Hindawi Publishing Corporation
International Journal of Agronomy
Volume 2009, Article ID 898396, 7 pages
doi:10.1155/2009/898396

Research Article

Genotype × Environment Interaction in Grass Pea (*Lathyrus sativus* L.) Lines

G. B. Polignano,[1] V. Bisignano,[1] V. Tomaselli,[1] P. Uggenti,[1] V. Alba,[2] and C. Della Gatta[2]

[1] *Dipartimento Agroalimentare, Istituto di Genetica Vegetale (IGV), Consiglio Nazionale delle Ricerche (C.N.R.), Via Amendola 165/A, 70126 Bari, Italy*
[2] *Dipartimento di Biologia e Chimica Agro-Forestale ed Ambientale, Università di Bari, Via Amendola 165/A, 70126 Bari, Italy*

Correspondence should be addressed to G. B. Polignano, giambattista.polignano@igv.cnr.it

Received 2 December 2008; Accepted 5 March 2009

Recommended by Rodomiro Ortiz

Eight grass pea lines grown in three different seasons were evaluated for the stability of seed yield, 100 seeds weight, flowering time, plant height, and biomass. Significant differences existed among years, lines, and lines × years interaction for all traits except for 100 seeds weight. Two methods of multivariate analysis cluster and principal components were utilized to determine: firstly, whether a pattern existed among lines in their response across years and secondly to examine the relationships among them. In both analyses, each line was presented as a vector whose elements were given by the performance of lines in each year. The analyses used arranged the lines into groups that were differentiable in terms of performances and stability. Our results provide useful information to aid the choice of grass pea lines in the Mediterranean marginal areas.

1. Introduction

Lathyrus sativus L. (grass pea, in italian "cicerchia") has been a traditional crop both for animal consumption as forage and grain, and for human consumption as a food grain. The main qualities of this grain legume consist of its sturdiness, drought tolerance, and adaptability to a wide range of soil types, including the marginal ones. Also, high protein content makes this species interesting as a forage crop (Polignano et al. [1]; Crinò et al. [2]; Polignano et al. [3]; Polignano [4]). Although rich in protein, the utilization of grass pea grain is limited by the presence of a water soluble, nonprotein amino acid β-N-oxalyldiaminopropionic acid (β-ODAP) which acts as a neurotoxin crippling the lower limbs when consumed in large amounts during a prolonged period can cause the disease neurolathyrism (up to 6% of the population) (Sharma et al. [5]). This has lead to the crop being excluded from agricultural improvement efforts. In fact, the sale of *Lathyrus* has been officially banned in some countries (Riley [6]). In Italy, since the early 70s the culture of the crop has decreased alarmingly and has almost disappeared. More recently, a renewed interest in grass pea cultivation is justified by the need to recover marginal lands and to provide an efficient alternative to wheat in the areas overexploited by cereal cultivation. Also, research on the use of grass pea for animal feeding will be of great importance in order to stimulate the expansion of grass pea cultivation in sustainable and low-input agricultural systems (Crinò et al. [2]). Breeding programs involving genotypes combining high yield with high protein content and low or no neuro-toxin (β-ODAP) are in progress all over the world (Dorrestein et al. [7]; Addis and Narayan [8]; Hanbury et al. [9]; Robertson and Abd El Moneim [10]; Mehta and Santha [11]; Crinò et al. [2]; Vaz Patto et al. [12]; Poma et al. [13]). For these reasons several research programs aimed at the collection, characterization, and evaluation of grass pea germplasm have been conducted. Considerable genetic diversity, as revealed by phenological, morphological, agronomical, biochemicals, molecular, and quality polymorphism exists in grass pea throughout the world (Alfaro et al. [14]; Chowdhury and Slinkard [15]; Chtourou-Ghorbel et al. [16]; Przybylska et al. [17]; Alba et al. [18]; Siddique et al. [19]; Sarker et al. [20]; Bisignano et al. [21]; Polignano et al. [1]; Granati et al. [22, 23];

