintained in an isolation field at the Experimental Station of the Forest Research Institute of Thessaloniki located in Serres, Macedonia (41°15'N, 23°28'E), an area with a mean annual precipitation of 555mm, a mean maximum temperature of 28°C (hottest month - July) and a minimum of -0.5°C (coldest month - January). During the period 1969-1988 plants were freely intercrossed. They showed remarkable persistence and increased their size by tillering. In the summer of 1988 seed was harvested from individual plants (HS families) and clones were excised as well. Thus each of the eighty mother plants (genotypes) was represented by a clone and a corresponding HS family.

Two separate progeny test trials were established in the spring of 1989, one for HS families and another for clone evaluation. An incomplete block experimental design with eight blocks and three replications per block was used for both trials. Ten families were randomly assigned to each block. The same 10 HS plant progenies which were evaluated in a block in the HS trial were also kept together in a separate block in the clones trial. One row plots with ten plants per row were used. Spacing was 50 cm among plants within and between rows. Plants used in the HS family trial were raised in containers from seeds of each family and transplanted in the field as two month plantlets in May 1989. For the clone trial, tillers were excised from each mother plant and planted in the field in April 1989. Number of flowering stems was recorded for each plant after flowering was completed and just before forage harvesting, at the end of June 1991 and 1992.

Data for each year were analysed on a per block basis and the individual analyses of variance were pooled over blocks for each trial and year. Block, replication and family effects were assumed to be random. A combined analysis over years was made on per block basis and pooled over blocks, with the year effect assumed to be fixed (Cochran and Cox, 1957). The genetic parameters estimated were the family and clone genetic variance component (σ^2_g) and the genetic coefficient of variation, GCV = $\sqrt{\sigma^2_g}$ /mean (Goulas and Lonnquist, 1976). A regression analysis between forage yield (Y variable) and number of flowering stems (X variable) was also done.

RESULTS AND DISCUSSION

Considerable variation for the number of flowering stems per plant was observed as indicated by the wide ranges (Table 1) among HS families and clones in both years, although drastically reduced in 1992, as compared to 1991.

The year effect was significant for both HS families and clones (Table 2) and could be attributed to the extreme dry winter and early spring in 1992 (128 mm of precipitation from December to April as compared to 262 mm in the corresponding period in 1991). A 58% reduction in the number of flowering stems per plant for HS families was observed in 1992, while clones were much more affected, with a reduction of 79%. The reduction in number of flowering stems per plant in 1992, for both types of progenies, followed the same trend of that observed for forage yield losses during the same period which was 67% for HS families and 74% for the clones (Dini - Papanastasi and Goulas, 1993). This trend was further confirmed with results of the regression analysis, which will be discussed later. The average number of flowering stems per plant of the clones relative to the corresponding HS was 79% and 40% in 1991 and 1992, respectively, indicating that clones are more severely affected by stresses than HS families, apparently because of inbreeding depression.

The analysis of variance combined over years (Table 2) showed no interaction effect suggesting that the trait was stable. In spite of the wide ranges discussed before, variances

associated with differences among families were not significant for HS families but highly significant for clones, suggesting that the trait was better expressed in clones and, hence, that selection should be mainly based upon their performance.

The genetic parameters are shown in table 3. The genetic variance component (σ^2_g) was much higher in the favourable year 1991 for both types of progenies, especially for clones, which also appeared to have higher σ^2_g values than those of HS families, implying that genetic variance might be better expressed under favourable conditions. This is further supported by the ranges observed (Table 1). GCV values for HS families were quite satisfactory and high for clones confirming that genetic variance for this trait is present in the population for effective selection to be carried out. The data on GCV contradicted the evidence provided by the observed ranges (Table 1) and by σ^2_g estimates, indicating that genetic variance could be higher under stress conditions. More data are needed before a definite indication on which condition enhance genetic variance can be given.

The relationship between forage yield and number of flowering stems per plant was positive as expected, for both types of progenies and years (Table 4). Correlation coefficients were highly significant but accounted for only about 60% of the variation. Selection for high forage yield combined with low number of flowering stems seems possible.

Table 1: *Mean number of flowering stems per plant and range observed in progeny evaluation.*

	HS			Clones		
	1991	1992	Combined	1991	1992	Combined
Mean	72	30	50	57	12	34
Range	(26 - 129)	(7 - 87)		(2 - 137)	(1 - 52)	

Table 2: Combined Analysis of Variance for number of flowering stems per plant[1]

		HS	Clones	
Source	DF	MS	MS	EMS
Year	1	9512**	10356**	
Families in blocks (F/B)	72	135	186**	$\sigma^2_e + y\sigma^2_{(yxg)} + ry\sigma^2_g$
Families x year in blocks (F x Y / B)	72	59	137	$\sigma^2_e + y\sigma^2_{(yxg)}$
Error	288	146	152	σ^2_e

* $P < 0.05$ ** $P < 0.01$

Table 3: Genetic parameters for HS families and clones.

	HS			Clones		
	1991	1992	Combined	1991	1992	Combined
GCV	11.2	14.9	2.0	22.4	38.9	7.3
σ^2_g	65	20	1.0	163	21.8	6.2

[1]A pooled MS (error and interaction with 360 df) was used for the F test and genetic variance estimates.

Table 4: Relationship between forage yield and number of flowering stems per plant. Data of regression analysis.

Type of progeny	Equation	r	P
HS families			
1991	Y = 40.02 + 1.44 X	0.697	0.001
1992	Y = 14.62 + 1.10 X	0.783	0.001
Combined	Y = 13.50 + 1.61 X	0.794	0.001
Clones			
1991	Y = 10.74 + 1.69 X	0.817	0.001
1992	Y = 15.09 + 1.04 X	0.650	0.001
Combined	Y = 9.19 + 0.915 X	0.860	0.001

Y = (g/plant) and X= number of flowering stems per plant

RÉFÉRENCES

Arnold G.V., 1960. Aust. J. agric. Res. 10, 219.

Clements R.J., Oram R.N., Scowcroft W.R., 1970. Variation among strains of *Phalaris tuberosa* L. in nutritive value during summer. *Aust. J. of Agric. Res., 21, 661-675.*

Cochran, W.G., Cox G.M., 1957. *Experimental Designs.* (Second Ed.) John Wiley and Sons, New York.

Dini - Papanastasi O., Panetsos C., 1989. Cytogenetic study of certain greek population of forage grass *Phalaris aquatica* L. *Annals of the Department of Forestry and Natural Environment. Aristotelian University of Thessaloniki. Volume ËÂ (2):261-290.*

Dini - Papanastasi O., Goulas C., 1993. Forage Yield Variation in a Population of *Phalaris aquatica* L. in Greece. *In Management of Mediterranean shrublands and related forage resources. FAO, PEUR Technical Series 28:47-49.*

Goulas C. K., Lonnquist J.H., 1976. Combined Half-sib and S_1 Family Selection in a Maize Composite Population. *Crop Sci. 36: 461-464.*

Liacos L., Papanastasis V., Papademetriou K. Selection of orchard grass (*Dactylis glomerata* L.) from indigenous populations of Northern Greece. *Annals of the Department of Forestry and Natural Environment. Aristotelian University of Thessaloniki (In press).*

Oram, R. N., 1984. Australian cultivars of *Phalaris. Australian Seed Industry Magazine. 2 (3): 29-30.*