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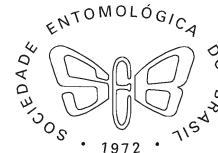
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No Correlation of Morpho-Agronomic Traits of *Phaseolus vulgaris* (Fabaceae) Genotypes and Resistance to *Acanthoscelides obtectus* (Say) and *Zabrotes subfasciatus* (Boheman) (Coleoptera: Chrysomelidae)

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Abstract

Resistance of common bean (*Phaseolus vulgaris*) varieties is an important tool to control *Acanthoscelides obtectus* (Say) and *Zabrotes subfasciatus* (Boheman) (Coleoptera: Chrysomelidae: Bruchinae) worldwide. However, bioassays to characterize the resistance of a genotype can be difficult to perform. Therefore, the current study sought to correlate the morpho-agronomic traits of *P. vulgaris* genotypes with their resistance to *A. obtectus* and *Z. subfasciatus* to facilitate genotype characterization. Bean samples of each genotype were infested with newly emerged insect couples, and the number of adults obtained in each genotype was quantified (value used as a resistance parameter). The resistance index was calculated by dividing the number of adults obtained in each genotype by the one obtained in the cultivar Bolinha, used as the standard for susceptibility. Fifty genotypes were evaluated for *A. obtectus* and 202 for *Z. subfasciatus*. All genotypes were characterized according to their resistance to each insect and 18 other morpho-agronomic traits, for a total of 19 descriptors. Principal component analyses did not show any correlation between insect resistance and the morpho-agronomic traits of the genotypes. Further, the thousand seeds weight (TSW), which is indicative of the genotype center of origin was tested considering genotypes from Mesoamerican with low TSW, while those from Andean with high TSW. Thus, the lack of correlation between genotype resistance and TSW indicates that resistance to *A. obtectus* and *Z. subfasciatus* in *P. vulgaris* is not related to the host center of origin.

Introduction

The common bean *Phaseolus vulgaris* (Fabaceae) originated from the Americas, and its domestication may have occurred independently through two distinct wild varieties—*P. vulgaris* var. *mexicanus* in the Mesoamerican region and *P. vulgaris* var. *aborigineus* in South America (Hancock 2004). These varieties differ in a

number of features and form hybrids that are mostly sterile (Graham & Ranalli 1997, Hancock 2004). Over the last 10,000 years, *P. vulgaris* may have acquired characteristics through its domestication, such as adaptation to neutral photoperiod, changes in plant architecture, the switch from perennial to annual behavior, production of larger and more tender seeds, and the development of more persistent pods (Hancock 2004).

According to Graham & Ranalli (1997), insects are the pests that cause the greatest losses in beans in some parts of the world. In Latin America, the predominant pests include the green leafhopper, chrysomelids, and bruchids; while in Africa, stem borers and bruchids are the most significant pests. In Brazil, the seed beetles *Acanthoscelides obtectus* (Say) and *Zabrotes subfasciatus* (Boheman) (Coleoptera: Chrysomelidae: Bruchinae) are the main pests of *P. vulgaris* under storage conditions and may coexist in the same warehouse (Vilca Mallqui et al 2013). These two species can be found in all regions of the world where beans are stored (Rossetto 1966), and together, they can cause losses of approximately 25% in stored beans (Gatehouse et al 1989). Damage caused by *A. obtectus* and *Z. subfasciatus* is similar, and the larvae of both pests bore into the seed cotyledons. Several individuals may be found within a single grain, which may result in the complete destruction of the seed (Athié & Paula 2002, Hill 2002, Lorini 2002).

The use of resistant varieties is usually considered the ideal solution for insect pest control among the various control methods available, as resistant varieties maintain pest populations below the economic loss threshold without causing disturbance or environmental pollution and without the need for specific knowledge from the farmer. Additionally, the use of resistant varieties is within the principles of Integrated Pest Management (Smith 2005).

The identification of resistant varieties may be based on parameters related to either the plant or the insect (Vendramim & Guzzo 2009, 2012), and bioassays for characterization of resistance can be time-consuming and labor-intensive. Moreover, such analyses depend on pest colonization in the laboratory as well as the availability of large amounts of the material to be characterized. Thus, the present study sought to correlate the resistance of *P. vulgaris* genotypes to *A. obtectus* and *Z. subfasciatus* with plant morpho-agronomic traits, with the goal to facilitate the characterization of resistant and susceptible genotypes.

Material and Methods

Insects

The seed beetles *A. obtectus* and *Z. subfasciatus* used in the bioassays were obtained from the stock colony maintained separately on the susceptible cultivar Bolinha under ambient conditions for several generations.