De La Rosa and Varela [24]; Costa et al. [25]; Sardinha et al. [26]; Pankiwicz [27]; Polignano et al. [28]; Polignano [4]). In our previous work we have developed a core collection to include accessions relevant for genetic studies and breeding (Polignano et al. [29]). In addition we have evaluated and identified a set of elite grass pea lines useful for breeders and farmers (Polignano et al. [28]). Genotype x environment interaction is one of the most important steps in order to encourage the utilization of the most stable genotypes by the growers. Relatively few reports provide information on the G x E interaction studies in grass pea. Abd El-Moneim and Cocks [30] compared sixteen promising lines of *Lathyrus* spp. evaluated under rainfed conditions in Syria. While, Hanbury et al. [31] evaluated a selected number of lines for seed yield and ODAP concentration in Mediterranean-type environments. Their results clearly demonstrate the role of the environment on the lines tested and the importance of G x E interaction studies in grass pea breeding strategies. Numerical classificatory or pattern analysis methods have been applied more widely in comparing the responses of cultivars and/or breeding lines across environments (Mungomery et al. [32]; Shorter et al. [33]; Polignano et al. [34]; Polignano and Alba [35]; Alba et al. [36]; Hanbury et al. [31]) The present research provided additional information concerning the behavior of a set of selected grass pea lines over different years and grown in a marginal hill area of South Italy characterized by a mild winter and annual rainfall less than 400 mm.

2. Materials and Methods

Eight elite lines extracted from the Bari grass pea core collection were compared in a replicated randomized complete block design in Matera's Experimental Field at the "Chiancalata" Farm of the Basilicata Region in South Italy during three growing seasons: 2003–2006 (Table 1). The line were grown in six-row plots with plants placed continuously within rows, each 30 m^2. Distance between the rows was 1.50 m with a plot density of 360, 300, and 210 g, respectively, for small, medium, and large seed size. The soil is a clay-loam of generally medium nutrient status lacking in phosphorus, so only presowing fertilizer applications were made (120 kg ha-1 of P_2O_5). A brief summary of both effective rainfall and mean monthly temperatures for each season is given in Figure 1. Rainfall and temperature patterns for three growing seasons, as usually in the Mediterranean countries, have shown rainy autumns and declining temperatures with a final drought period and increasing temperatures in late spring. Growing season rainfall (November to June) was greater in 2005-06 relative to the other two seasons 2004-05 and 2005-06, being 725 mm, 321 mm, and 447 mm, respectively. Mean monthly temperatures at the end of each season were similar in the three seasons: 11.5°C in 2004-05, 11.4°C in 2005-06, and 11.3°C in 2003-04 (Figure 1). Five traits selected for their agronomic interest were recorded as average of five plants randomly chosen in each plot: plant height as it is in the canopy (cm from ground level to plant tip when plants were fully mature), flowering time (as days from

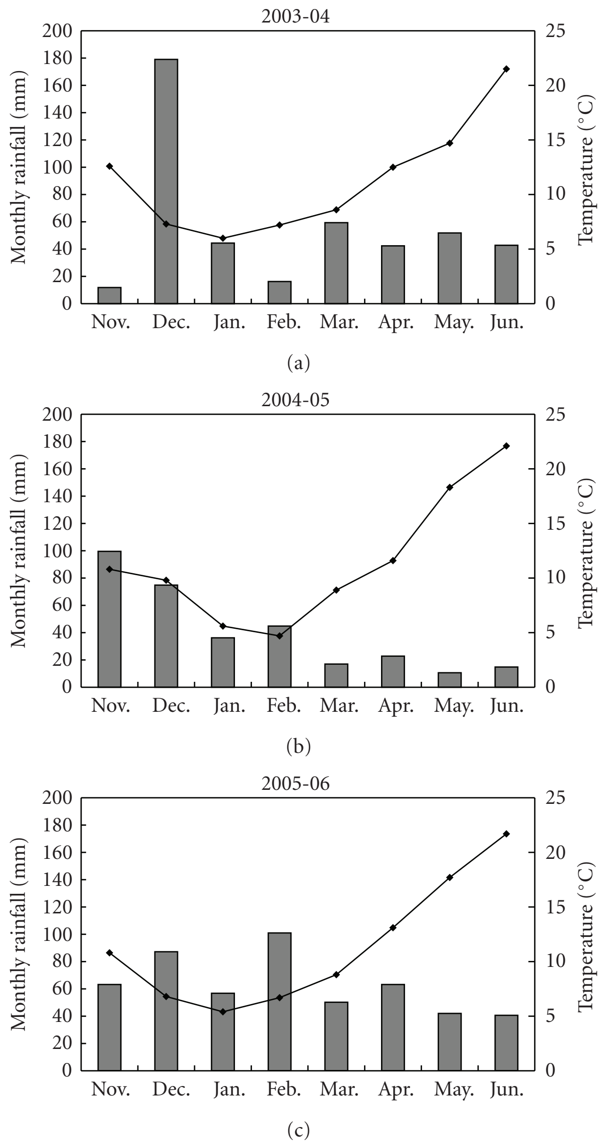


Figure 1: A graphic representation of the behavior of the lines according the first three principal components and identification of clusters. The behavior in each year is represented by a letter (line code) and a number (1 = 2004; 2 = 2005; 3 = 2006).

