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ARTICLES

QTL mapping for common bean grain yield in different environments

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ABSTRACT - *Objectives of this research were to identify QTLs that control the grain yield of common bean in different environments, to evaluate interactions of the QTLs with the environments, and to compare the mapping and multiple regression methods. One hundred and ninety-six recombinant inbred lines derived from the cross of Carioca with Flor de Mayo cultivars sown in two periods in 1996, 1997, and 1998 were evaluated at two sites. Seven field experiments were conducted for the phenotypic evaluation of the families in a 14 x 14 simple square lattice design. The QTLs x sites interaction was significant, but some stable QTLs were identified. The results of the two studied methods were not in line. The most stable and promising molecular markers for a marker-assisted selection for grain yield were OPO-19 (1412 pb), OPO-20 (1585 pb), and OPN-07 (1445 pb).*

Key words: *Phaseolus vulgaris*, yield, QTLs x environments interaction, RAPD markers.

INTRODUCTION

Although a considerable number of traits in plant species is controlled by qualitative genes, most characters of economic importance are of quantitative nature, in other words, they are result of the joined action of several gene loci. Such gene groups are the so-called quantitative trait loci (QTL). The study of these quantitative characters is undertaken through analyses and statistical inferences, which intend to describe the characteristics of a continuous phenotypic distribution. An alternative to this approach consists in the identification of QTLs by molecular markers which can provide more precise and detailed information about the architecture of the genes that control quantitative traits as well as support the process of selecting superior genotypes. Grain yield, in a field-bean breeding program, is one of the most important traits, despite being also the most complex one, since it depends on several other characters and on countless environmental factors as well.

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The increase of the productivity potential of common bean (*Phaseolus vulgaris*) cultivars has been low and gradual, in spite of the broad variation in the majority of the characters, including grain yield itself. In Brazil, one of the main reasons for such a low increment in the potential yield is the consumer's preference for cultivars of the "carioca" common bean type (beige with brown stripes). This demand imposes considerable restriction regarding the utilization of germplasm sources, limiting the available genetic variability to breeding programs since it is not possible to develop new cultivars by crosses among genotypes of a very different grain type from the Carioca standard.

The utilization of similar genetic materials became more evident after Singh (1988) clustered common bean germplasm into twelve gene clusters and later into six races (Singh et al. 1991). Thus, it became clear that breeders have traditionally realized their hybridizations involving genotypes of a single gene group. Singh (1988) observed that the variability in grain yield, its main components, and in other traits was greater among the gene groups than within them.

The field-bean plant belongs to a species with a small genome (Arumuganatham and Earle 1991) and predominantly with simple copy sequences (Talbot et al. 1984). This feature makes it easier to obtain molecular markers distributed uniformly across the whole genome, which in turn increases the possibility of QTL detection by making the obtaining of highly saturated genetic maps possible. The genetic mapping of common bean began with the development of an empiric linkage map, in which most markers were morphologic and a few isoenzymatic (Basset 1991). Later, Vallejos et al. (1992) and Nodari et al. (1993) constructed maps based mainly on RFLP markers, covering 82% and 69% of the genome, respectively.

Taram et al. (2000), using the RFLP, SSR, AFLP, and RAPD markers, identified 29 QTLs associated to agronomic traits in common bean. QTLs were identified for growth habit, days to flowering, days to maturity, plant lodging, and grain yield, demonstrating the possibility of identifying useful molecular markers for the improvement of common bean. If such markers are utilized in marker-assisted selection, they may contribute to the increase of the efficiency of the selection process and thus increase the efficiency of the breeding program. Faleiro et al. (2003) mapped loci associated with eight quantitative characters in common bean, in which the phenotypic variance attributed to the markers varied from 14.03% to 40.14%. According to the authors, these results provide the basis for the development of specific saturated maps of utility for common bean breeding programs.

Objectives of this research were: i) to map RAPD (Random Amplified Polymorphic DNA) markers linked to QTLs controlling common bean grain yield in a segregating population, at different sowing times and sites; ii) to evaluate the existence of the interaction QTLs x sites, and; iii) to compare the detection processes of QTL-linked markers by the composite interval method and multiple regression analysis.

