

**GENOTYPE-ENVIRONMENT INTERACTION FOR FORAGE YIELD OF VETCH
(*VICIA SATIVA* L.) IN MEDITERRANEAN ENVIRONMENTS**

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Abstract

Genotype x environment (GE) interactions limit the effectiveness of selection when selection is based only on mean yields. The objective of this study was to evaluate the amount of GE interaction for vetch forage yield in some environments of Southern Italy, and to analyze some stability parameters that can be useful in the selection of genotypes adapted to Mediterranean environmental conditions. Eleven vetch genotypes were grown in a total of 16 environments in Southern Italy. The combined analysis of variance for forage yield showed that the environment, genotype and GE interaction terms were significant at 0.01 level, suggesting a broad range of genotype diversity and environmental variation. Production stability for yield was measured by computing five stability parameters: (i) mean forage yield, (ii) the regression coefficients of the yields of a genotype on to mean yields of the 16 environments (b), (iii) the deviations from regression mean square (s_{di}^2), (iv) the determination coefficient (r^2), and (v) the ranking indices (R_1 and R_2) of genotypes productivity. Phenotypic correlations between forage yield and stability parameters were also calculated. More than 90% of yield variability of single vetch genotype is due to the linear regression. The mean forage yield and the adaptability (b) and stability (s_d^2 and r^2) parameters showed a significant variability. No significant correlation was observed between yield and adaptability and stability parameters, whereas the correlation between r^2 and s_d^2

parameters was highly significant ($r = -0,978^{**}$). Three genotypes, useful for Mediterranean environments, were selected.

Keywords: Genotype-environment interaction, stability parameters, selection, adaptation, vetch.

Introduction

In breeding programmes many genotypes are evaluated in a range of environments in order to obtain information about their adaptation across environments and enable breeders to select the more consistent-performing ones. Genotype-environment (GE) interactions encountered in yield trials are a challenge to plant breeders, and its cause, nature, and implications must be carefully considered in breeding programs (Kang and Martin, 1987).

Several attempts were made to solve the problems related to the GE interaction and many stability measures have been proposed. An approach subdivides the total variability due to GE interactions into components attributable to the single genotype. For such a splitting, different methods were proposed (Plaisted and Paterson, 1959; Wricke, 1962; Shukla, 1972), each allowing to obtain parameters that are very similar to each other. Another way is the regression analysis (Frinlay and Wilkinson, 1963; Eberhart and Russel, 1966; Perkins and Jinks, 1968; Tai, 1971). This analysis allows two stability parameters to be obtained: the regression coefficient (b) and the estimate of the sum of deviations from the regression line (s_d^2). Such a type of analysis was extensively utilised in the study of the GE interactions in many crops (Pacucci and Frey, 1972; Bilbro and Ray, 1976; Kang and Gorman, 1989; Helms, 1993; Alvarez et al., 1999). Afterwards, Pinthus (1973) proposed the use of the determination coefficient (r^2); Langer et al. (1979), instead, proposed two additional indices (R_1 and R_2), which are related to the yield ranking of genotypes.

The objectives of this study are: (i) to assess, for forage production, the yield potential of some vetch genotypes, (ii) to study, through some stability parameters, their adaptability to Southern Italian environments, and (iii) to check the possibility to select some genotypes using the stability parameters considered.

Material and Methods

Eleven vetch genotypes were evaluated in yield trials at 8 locations in Apulia and Basilicata regions, in Southern Italy, during the 1980-1983 period. A total of 16 trials were run in the locations: 3 at Cerignola, Bari, and Policoro; 2 at Locorotondo and Corleto Perticara; and 1 at Gravina, Lecce and Matera. All locations were characterized by different soil types: clay, silty-clay, clay-loam, sandy-loam, and loam; the elevation of the locations ranged from 5 to 722 m. The genotypes were grown, in each trial, in a randomized complete-block design with four replications. The plant density was of 150 seeds m⁻², corresponding to a sowing rate ranging from 80 to 140 Kg ha⁻¹, due to seed weight variability. Sowing date ranged from 20 October to 8 January, whereas the harvest date ranged from 5 May to 10 June, showing the great variability of the 16 “environments”. Cultural practices such as fertilizing and cultivating were the same as used in the farm in which each test was located, and, therefore, varied across locations.

A combined analysis of variance was conducted for dry matter yield (DMY). The genotype x environment interaction was significant ($P = 0,01$), so that some stability parameters were determined. They were: (i) the mean yield as productivity index; (ii) the regression coefficient b (Eberhart and Russel, l.c.), (iii) the parameter s_d^2 (Eberhart and Russel, l.c.) that estimates, for each genotype, the mean square of deviations from the regression over environmental indices; (iv) the coefficient of determination r^2 (Pinthus, l.c.) to estimate the yield of a genotype and its repetitiveness in different environments; (v) the

indices R_1 and R_2 that take into account the genotype yield ranking (Langer et al., l.c.). Lastly, any possible correlation was calculated between mean DMY and the different adaptability and stability indices being considered.

Results and Discussion

Highly significant differences were observed not only for the genotype-environment interaction, but also within the genotypes and the environments. As to the significant differences between the environments, they can be explained, both because trials were run in environments characterized by different soil and climatic conditions and because in the same location different climatic patterns were observed from year to year. The yield, adaptability and stability indices of each vetch genotype under study are reported in Table 1.