January 1st to 50% plants with flowers), 100 seeds weight, seed yield, and biomass. A univariate analysis of variance was performed with the years assumed as random, and the lines as the fixed effect. Thereafter the plot means were processed using an analysis which combined multivariate methods (Mungomery et al. [32]; Polignano et al. [34]; Alba et al. [36]). A pattern analysis approach, based on ordination and classification, is presented to identify differences among lines in mean performances and response across seasons. In particular, data analysis followed two steps: (1) an analysis of the main components in order to summarise the information contained in the original traits in a smaller and unrelated number of variables to be represented on a smaller number of orthogonal axes; (2) a cluster analysis utilizing the first three

Table 1: Means and LSD for five characters observed in 8 grass pea (*Lathyrus sativus* L.) lines over three consecutive years (2003–2006).

Lines	Code	Years				
		2003-04	2004-05	2005-06	*Mean*	*LSD*
			Flowering time (days)			
1. MG 110437-4	A	119	117	123	**119**	*1.26*
2. MG 112251-3	B	119	118	122	**119**	*0.99*
3. MG 110435-3	C	120	119	123	**120**	*1.24*
4. MG 113873-1	D	120	118	122	**120**	*1.37*
5. MG 113089-5	E	120	118	124	**120**	*1.12*
6. MG 110957-4	F	121	121	124	**122**	*0.99*
7. MG 103203-1	G	119	118	120	**119**	*0.84*
8. MG 110492-4	H	117	117	118	**117**	*0.76*
Mean		**119**	**118**	**122**		
LSD		*1.02*	***1.26***	*0.98*		
			Plant heigth (cm)			
1. MG 110437-4	A	55.9	54.9	60.3	**57.0**	*2.60*
2. MG 112251-3	B	58.1	53.3	60.2	**57.2**	*2.30*
3. MG 110435-3	C	53.3	47.3	56.6	**52.0**	*1.83*
4. MG 113873-1	D	56.0	46.7	57.9	**53.5**	*3.48*
5. MG 113089-5	E	58.1	56.7	60.0	**58.2**	*3.27*
6. MG 110957-4	F	59.6	49.9	62.4	**57.3**	*3.52*
7. MG 103203-1	G	45.2	42.4	46.0	**44.5**	*1.20*
8. MG 110492-4	H	41.8	41.2	45.7	**42.9**	*1.16*
Mean		**53.1**	**49.5**	**56.1**		
LSD		*3.01*	*1.36*	*2.52*		
			Seed Yield (kg/plot)			
1. MG 110437-4	A	**3.3**	4.8	5.4	**4.5**	*0.90*
2. MG 112251-3	B	3.6	3.0	3.9	**3.6**	*0.60*
3. MG 110435-3	C	3.3	3.0	4.2	**3.6**	*0.42*
4. MG 113873-1	D	3.6	3.3	4.2	**3.6**	*0.33*
5. MG 113089-5	E	3.6	3.3	3.9	**3.6**	*0.57*
6. MG 110957-4	F	3.0	2.4	3.6	**3.0**	*0.39*
7. MG 103203-1	G	4.2	4.2	4.5	**4.2**	*0.42*
8. MG 110492-4	H	4.5	3.6	4.8	**4.2**	*0.30*
Mean		**3.6**	**3.3**	**1.4**		
LSD		*0.39*	*0.39*	*0.23*		
			Biomass (kg/plot)			
1. MG 110437-4	A	9.6	9.0	11.7	**10.2**	*0.42*
2. MG 112251-3	B	8.1	6.3	9.0	**7.8**	*0.60*
3. MG 110435-3	C	9.3	7.8	10.8	**9.3**	*0.48*
4. MG 113873-1	D	9.9	10.5	11.1	**10.2**	*0.93*
5. MG 113089-5	E	8.4	7.8	9.9	**8.7**	*0.60*
6. MG 110957-4	F	7.8	6.9	9.0	**7.8**	*0.63*
7. MG 103203-1	G	9.9	9.3	11.1	**10.2**	*0.51*
8. MG 110492-4	H	9.9	9.3	10.5	**9.9**	*0.54*
Mean		**9.0**	**8.4**	**10.5**		
LSD		*0.48*	*0.66*	*0.66*		
			100 seeds weight (g)			
1. MG 110437-4	A	23.8	23.3	23.9	**23.7**	*4.06*
2. MG 112251-3	B	30.4	30.1	31.0	**30.5**	*7.01*
3. MG 110435-3	C	38.5	38.3	39.3	**38.7**	*6.20*
4. MG 113873-1	D	40.7	39.9	41.0	**40.5**	*5.49*

Table 1: Continued.