MATERIAL AND METHODS

One hundred and ninety-six families originated from the cross of Carioca (gene group 3) and Flor de Mayo (gene group 6) parents were utilized in this study. The F_2 through F_5 generations were obtained from a F_1 generation conducted by the bulk-population method. In the F_5 generation, seeds were harvested from 196 randomly selected individual plants, which in turn originated 196 $F_{5:6}$ families. Seeds from these families were multiplied in one cycle to produce $F_{5:7}$ families. The families were evaluated in two traditional sowing periods in 1996, 1997, and 1998, on the experimental area of the Biology Department of Universidade Federal de Lavras, Lavras, State of Minas Gerais, and on the experimental farm of Empresa de Pesquisa Agropecuária de Minas Gerais (EPAMIG), in Patos de Minas, State of Minas Gerais.

Seven experiments (two in winter in Lavras, one in winter in Patos de Minas, two during the dry season in Lavras and also in Patos de Minas) were conducted in order to evaluate the families phenotypically. The experimental design for all experiments was a partially balanced double-replicate Lattice Square (14 x 14). Each plot consisted of two 2m rows spaced 50 cm apart, along which 15 seeds were sown per meter. Normally recommended cultural practices were applied, plus irrigation whenever needed. Grain yield (in kg ha^{-1}) was obtained by means of weighing the grains harvested in each plot after drying them to around 13% moisture.

Initially, variance analyses were run individually for each experiment, considering the family effects as random. Later on, a joint variance analysis was performed using the adjusted means of the individual analyses, in which both sowing time and location effects were considered fixed. The layout for the joint variance analysis and the mean square expectations were obtained according to Vencovsky and Barriga (1992). Based on the mean square expectations, the genetic and phenotypic variances as well as some genetic parameters (broad-sense heritability, coefficient of genetic variation, and the b coefficient) were estimated among the families, according to Vencovsky and Barriga (1992). As for heritability, the lower and upper confidence limits were estimated with a confidence coefficient of $1 - \alpha = 0.95$ (Kanapp et al. 1985).

The DNA extraction, the achievement of RAPD markers, as well as the construction of the linkage map between the RAPD markers were described previously (Melo et al. 2002). A multiple

regression analysis was performed involving all markers that presented Mendelian segregation for each individual experiment and also with the means of each location and time of sowing separately, besides the overall analysis with the means of all experiments. The multiple linear regression analysis of the markers was performed using the procedures described by Edwards et al. (1987), who considered the molecular markers as independent variables and the phenotypic characters as dependent variables. The most important markers were identified through the significant values of partial F (P<0.05). The percentage of the phenotypic variation explained by the markers was estimated by the partial determination coefficient (Draper and Smith 1981).

Based on the RAPD marker molecular map developed by Melo et al. (2002), who used the same recombinant lines as the ones in this research, the QTL map was constructed using the composite interval method (CIM) (Zeng 1993, 1994), which is a combination of interval mapping and multiple linear regression in which the markers are considered independent variables. The mapping analyses were performed with the QTL Cartographer software for Windows (version 1.01). The parameters defined in the QTL Cartographer to assemble the QTL maps were: Walk speed set to 2; Threshold selection – By Manual set to 2.6 CIM Model – Standard Model, which utilizes a variable number of markers to control the genetic background; Control Markers Number set to 5; Regression Method Selection – Stepwise; Windows Size set to 10 cM. The mapping for each experiment was carried out individually, considering the means of each location and sowing time separately, besides the analysis involving the means of all experiments.

RESULTS AND DISCUSSION

Phenotypic evaluation

According to Singh (1988), the two specific parentals employed in this research have a high potential of allelic complementation for high yield, which is the reason why they were chosen for this research. Abreu (1997), who evaluated several populations originated from inter racial crosses, identified the cross Carioca x Flor de Mayo as one of the most auspicious as far as grain yield is concerned, thus confirming Singh's report (1988).

It is worth mentioning that in spite of the great chances to obtain a higher yielding material, this population presents quite serious problems. One aspect is the prostrate habit, which provokes a direct contact of the pods with the soil surface leading to a higher disease incidence and reduced grain quality if there is rain at maturation or harvest. Besides,

the grain type is another problem. Despite one of the parents was the Carioca cultivar with the ideal grain type, the grains of the other parent had a non-commercial pattern. This caused an enormous grain type variability in the segregant population, ranging from the carioca (standard) to a dark blue type, encompassing practically all possible variants.