Bean genotypes

The *P. vulgaris* genotypes tested were obtained from the Bean Germplasm Bank of the Instituto Agronômico (IAC), Campinas, SP, Brazil. The genotypes studied included wild

genotypes, improved materials, cultivars, special seed strains, and others. All of them were multiplied simultaneously to promote uniformity. After harvest, grains were dried in a forced air oven at 28°C. Final moisture content (13%) was determined using the oven-drying method at 105 ± 3°C for 24 h (Brasil 2009). Then, dried grains were kept in a freezer at 0°C until their use to prevent degradation and to eliminate any previous infestation by insect species. Fifty genotypes were evaluated for *A. obtectus* (Table 1) and 202 for *Z. subfasciatus* (Table 2).

Evaluation of genotype resistance

For *A. obtectus*, circular transparent plastic pots (6 cm diameter and 2 cm height) were used for each genotype with each one containing 20 bean grains. Two 0–24-h-old couples were released per pot for oviposition for 3 days. Afterwards, adults were removed and the number of emerged adults in each pot was determined 50 days later. The mean value of emerged adults for the genotype was used as a resistance parameter. Five replicates were used for each genotype. The same procedure was followed for *Z. subfasciatus*; however, due to the large number of genotypes, they were randomly divided into five sets that were sequentially infested. The susceptible cultivar Bolinha was used in each set to allow the comparison among genotypes.

The resistance level of each genotype was determined according to the relative emergence (RE), which was calculated independently for *A. obtectus* and *Z. subfasciatus* using the following formula: $RE = (G/C) \times 100$; where *G* is the number of insects emerged in the respective genotype and *C* is the number of insects emerged in the control ('Bolinha') of the same set.

Statistical analysis

The RE and 18 botanical characteristics related to the plant, pods, and seeds of each genotype, as suggested by Singh (1989), Singh et al (1991), and Voysest et al (1994), were used in the analysis, for a total of 19 descriptors. The morpho-agronomic descriptors were the thousand seeds weight (TSW), primary seed color, seed brightness, seed shape, number of seed colors, seed halo color, seed profile, seed size, primary pod color, secondary pod color, pod length, pod width, pod profile, number of seeds in the pod, flower wing color, bracteole shape, growth habit, and number of days to flowering. All quantitative variables were categorized, and the results were subjected to principal component analysis using the GENES software (Cruz 2013) independently for *A. obtectus* and *Z. subfasciatus*, following Chiorato et al (2006).

Additionally, bean genotypes were grouped into categories according to their resistance to both beetle species.

Table 1 Average number of *Acanthoscelides obtectus* adults emerged from *Phaseolus vulgaris* genotypes at 50 days post-infestation, under confinement testing.

Acessions [Genotype name]	Adults ^a	Classification ^b
IAC 457 [Cavalo Amarelo] and IAC 612 [Bat-93]	14.4±0 (14.4)	HS
IAC 834 [FT Bonito], IAC 618 [Mex-54], IAC 21 [Baio da Praia], IAC 623 [G5686], IAC 937 [Contender], IAC 628 [Cal-143], IAC 528 [Type Baetão], IAC 678 [MAR 3], IAC 911 [Goytacazes], IAC 622 [G2858], IAC 114 [Bataav], IAC 121 [Type Rosinha], IAC 71 [Vermelhinho], IAC 568 [IAPAR-57], IAC 297 [I-114], IAC 624 [MAR 1], IAC 152 [STO ROSS], IAC 855 [Bolinha CB] , IAC 1 [Frijol Negro], IAC 596 [IAPAR-BAC 6 R. Bac.], IAC 610 [Oito e Nove], IAC 707 [IAC-Una], IAC 374 [Monte Negro-1349], IAC 478 [México-12], IAC 655 [A-55], IAC 630 [HF 465-63-1], IAC 28 [Uberabinha], IAC 597 [IAPAR-31], IAC 606 [Apetito Branco], IAC 544 [IAPAR-80], IAC 633 [RG 1342 CH60 (MA)], IAC 921 [Batista Brilhante (CB)], IAC 445 [B. Porrillo-70], IAC 586 [ARC-4], IAC 171 [Vermelho de Minas], IAC 112 [Type Baetão], IAC 674 [DOR-390], IAC 533 [Puebla-152], IAC 89 [Venezuela-350], IAC 179 [Manteiguinha], and IAC 251 [Costa Rica]	7.0±3.37 (13.6–1.6)	S
IAC 215 [Pirata-1], IAC 556 [Rico-23], IAC 816 [RAZ-49], IAC 749 [Car Marrom], IAC 525 [Type Baetão], IAC 584 [ARC-2], and IAC 615 [A-439 (R.Nem.)]	0.3±0.28 (0.6–0)	R

^a Overall mean±standard deviation considering all genotypes within a group. Values in parenthesis indicate the extreme values (amplitude) for the genotypes in the group.

^b Genotypes were classified according to their resistance level based on the 95% confidence interval (95% CI) for the *A. obtectus* adults emerged from the susceptible standard cultivar Bolinha. HS (highly susceptible)=values above the 95% CI; S (susceptible)=values within the 95% CI; R (resistant)=values below the lower limit of the 95% CI.