Lines	Code		Years			
5. MG 113089-5	E	26.1	26.9	26.7	**26.6**	*7.57*
6. MG 110957-4	F	27.9	27.0	27.6	**27.5**	*0.96*
7. MG 103203-1	G	34.2	34.1	34.2	**34.2**	*1.32*
8. MG 110492-4	H	32.6	32.5	32.6	**32.6**	*0.86*
Mean		**31.8**	**31.5**	**32.0**		
LSD		*3.30*	*3.46*	*3.31*		

Table 2: Analysis of variance for five characters observed in 8 grass pea lines over three consecutive years (2003–2006).

Source	Year (Y)	*Error a*	Line (L)	L x Y	*Error b*	Total
d. of f.	**2**	**6**	**7**	**14**	***331***	**359**
Character						
Flowering time (days)	489.91***	*11.29*	85.16***	11.51***	*2.46*	
Plant height (cm)	1538.82***	*118.50*	1635.31***	67.42***	*11.84*	
100 seeds weight (g)	7.50 n.s.	*96.4*	1567.09***	1.61 n.s.	*24.96*	
Biomass (t ha-1)	1356.22***	*34.20*	480.53***	50.71***	*8.99*	
Seed Yield (t ha-1)	317.59***	*10.12*	134.04***	31.92***	*5.95*	

***$P \leq .001$; n.s. = not significant.

principal components in order to differentiate the behavior of the lines during the growing seasons. With this approach, a stable line could show similar behavior in different years. In other words, each line is represented by three vectors whose elements correspond to the behavior of each line in each year. The analysis starts with a cluster containing the two most similar behavior and continues for the remaining ones until it reaches a single cluster. For statistical analysis, ANOVA, PRIN COMP, and PROC CLUSTER procedures from the SAS (1989) statistical software package were performed. In addition, the Stat Graph procedure from the STATISTICA for Windows software was performed to get a 3D graphical presentation.

3. Results and Discussion

Mean values and least minimum differences (LSDs) of five traits for eight grass pea lines estimated in each year of cultivation are presented in Table 1. Lines did show differences among growing seasons. Growing conditions were fairly typical in 2003-04 and 2005-06 with slightly warmer than normal temperatures in 2004-05. There was sufficient moisture for productive plant growth in 2003-04 and 2005-06, but not in 2004-05, when a severe drought occurred and temperatures were above normal. So, the growing season in 2005-06 gave higher mean values for all traits. On the contrary, the growing season in 2004-05 gave lower mean values. Intermediate mean values were shown for the years 2003-04. Variance, mean square, and significance for lines and their interaction with years are given in Table 2. All main effects and interaction were highly ($P \leq .001$) significant. For all traits, except for 100 seeds weight, the effects associated with years were most important in determining differential line responses. In other words, the year component of variance was larger than the line component for days to flowering, biomass, and seed yield. Similar results for seed yield are reported by Hanbury et al. [31] and Tadesse [37]. On the contrary, the line effect was larger for plant height and 100 seeds weight. For all traits the interaction line x year was lower than the main effects. These interactions indicate that from a statistical point of view, the relative performance among lines was not the same from one year to the next, which is not surprising considering the climatic differences among growing seasons. This indicates that genetic variation for flowering time, plant height, seed yield, and biomass existed among the lines and that selection should be effective for these traits in future improvement work. For 100 seeds weight, there was no interaction between years and lines indicating that the lines behaved similarly in all years. The mean values of each line in the three growing seasons were used in the subsequent pattern analysis based on ordination and classification procedures. The principal component analysis was done to reduce efficiently the information on response across the three growing seasons to a smaller number of dimensions. In other words, the ordination procedure allowed the relative proximity of line performances to be visualized in a spatial model of reduced dimensions and also indicate directions of major variation. The first three vectors obtained by the ordination procedure for all traits accounted for 93% of total variation (Table 3). In particular, if we consider the association coefficients between the original and transformed variables "eigenvectors," the first component (37%) displayed differences in the behavior of the lines for the following traits: seed yield (.62) and biomass (.68); the second component (36%) showed different behavior for the following traits: plant height (.64) and flowering time (.65); while, 100 seeds weight (.83) showed high loadings in the third component. A cluster analysis arranged the line

Table 3: Principal component analysis: eigenvalues, eigenvectors, and percent of variation accounted for the first three principal components (PCs).