The combined analysis for grain yield (Table 2), for sowing times, and locations revealed the existence of significant interactions for both families x sowing times and families x locations. The correlation between the family means of the two sowing periods was 0.01 and of the two locations 0.14; both values were not statistically different from zero according to the t test at P<0.05. This indicates that the major part of the interactions for this trait is of the complex type (Ramalho et al. 1993) with a greater importance of the interactions genotypes x sowing times, since they presented a reduced estimate of the correlation and a greater interaction mean square (Table 2) in comparison to the locations. Thus, such low correlations largely increase the chances that an outstanding material in a certain environment will not repeat its performance in another, hindering the selection efforts.

In order to confirm the effect of the families x environment interactions (sowing time and locations) on grain yield, the heritability was estimated considering all factors involved in the model as random (Vencovsky and Barriga 1992). Therefore, the calculation of the genetic variance obtained the estimate of this parameter totally free from the interaction effect. Under this condition, the estimated heritability value was 0.0%, which confirmed the intense effect of the interaction on the phenotypic expression of grain yield in common bean. This is the reason why this character should be evaluated at different sowing periods and sites, since the family performance strictly depends on both the chosen sowing time and site. Therefore, when mapping QTLs for this trait, one must always try to identify both those that are only expressed in specific environments as well as the more constant ones, which are expressed in most environments.

Multiple linear regression analysis

The regression analysis for grain yield (Table 2) for the first experiment (Lavras - F_7 - winter - 1996) permitted an identification of five QTLs linked markers that participate in the genetic control of this trait. Three of them presented a negative and two a positive effect. Marker OPG-16 (851 bp) explained the greatest part of the phenotypic variation (10.05%) in this experiment; all markers together explained 22.06% of the variation. Therefore, the RAPD markers in

this experiment explained more than one fifth of all phenotypic variation observed for this character, demonstrating that, even in the case of complex traits, they could represent important tools in the selection process. Nevertheless, in spite of explaining a considerable fraction of the phenotypic variation, the heritabilities estimated for this and the other locations were of low magnitude (Table 1) thus making the precise quantification of the marker effects difficult and also reducing their efficiency in a future marker-aided selection.

Five QTLs-linked markers were found again in the second experiment, four of them with negative and one with a positive effect (OPN-07 marker - 1698 bp), which explained the most part of the phenotypic variation (5.61%). None of these had been identified in the previous experiment. In the third experiment, six linked markers were identified and marker OPN-07 (1072 bp) was the one that explained the greatest part of the phenotypic variation (4.75%). Three markers linked to QTLs were found in the fourth experiment, where the marker OPO-20 (1585 bp) was the most important for the explanation of the phenotypic variation (9.92%).

In the fifth experiment, four markers were found and OPN-07 (1445 pb) was outstanding in relation to the others at explaining the phenotypic variation (6.11%). Three markers were identified in the sixth experiment, but explained a small fraction of the phenotypic variation (less than 4%). In the seventh experiment, three QTL-linked markers related to grain yield were found but again, they explained less than 4% of the total phenotypic variation for the trait.

The joint regression analysis, considering only the experiments carried out in Lavras, identified three markers linked to grain yield controlling QTLs. Marker OPN-07 (1072 bp) was the one that explained the major part of the phenotypic variation (5.23%), specifically for this location. This particular marker had already been identified in two other trials and in the first experiment, conducted in Lavras, it had explained 3.55% of the phenotypic variation for grain yield. Hence, this marker could be useful in the selection procedures in Lavras, selecting for its absence, since its presence is related to a grain yield reduction. Nevertheless, it is worth noting that selection based on band absence has not been utilized due to its low efficiency, mainly in the case of RAPD markers, once the absence of the band can be caused by different mutation types, which does not characterize a stable and dependable linkage group. Besides, the absence of the band on an individual basis can occur due to an amplification failure and would, in this case, lead to the selection of undesirable individuals.