Forage yield, expressed in $t\ ha^{-1}$ of dry matter (DMY) and, for each genotype, in terms of average of the 16 environments being studied, ranged between $5.21\ t\ ha^{-1}$ of the genotype M30 and $3.85\ t\ ha^{-1}$ of 'Cipro' ecotype. For Southern Italy environments, such variability is quite large. If we consider, instead, the yield of the genotypes under selection, such variability is by far lower: from 5.21 to $4.56\ t\ ha^{-1}$. This points out that the selection made throughout the years has been quite effective.

The regression coefficients (b) varied from 0.82 to 1.32 and showed a moderate variability. Only the b value of genotype M30 (1.32) was significantly higher than 1, hence showing a good adaptability to more favourable environments. The b values of genotypes M32 ($b = 0.84$) and 775 ($b = 0.82$) were significantly lower than 1 thus showing, for these genotypes, a moderate adaptability to less favourable environmental conditions; for all other genotypes, the b values observed were not significantly different from 1.

The linear regression (r^2) explains 72.9 to 98.3 % of the variation in yield of the 11 genotypes. The higher values were observed in the genotypes under selection, whereas for

'Mirabella' and 'Cipro' ecotypes, the linear regression accounts for only a small portion of the variability.

As to s_d^2 values, such a parameter was, as expected, significantly correlated with r^2 ($r = -0.978^{**}$, Table 2), so that the same considerations made for the determination coefficient hold true. Moreover, such a correlation indicates that both parameters can be satisfactorily used to measure stability and perform the selection (Easton and Clement, 1973). Therefore, we agree with Langer et al. (1979) in stating that the determination coefficient (r^2) should be utilised because its values are standardised and the results of different trials may be compared with each other directly, without taking into account the scale of measurement applied in trials.

As to the R_1 and R_2 indices, proposed by Langer et al. (1979) to have a much simpler method than the regression for assessing and characterising genotypes in preliminary agronomic trials, the values observed (Table 1) are very similar to each other, except a couple of exceptions. It would seem, for the trial conditions, that the genotypes show extreme yield values under more and less favourable conditions.

The significant correlation between b and R_1 ($r = 0.647^*$) and R_2 ($r = 0.769^{**}$) (Table 2) cannot confirm what is suggested by Langer. Indeed in our trial the correlation between b and R_1 is quite low, whereas that between b and R_2 is in the same order of magnitude as observed by Langer.

The correlations between the traits under study (Table 2) show, except those previously considered and analyzed, non significant values, which indicate a lack of association between yield and different adaptability and stability indices. The lack of such correlation might be explained, as suggested by Langer, by the degree of selection applied to the genotypes being compared.

As a whole, the results obtained in the present research show that in vetch selection programmes for forage yield, breeders can use adaptability and stability with the mean yield, whenever significant genotype and environment interactions do exist.

The results obtained have enabled the selection of three genotypes for Southern Italy environments 'M30', '782' and '576', which show good adaptability and stability, besides a high or good yield. The above genotypes have been recorded in the Italian register of varieties as 'Itria', 'Sauro' and 'Murgia', respectively. The variety 'Itria' is also more suitable for more favourable environmental conditions.

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Table 1 - Dry matter yield (DMY), regression (b) and determination (r^2) coefficients, standard deviation from regression (s^2_d), and R_1 and R_2 indexes in 11 vetch genotypes.

Genotype	DMY ⁽¹⁾ (t ha ⁻¹)	b	r^2	s^2_d	R_1	R_2
M 30	5.21 A	1.32 ^{**}	0.983	21.4	87.2	89.2
782	5.20 A	0.96	0.964	20.8	70.7	60.1
576	5.04 AB	1.12	0.927	48.7*	73.8	73.2
571	4.98 AB	1.03	0.872	68.5*	85.8	84.8
681	4.94 ABC	1.10	0.941	29.7	75.1	76.4
M32	4.85 ABC	0.84 [°]	0.960	18.4	60.4	54.6
775	4.73 CD	0.82 [°]	0.825	97.6 ^{**}	69.8	36.1
Pietranera	4.63 D	0.98	0.973	30.2	65.4	66.3
Linea 6	4.56 D	0.97	0.898	41.9*	76.3	78.7
Mirabella	4.54 D	0.93	0.729	80.9*	84.8	57.2
Cipro	3.85 E	1.13	0.786	101.7 ^{**}	79.2	79.1

⁽¹⁾ The values with different letters in the column are significantly different at 1% level ($P < 0.01$).

^{**} Significantly greater than 1 at ($P < 0.01$) ; [°] significantly lower than 1 at ($P < 0.05$) and ($P < 0.01$).

* Significantly greater than 0 at ($P < 0.05$) and ($P < 0.01$).

Table 2 - Phenotypic correlation coefficients between DMY and stability parameters in 11 vetch genotypes.

	b	r^2	s_d^2	R_1	R_2
DMY	0,317	0,538	-0,565	0,046	0,161
b		0,361	-0,234	0,647*	0,769**
r^2			-0,978*	-0,158	0,427
s_d^2				0,264	-0,293
R_1					0,625*

* · ** Significant at ($P < 0.05$) and ($P < 0.01$) respectively.