	PC1	PC2	PC3
Eigenvalue	*1.85*	*1.81*	*0.98*
Variance (%)	**37**	**36**	**20**
Cumul. (%)		73	**93**
Character		*Eigenvector*	
Seed yield	**0.62**	0.18	−.41
Flowering time	−.00	**0.65**	0.39
Plant height	−.26	**0.64**	0.08
Biomass	**0.68**	0.20	0.04
100 seeds weight	0.29	−.28	**0.82**

performances into groups that were differentiable in terms of means and stability. In the classification of the lines, the hierarchy was truncated at 8-group level according to the number of lines tested. All lines responses in each cluster were closely related. The results of clustering were combined with those of the principal component analysis as a visual aid for discerning clusters in subsequent graphical presentation (Figure 2). MG 103203-1 (code G) and MG 110492-4 (code H) grass pea lines showing similar behavior in three different years turned out to be the ones characterized by a greater stability than the other lines. Lower uniformity of behavior was displayed by MG 110437-4 (code A), MG 112251-3 (code B), MG 113089-5 (code E), and MG 110957-4 (code F) lines. The remaining lines showed less similar behavior and therefore are present in all clusters. Our results confirmed that the grouping and ordination procedures were effective in delimiting groups of lines which differed in their environmental responses and within which the individual lines had a relatively homogeneous response.

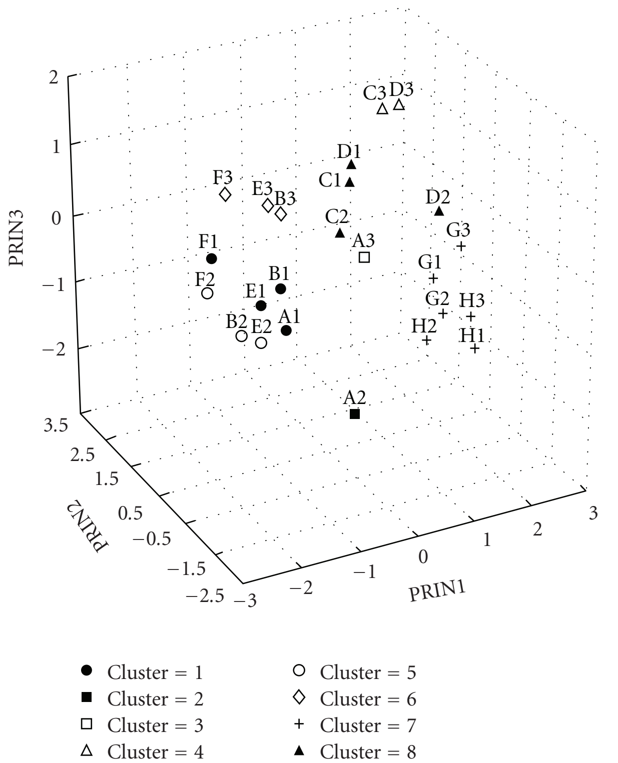


Figure 2: Rainfall and monthly temperatures during the growing seasons.

4. Conclusions

The results presented in this paper have given an idea of the relative stability of selected grass pea lines in three different growing seasons. The range of climatic conditions was sufficiently broad to provide for a substantial test of the lines. In fact, the effect of year was much more important than the other effects at least for flowering time, seed yield and biomass. Clear differences for these traits between the grass pea lines across growing seasons were evident. On the contrary, the effect of line on 100 seed weight is clearly most important, while the year and year x line interaction effects were of little importance. This suggests that the seed size is a stable trait in the tested grass pea lines which have shown a good potential to respond better in most favourable growing conditions; similar results are reported by Abd El-Moneim and Cocks [30]. Our results provide useful information to aid the choice of grass pea lines in the Mediterranean marginal areas. However, it is important to underline that in other specific edaphic conditions as in drought prone areas around the world (i.e., Ethiopia, India), characterized by a different soil management, more detailed analyses of adaptation including the soil fertility effect are necessary. Utilizing a combined principal components and cluster analyses to examine genotype performance, the advanced grass pea lines that had a significant stability over different years were identified (MG 103203-1; MG 110492-4). These lines were relatively indifferent to environmental variation and always had good performance. The analysis also identified lines with average sensitivity (MG 110435-3; MG113873-1) and lines with extreme or undesirable sensitivity (MG 110437-4; MG 112251-3; MG 113089-5; MG 110957-4). Consequently, the stable grass pea lines could be considered suitable for a broad “general” adaptability; while, development of specific grass pea lines for specific regions of production would utilize to advantage lines with narrow “specific” adaptability. The pattern analyses used provided effective methodology to systematically investigate the response patterns of a set of genotypes.