When considering only the experiments carried out in Patos de Minas, six QTL-linked grain yield controlling markers were identified. Marker OPH-03 (1258 bp) was the

one that explained the greatest part of the phenotypic variation (6.04%), specifically for this location. This marker had already been identified in another experiment (E3) conducted in Patos de Minas, where it explained 2.43% of the phenotypic variation for grain yield.

The joint analyses for Lavras and Patos de Minas did not specify any markers in common, thus indicating the difficulty to obtain simultaneous gains for both locations, reinforcing the results of the significant interaction families x locations and also the low correlation between the family means at both sites for grain yield, as determined in the previous analyses (Table 2). However, 22.27% of the phenotypic variation was explained by the markers identified specifically at Patos de Minas, while in Lavras, this value was only 11.62%. The trials conducted specifically in wintertime were capable of identifying six QTL-linked markers that control grain yield. Marker OPO-20 (1585 bp) explained the greatest part of the phenotypic variation (9.90%) at this sowing time. This marker had already been identified in another experiment (E4), conducted in wintertime, where it explained 9.92% of the phenotypic variation for grain yield, thus demonstrating a certain stability not only due to its presence but also to the magnitude of its effect.

The joint regression analysis took only the experiments conducted in the dry season into account and identified four QTL-linked markers. Marker OPJ-04 (2344 bp) was the one that explained most (4.98%) of the phenotypic variation among families in that sowing time. This marker was also found in experiments E3 and E6, which were also conducted in the dry season, however in all cases, it was responsible for less than 4.0% of the total phenotypic variation for this character. The combined analyses for both wintertime and dry season sowing times did not identify any marker in common, which demonstrated the difficulty of pursuing gains for both sowing times simultaneously. This is reinforced by the results of the significant interaction families x sowing times (Table 2) and also by the low correlation between the means of the families at the two sowing times found for grain productivity in the previous analyses.

Considering all experiments, two QTL-linked markers that control grain yield were detected, both with positive effect. Marker OPN-07 (1445 bp) explained 4.84% of the among-family phenotypic variation for grain yield and the two markers together were responsible for only 7.80% of this variation. Marker OPN-07 (1445 bp) had only been detected for wintertime in Patos de Minas and in the combined wintertime analysis, while OPO-20 (1585 bp) was identified only in generation F_9 in Lavras, also in the winter season.

Table 1. Multiple linear regression analysis for weight of 100 seed utilizing stepwise procedure

Markers	Parameter estimates	R² partial	Standard error	t test*
E1- LAVRAS, F_7, WINTER, 1996				
Intercept	2646.94		85.52	30.95
OPN-07 (1072 bp)	-211.59	0.0355	73.77	-2.87
OPD-08 (759 bp)	174.74	0.0237	73.23	2.39
OPR-02 (1230 bp)	239.98	0.0356	73.00	3.29
OPR-02 (832 bp)	-165.66	0.0253	76.55	-2.16
OPG-16 (851 bp)	-210.44	0.1005	78.92	-2.67
E2 - LAVRAS, F_8, DRY, 1997				
Intercept	2937.48		93.95	31.27
OPN-07 (1698 bp)	-264.26	0.0561	66.94	-3.95
OPG-19 (851 bp)	-137.09	0.0236	67.33	-2.04
OPH-03 (1258 bp)	-218.80	0.0299	61.59	-3.55
OPH-03 (759 bp)	-161.02	0.0316	64.05	-2.51
OPG-16 (676 bp)	160.12	0.0383	59.07	2.71
E3 - PATOS DE MINAS, F_8, DRY,1997				
Intercept	1361.45		50.02	27.22
OPJ-04 (2344 bp)	-114.73	0.0263	44.65	-2.57
OPN-07 (1072 bp)	141.76	0.0475	48.07	2.95
OPAA-09 (1059 bp)	-132.49	0.0327	50.97	-2.60
OPN-02 (436 bp)	-112.29	0.0321	46.25	-2.43
OPH-03 (1258 bp)	-87.53	0.0243	43.93	-1.99
OPS-13 (1950 bp)	188.18	0.0239	51.57	3.65
E4 - LAVRAS, F_9, WINTER, 1997				
Intercept	2523.22		82.52	30.58
OPG-19 (851 bp)	213.59	0.0410	80.69	2.65
OPS-10 (794 bp)	-173.68	0.0266	80.44	-2.16
OPO-20 (1585 bp)	345.33	0.0992	80.81	4.27
E5 - PATOS DE MINAS, F_9, WINTER, 1997				
Intercept	2389.16		69.18	34.54
OPE-20 (891 bp)	134.81	0.0373	57.16	2.36
OPN-07 (1445 bp)	173.92	0.0611	59.59	2.92
OPD-08 (759 bp)	120.76	0.0248	58.66	2.06
OPAA-09 (1059)	-144.79	0.0281	59.22	-2.45
E6- LAVRAS, F_{10}, DRY, 1998				
Intercept	2451.21		63.16	38.81
OPF-10 (1000 bp)	123.51	0.0249	61.80	2.00
OPJ-04 (2344 bp)	-157.19	0.0374	59.97	-2.62
OPO-20 (933 bp)	122.07	0.0281	59.94	2.04
E7 - PATOS DE MINAS, F_{10}, DRY, 1998				
Intercept	1224.03		41.86	29.24
OPM-06 (1096 bp)	-95.20	0.0316	42.30	-2.25
OPO-10 (525 bp)	123.57	0.0289	42.19	2.93
OPO-20 (1698 bp)	-107.98	0.0274	41.32	-2.61
MEAN – LAVRAS				
Intercept	2655.38		44.93	59.10
OPN-07 (1072 bp)	-92.37	0.0523	38.37	-2.41
OPB-18 (1412 bp)	91.52	0.0332	39.32	2.33
OPG-16 (851 bp)	-88.59	0.0307	39.32	-2.25