References

[1] G. B. Polignano, P. Uggenti, V. Bisignano, and E. Alba, "Patterns of variation in *Lathyrus sativus* and some related species," *Agricoltura Mediterranea*, vol. 133, no. 1, pp. 81–88, 2003.

[2] P. Crinò, G. B. Polignano, and S. Tavoletti, "Grass pea, a potentially important crop in Mediterranean agriculture," *Grain Legumes*, no. 40, pp. 6–7, 2004.

[3] G. B. Polignano, P. Uggenti, V. Alba, V. Bisignano, and C. Della Gatta, "Morpho-agronomic diversity in grass pea (*Lathyrus sativus* L.)," *Plant Genetic Resources*, vol. 3, no. 1, pp. 29–34, 2005.

[4] G. B. Polignano, "Conservation, analysis of genetic diversità and maintenance of grass pea and other species (*Lathyrus* spp.) in Italy," *Plant Genetic Resources Newsletter*, no. 152, pp. 73–76, 2007.

[5] R. N. Sharma, M. W. Chitale, G. B. Ganvir, A. K. Geda, and R. L. Pandey, "Observations on the development of selection criterion for high yield and low neurotoxin in grass pea based on genetic resources," *Lathyrus Lathyrism Newsletter*, no. 1, pp. 15–16, 2000.

[6] K. W. Riley, "A network approach for the conservation and use of *Lathyrus sativus* genetic resources," in *Lathyrus Genetic Resources in Asia*, R. K. Arora, P. N. Mathur, K. W. Riley, and Y. Adham, Eds., pp. 149–158, International Plant Genetic Resources Institute, Rome, Italy, 1996.

[7] B. van Dorrestein, M. Baum, and A. Abd El-Moneim, "Use of somaclonal variation in *Lathyrus sativus* (Grass pea) to select variants with low β-ODAP concentration," in *Proceedings of the 3rd European Conference on Grain Legumes*, p. 364, Valladolid, Spain, November 1998.

[8] G. Addis and R. K. J. Narayan, "Interspecific hybridisation of *Lathyrus sativus* (Guaya) with wild *Lathyrus* species and embryo rescue," *African Crop Science Journal*, vol. 8, no. 2, pp. 129–136, 2000.

[9] C. D. Hanbury, C. L. White, B. P. Mullan, and K. H. M. Siddique, "A review of the potential of *Lathyrus sativus* L. and *L. cicera* L. grain for use as animal feed," *Animal Feed Science and Technology*, vol. 87, no. 1-2, pp. 1–27, 2000.

[10] L. D. Robertson and A. M. Abd El Moneim, "*Lathyrus* germplasm collection, conservation and utilization for crop improvement at ICARDA," in *Lathyrus Genetic Resources in Asia*, R. K. Arora, P. N. Mathur, K. W. Riley, and Y. Adham, Eds., pp. 97–111, International Plant Genetic Resources Institute, Rome, Italy, 1996.

[11] S. L. Mehta and I. M. Santha, "Plant biotechnology for development of non-toxic strains of *Lathyrus sativus*," in *Lathyrus Genetic Resources in Asia*, R. K. Arora, P. N. Mathur, K. W. Riley, and Y. Adham, Eds., pp. 129–138, International Plant Genetic Resources Institute, Rome, Italy, 1996.

[12] M. C. Vaz Patto, B. Skiba, E. C. K. Pang, S. J. Ochatt, F. Lambein, and D. Rubiales, "*Lathyrus* improvement for resistance against biotic and abiotic stresses: from classical breeding to marker assisted selection," *Euphytica*, vol. 147, no. 1-2, pp. 133–147, 2006.

[13] I. Poma, L. Gristina, A. Davi', V. Bisignano, C. Della Gatta, and G. B. Polignano, "Performance of selected grass pea lines in Sicily (Italy)," in *Proceedings of the 6th European Conference on Grain Legumes*, p. 103, Lisbon, Portugal, November 2007.

[14] M. Alfaro, O. M. Paredes, and V. L. Becerra, "Genetic variation in *Lathyrus sativus* and their relationships with other species," in *Proceedings of the 3rd International Food Legume Research Conference*, p. 134, Adelaide, Australia, September 1997.

[15] M. A. Chowdhury and A. E. Slinkard, "Genetic diversity in grass pea (*Lathyrus sativus* L.)," *Genetic Resources and Crop Evolution*, vol. 47, no. 2, pp. 163–169, 2000.

[16] N. Chtourou-Ghorbel, B. Lauga, D. Combes, and M. Marrakchi, "Comparative genetic diversity studies in the genus *Lathyrus* using RFLP and RAPD markers," *Lathyrus Lathyrism Newsletter*, vol. 2, no. 2, pp. 62–68, 2001.

[17] J. Przybylska, Z. Zimniak-Przybylska, and P. Krajewski, "Diversity of seed globulins in *Lathyrus sativus* L. and some related species," *Genetic Resources and Crop Evolution*, vol. 47, no. 3, pp. 239–246, 2000.

[18] E. Alba, G. B. Polignano, D. De Carlo, and A. Mincione, "Electrophoretic phenotypes of different enzymes in some entries of *Lathyrus sativus* L.," *Lathyrus Lathyrism Newsletter*, vol. 2, no. 1, pp. 15–20, 2001.

[19] K. H. M. Siddique, C. D. Hanbury, A. Sarker, M. W. Perry, and C. M. Francis, "*Lathyrus* germplasm evaluation in a Mediterranean-type environment of south western Australia," in *Lathyrus Genetic Resources in Asia*, R. K. Arora, P. N. Mathur, K. W. Riley, and Y. Adham, Eds., pp. 113–125, International Plant Genetic Resources Institute, Rome, Italy, 1996.

[20] A. Sarker, A. Abd El Moneim, and N. Maxted, "Grass pea and chicklings (*Lathyrus* L.)," in *Plant Genetic Resources of Legumes in the Mediterranean*, N. Maxted and S. J. Bennett, Eds., pp. 159–180, Kluwer Academic Publishers, Dordrecht, The Netherlands, 2001.

[21] V. Bisignano, C. Della Gatta, and G. B. Polignano, "Variation for protein content and seed weight in grass pea (*Lathyrus* spp.) germplasm," *Plant Genetic Resources Newsletter*, no. 132, pp. 30–34, 2002.

[22] E. Granati, V. Bisignano, D. Chiaretti, G. B. Polignano, and P. Crinò, "Grain qualità in accessions of *Lathyrus* spp," *Lathyrus Lathyrism Newsletter*, vol. 2, no. 2, pp. 69–71, 2001.

[23] E. Granati, V. Bisignano, D. Chiaretti, P. Crinò, and G. B. Polignano, "Characterization of Italian and exotic *Lathyrus* germplasm for qualità traits," *Genetic Resources and Crop Evolution*, vol. 50, pp. 273–280, 2003.

[24] L. De la Rosa and F. Varela, "Phenotypic variability in spanish landraces of *Lathyrus cicera*," in *Proceedings of the 3rd European Conference on Grain Legumes*, p. 402, Valladolid, Spain, November 1998.

[25] R. Costa, T. Carita, G. Pereira, and M. Tavares-de-Sousa, "Characterization of grass pea genotypes by RAPD markers," in *Proceedings of the 6th European Conference on Grain Legumes*, p. 131, Lisbon, Portugal, November 2007.

[26] J. Sardinha, N. Almeida, and M. C. Vaz Patto, "Molecular characterization of *Lathyrus sativus* using AFLP markers," in *Proceedings of the 6th European Conference on Grain Legumes*, p. 131, Lisbon, Portugal, November 2007.

[27] K. Pankiwicz, "Differences within and between populations of *Lathyrus sativus* and *Lathyrus ciucera* (Fabaceae) revealed by isoenzimatic markers," in *Proceedings of the 6th European Conference on Grain Legumes*, p. 132, Lisbon, Portugal, November 2007.

[28] G. B. Polignano, P. Uggenti, G. Olita, V. Bisignano, E. Alba, and P. Perrino, "Characterization of grass pea landraces using agronomically useful traits," *Lathyrus Lathyrism Newsletter*, vol. 4, pp. 10–14, 2005.

[29] G. B. Polignano, D. Chiaretti, L. Iommarini, V. Bisignano, P. Crinò, and S. Tavoletti, "Genetic diversity of grass pea (*Lathyrus* spp.) and establishment of Italian core collections," in *Proceedings of the 5th European Conference on Grain Legumes*, p. 108, Dijon, France, June 2004.