To be continued

		MEAN – PATOS DE MINAS		
Intercept	1776.80		35.50	50.05
OPM-06 (1096 bp)	-68.56	0.0269	30.83	-2.22
OPAA-09 (1059 bp)	-123.19	0.0534	35.15	-3.51
OPH-03 (1258 bp)	-76.40	0.0604	30.35	-2.52
OPR-12 (794 bp)	84.00	0.0282	44.94	1.87
OPS-13 (1950 bp)	109.73	0.0256	47.45	2.31
OPO-20 (1698 bp)	-115.12	0.0282	35.72	-3.22
		MEAN – WINTER		
Intercept	2369.04		58.11	40.77
OPN-07 (1445 bp)	108.36	0.0384	44.89	2.41
OPN-07 (661 bp)	144.17	0.0455	45.29	3.18
OPD-08 (759 bp)	102.75	0.0221	44.53	2.31
OPR-02 (832 bp)	-126.20	0.0244	48.75	-2.59
OPG-19 (851 bp)	88.56	0.0221	43.09	2.06
OPO-20 (1585 bp)	91.68	0.0990	50.24	1.83
		MEAN – DRY		
Intercept	2046.79		43.25	47.33
OPJ-04 (2344 bp)	-119.14	0.0498	32.56	-3.66
OPI-06 (480 bp)	89.19	0.0349	32.01	2.79
OPH-03 (1258 bp)	-101.15	0.0306	33.46	-3.02
OPH-03 (759 bp)	-97.34	0.0422	36.10	-2.70
		MEAN - ALL EXPERIMENTS		
Intercept	2135.69		24.42	87.45
OPN-07 (1445 bp)	69.09	0.0484	27.13	2.55
OPO-20 (1585 bp)	57.22	0.0296	26.36	2.17

* Significant at the 5% probability level based on t test

Table 2. Joint analysis of variance and estimative of genetic coefficient of variation (CVg), the b coefficient, broad-sense heritability (h^2) with the upper (LU) and lower limits (LL) of the confidence intervals, for grain yield (kg ha^{-1})

Sources of variation	df	MS
Locations (L)	1	561819395.00**
Seasons (S)	1	306233921.20**
Families (F)	195	424431.56**
F x L	195	298317.66**
F x S	195	438656.68**
F x L x S	195	273160.68**
Mean error	1183	186327.28
Mean		2204.14
CV (%)		19.58
CVg (%)		5.92
b		0.30
h^2 (%)		56.10 (0.00)[a]
LU (h^2)		45.13
LL (h^2)		64.29

** Significant at the 1% probability level based on F test . [a] Heritability considering all model factors as random

Composite interval mapping (CIM)

QTLs related to grain yield in common bean were detected with the RAPD-marker molecular map developed by Melo et al. (2002) as reference, which was obtained by the analysis of the same lines used in the present research. In that map, seven linkage groups were found in the common bean genome. In average, groups of 112.24 cM length were obtained, the smallest with 16 cM and the largest with 252 cM. Thus, in average, the markers were mapped with an interval of 20.15 cM. Overall, it was possible to map a region that corresponds to approximately 785.7 cM. Since the size of the common bean genome is estimated at around 1200 cM (Vallejos et al. 1992), it is estimated that around 66% of the bean genome was mapped in this study, yet with a low marker saturation. Hence, the marker map utilized for this mapping may present some blank regions, which makes it difficult to

identify part of the QTLs for grain yield, but, anyhow, supplies important information on the detected ones.

The mapping for grain yield in the first experiment (Figure 1 and Table 3) (wintertime in Lavras) identified two QTLs. The first detected QTL presents a negative additive effect (presented in the smaller graph in the lower part of the figures) and the second a positive one. In the regression analysis, only marker OPS-16 was not identified as linked to QTLs that participate in the genetic control of grain yield.

In the second and third experiments, no QTLs were detected for this character. In the fourth experiment (wintertime in Lavras) one QTL was found with a positive additive effect (Figure 2). The regression analysis did not identify this marker as linked to QTLs that participate in the genetic control of grain yield. In the other individual experiments, as well as in the analyses using location means,
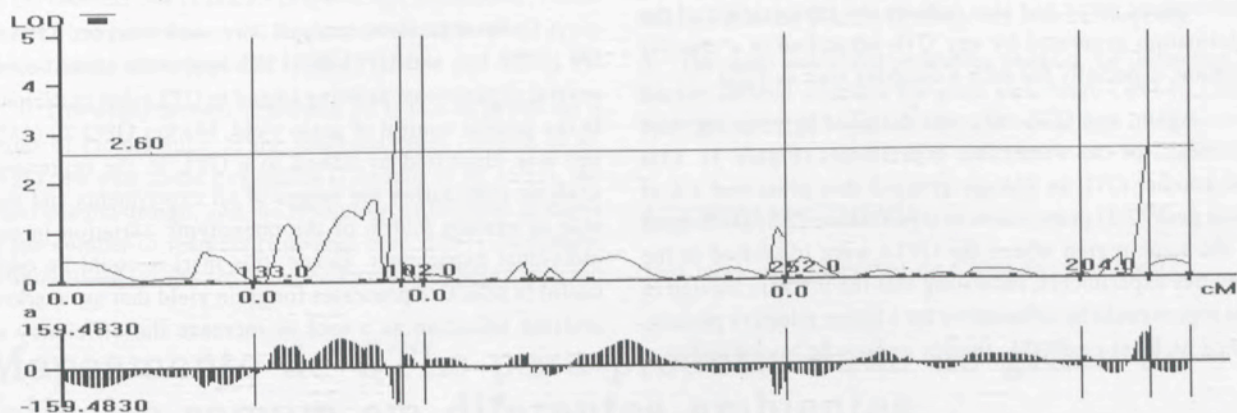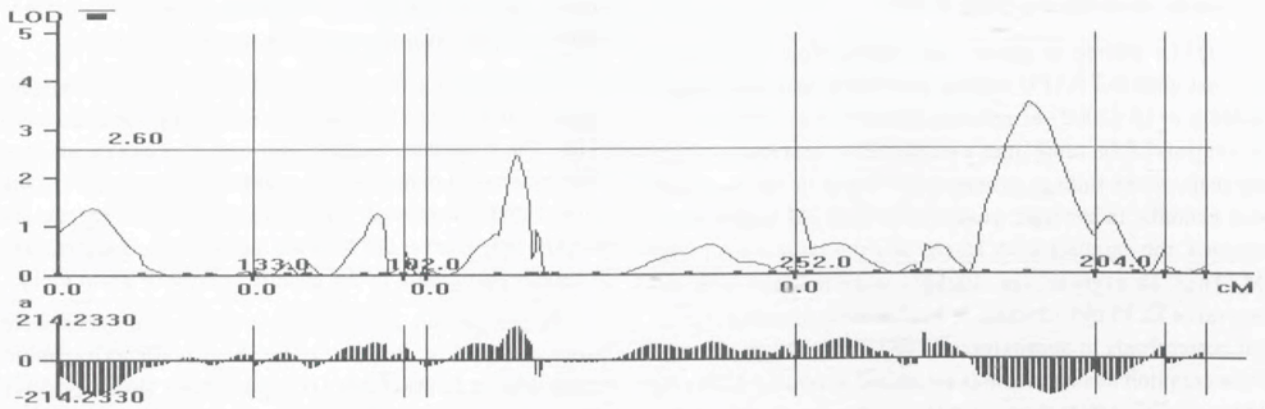