[30] A. M. Abd El-Moneim and P. S. Cocks, "Adaptation and yield stability of selected lines of *Lathyrus* spp. under rainfed conditions in West Asia," *Euphytica*, vol. 66, no. 1-2, pp. 89–97, 1992.

[31] C. D. Hanbury, K. H. M. Siddique, N. W. Galwey, and P. S. Cocks, "Genotype-environment interaction for seed yield and ODAP concentration of *Lathyrus sativus* L. and *L. cicera* L. in Mediterranean-type environments," *Euphytica*, vol. 110, no. 1, pp. 45–60, 1999.

[32] V. E. Mungomery, R. Shorter, and D. E. Byth, "Genotype × environment interactions and environmental adaptation—I: pattern analysis-application to soya bean populations," *Australian Journal of Agricultural Research*, vol. 25, pp. 59–72, 1974.

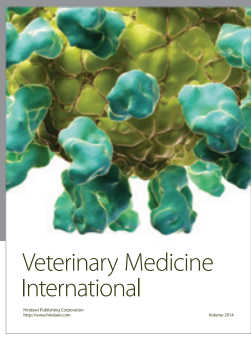
[33] R. Shorter, D. E. Byth, and V. E. Mungomery, "Genotype × environment interactions and environmental adaptation—II: assessment of environment contributions," *Australian Journal of Agricultural Research*, vol. 28, no. 2, pp. 223–235, 1977.

[34] G. B. Polignano, P. Uggenti, and P. Perrino, "Pattern analysis and genotypic × environmental interactions in faba bean (*Vicia faba* L.) populations," *Euphytica*, vol. 40, no. 1-2, pp. 31–41, 1989.

[35] G. B. Polignano and E. Alba, "Phenotypic stability analysis of safflower (*Carthamus tinctorius* L.) varieties over six years," *Agricoltura Mediterranea*, vol. 125, pp. 21–30, 1995.

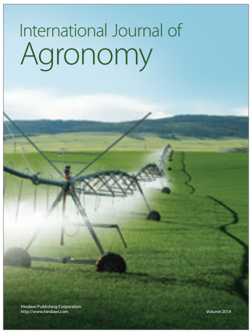
[36] E. Alba, G. B. Polignano, and L. Notarnicola, "Yield stability in a set of Amaranth entries in southern Italy," *The Italian Journal of Agronomy*, vol. 1, no. 2, pp. 65–71, 1996.

[37] W. Tadesse, "Stability of grass pea (*Lathyrus sativus* L.) varieties for ODAP content and grain yield in Ethiopia," *Lathyrus Lathyrism Newsletter*, vol. 3, pp. 32–34, 2003.

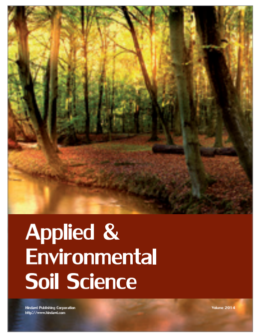

Scientifica

Veterinary Medicine
International

International Journal of
Food Science

Journal of
Botany

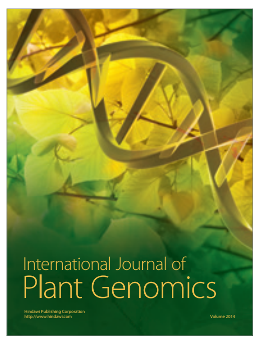
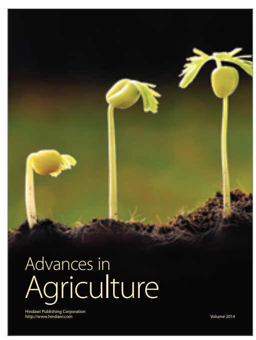
The Scientific
World Journal

International Journal of
Agronomy

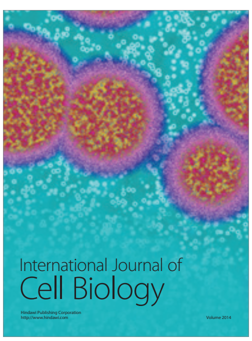

International Journal of
Ecology

International Journal of
Biodiversity

Applied &
Environmental
Soil Science

International Journal of
Forestry Research

Journal of
Nutrition and
Metabolism

International Journal of
Evolutionary Biology

International Journal of
Plant Genomics

Advances in
Agriculture

Biotechnology
Research International

International Journal of
Cell Biology

International Journal of
Genomics

International Journal of
Microbiology

Psyche