Figure 1. Mapping and additive effect of QTLs for grain yield in common bean, winter, Lavras, MG, 1996

Table 3. Summary of Composite Interval Mapping (CIM) in different experiments (E), with QTLs identified, linkage group, values of the Lod score (Lod), and distance (DM1 and DM2) for flanking markers of the QTL (M1 and M2)

E	Linkage Group*	QTL	Lod	M1	M2	DM1	DM2
						— cM —	— cM —
1	2	1	3.2	OPO-20 (1698 bp)	OPO-20 (933 bp)	5.5	4.9
1	6	2	2.6	OPB-18 (1412 bp)	OPS-16 (640 bp)	18.3	0.3
4	5	3	3.6	OPR-12 (1000 bp)	OPO-19 (1412 bp)	27.2	0.3
WINTER	2	4	2.9	OPO-20 (741 bp)	OPO-20 (1585 bp)	11.9	0.3

*Linkage map between RAPD markers are described in the paper published by Melo et al. (2002). E1: experiment in Lavras, F_7, winter, 1996; E4: Lavras, F_9, winter, 1997; WINTER: Analyses with all experiments in winter
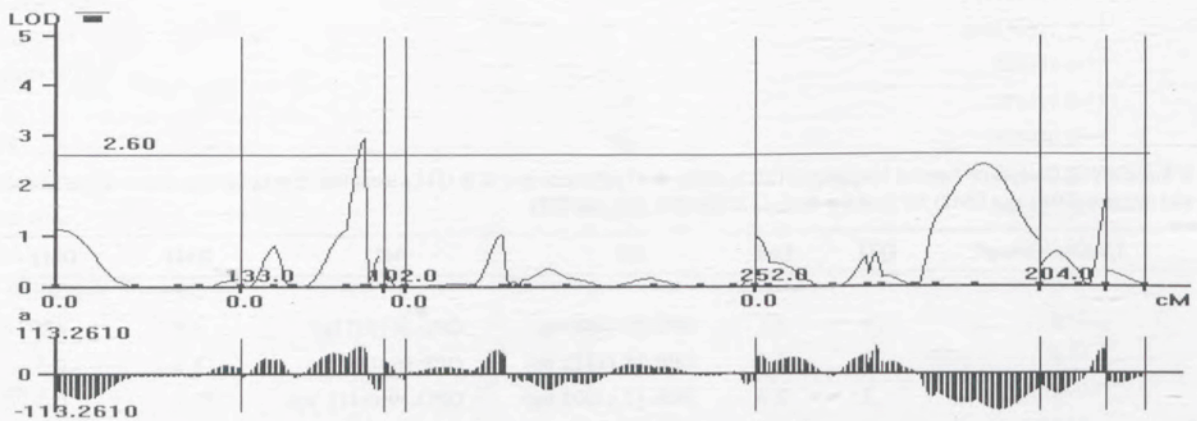
Figure 2. Mapping and additive effect of QTLs for grain yield in common bean, winter, Lavras, MG, 1997

no QTLs were identified for this character. This is, once more, evidence of the strong interaction effect with the locations, which greatly hinders the QTL detection in the environment mean and also reduces the repeatability of the information generated by any QTL identified in a specific location, especially for such a complex trait as yield.

Again, one QTL only was detected by mapping with the means of the wintertime experiments (Figure 3). This and another QTL in linkage group 5 that presented a Lod score peak (2.5) pretty close to significance (2.6) are located in the same region where the QTLs were identified in the previous experiments, indicating that the markers located in this region could be informative for a future selective process. Since at least one QTL that is expressed specifically at

wintertime was identified, the conclusion can be drawn that this cultivation period is more stable than the dry season, for which no specific QTL was detected.

In the regression analysis, two such markers [OPAA-O9 (1059 bp) and OPO-20 (1585 bp)] were identified in several experiments as being linked to QTLs that participate in the genetic control of grain yield. Marker OPO-20 (1585 bp) was identified as linked to a QTL in the regression analysis considering the means of all experiments and was able to explain 9.90% of the phenotypic variation in one individual experiment. Hence, this marker could be quite useful in selective processes for grain yield that use marker-assisted selection as a tool to increase the efficiency of selection.

Figure 3. Mapping and additive effect of QTLs for grain yield in common bean, all experiments in winter, Lavras and Patos de Minas, MG, 1996/1997

The multiple regression method identified a larger number of QTLs in comparison with the composite interval mapping, due to the greatest number of markers available for the regression analysis, since, in this process, there is no need to rank the markers into linkage groups. For mapping, on the other hand, this is mandatory, thus limiting the number of markers available for analysis, as not all of them were linked to a particular group, due also, certainly, to the low number of markers used. In most cases there was no correspondence between the markers identified by regression versus mapping. This can be explained by the low saturation of the map and also by the different number of markers used in the two procedures, reducing the precision of the inferences on the localization of QTLs in relation to the markers.

Faleiro et al. (2003) realized the QTL mapping for yield per common bean plant and found only one QTL linked to that trait, which is linked to marker rOC081820. The explanation for the identification of only one QTL is based on the fact that this character presents low heritability, which means a low precision in the measurements of the phenotypic values due to environmental effects.

The experimental detection of QTLs depends on a series of factors such as the analyzed cross (Beavis et al. 1991), the trait under evaluation (Edwards et al. 1992), the experimental design, and the resolution of the map in terms of the number of markers (Edwards et al. 1987). Naturally, differentiated results are obtained by each mapping realized under the specific conditions of each plant breeding program, so any obtained information has a greater chance of success if utilized under similar conditions to where it was obtained.

Results of this study confirm that it is very difficult to achieve the identification of a stable marker for grain yield, since this is a complex trait strongly influenced by the environment. The interaction observed between families with locations and with sowing times (Table 2) and the low correlations between those environments, once again, illustrate the great difficulty of finding stable QTLs for this character, insofar as changes in environments would lead to changes in the degree of importance (allele effect) of the countless genes that participate in the definition of the grain yield.

CONCLUSIONS

1. The interaction QTLs by locations is outstanding, but there are QTLs with a greater stability.

2. The multiple regression method identifies more QTL-linked markers than the process of composite interval mapping.

3. The most stable and promising markers for utilization in marker-assisted selection for grain yield were OPO-19 (1412 bp), OPO-20 (1585 bp), and OPN-07 (1445 bp).

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Mapeamento de QTLs para produtividade de grãos do feijoeiro comum em diferentes ambientes

RESUMO - *Os objetivos desse estudo foram identificar, em diferentes épocas e locais, QTLs de produtividade de grãos em feijoeiro comum, avaliar as interações de QTLs por ambientes e comparar os métodos de mapeamento e regressão múltipla. Foram avaliadas 196 linhagens recombinantes do cruzamento 'Carioca' x 'Flor de Mayo' nos anos de 1996, 1997 e 1998, em duas épocas e dois locais. Para a avaliação fenotípica foram conduzidos sete experimentos em látice quadrado simples 14 x 14. A interação QTLs por locais foi expressiva, mas foram identificados alguns QTLs com estabilidade. Não houve concordância entre os resultados apresentados pelos dois métodos de mapeamento. Os marcadores que se mostraram mais estáveis e promissores para serem utilizados na seleção assistida para produtividade de grãos foram OPO-19 (1412 pb), OPO-20 (1585 pb) e OPN-07 (1445 pb).*

Palavras-chave: *Phaseolus vulgaris*, produção, interação QTLs x ambientes, marcadores RAPD.

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