Genotypes were allocated to one of three resistance levels based on the 95% confidence intervals (95% CI) considering the mean number of emerged insects per genotype relative to the cultivar Bolinha, considered the standard for susceptibility, following the classification adopted by Silva *et al* (2014): resistant (R) for values below the lower limit of the 95% CI, susceptible (S) for values within the 95% CI, and highly susceptible (HS) for values greater than the upper limit of the 95% CI. For genotypes tested against *A. obtectus*, all of them were analyzed together. For genotypes tested against *Z. subfasciatus*, the procedure was done for genotypes within each set.

Results

The average number of *A. obtectus* adults obtained in the studied genotypes varied between 0 and 14.4 adults, resulting in RE values ranging from 0 to 189.5, respectively (data not shown). Principal component analysis revealed no correlation between genotype resistance to *A. obtectus* and any of the morpho-agronomic traits analyzed. The first axis explained 23.2% of the variation whilst the second axis explained 11.5%.

Based on the 95% confidence interval of the standard susceptible cultivar Bolinha, the tested bean genotypes were clustered into three groups: 2 genotypes were classified as highly susceptible, 41 as susceptible (including the standard susceptible cultivar Bolinha), and 7 as resistant (Table 1).

The average number of emerged adults of *Z. subfasciatus* from the tested genotypes ranged from 0 to 18.8. Considering that the genotypes of each group were compared to their respective control, the final RE values varied between 0 and

152.4 (data not shown). Similarly to what was found for *A. obtectus*, principal component analysis revealed no correlation between genotype resistance to *Z. subfasciatus* and the morpho-agronomic traits analyzed. The first axis accounted for 19.9% of the variation whilst the second axis for 11.3%.

Based on the 95% confidence interval of the standard susceptible cultivar (Bolinha), resistance of bean genotypes to *Z. subfasciatus* resulted in the formation of 3 clusters with 1 genotype classified as highly susceptible, 110 genotypes classified as susceptible (including the standard susceptible cultivar Bolinha), and 91 as resistant (Table 2).

Discussion

The RE based on the number of insects emerged 50 days after infestation alone is not a solid indicator for selection of resistant genotypes, although RE values directly reflect the sum of the possible types and causes of genotype resistance. A low number of emerged adults may be due to genotype antibiosis or to antixenosis for feeding and/or oviposition. These factors could result in high immature mortality, prolonged development, and/or reduced egg laying, all leading, singly or jointly, to a reduced number of adults. Moreover, Rêgo *et al* (1986) found that the assessment of emerged populations was one of the most consistent parameters for determining the resistance and/or susceptibility of *P. vulgaris* genotypes to *Z. subfasciatus*.

It was also observed that not all resistant genotypes to *Z. subfasciatus* were resistant to *A. obtectus* and vice versa. For example, the genotype IAC 215, which was found to be resistant to *A. obtectus*, was classified as susceptible to

Table 2 Average number of *Zabrotes subfasciatus* adults emerged from *Phaseolus vulgaris* genotypes at 50 days post-infestation, under confinement testing.

Set	Acessions [Genotype name]	Adults ^a	Classification ^b
1	IAC 674 [DOR-390]	14.2 (14.2)	HS
	IAC 478 [México-12], IAC 855 [Bolinha CB] , IAC 374 [Monte Negro-1349], IAC 112 [Type Baetão], IAC 834 [FT-Bonito], IAC 297 [I-114], IAC 1 [Frijol Negro], IAC 607 [Barbunya], and IAC 445 [B. Porrillo-70]	10.9±0.92 (12.4–9.8)	S
	IAC 635 [RIZ-30], IAC 597 [IAPAR-31], IAC 749 [Car Marrom], IAC 611 [Alemão], IAC 556 [Rico-23], IAC 678 [Mar 3], IAC 628 [Cal-143], IAC 596 [IAPAR-BAC 6 R. Bac.], IAC 615 [A-439 (R.Nem.)], IAC 618 [Mex-54], IAC 121 [Type Rosinha], IAC 21 [Baio da Praia], IAC 683 [Xan-251], IAC 49 [IAC Carioca], IAC 624 [MAR 1], IAC 521 [Chileno/Preto], IAC 114 [Bataav], IAC 457 [Cavalo Amarelo], IAC 630 [HF 465-63-1], IAC 179 [Manteiguinha], IAC 612 [Bat-93], IAC 533 [Puebla-152], IAC 623 [G5686], IAC 75 [Bagajo], IAC 672 [IAPAR 81], IAC 588 [Ovo de Codorna Tynaga Vermelho], IAC 568 [IAPAR-57], IAC 595 [CNF-86-9], IAC 528 [Type Baetão], IAC 83 [Type Baetão], IAC 544 [IAPAR-80], IAC 614 [Pinto-114], IAC 577 [Jalo], IAC 71 [Vermelhinho], IAC 682 [Xan-159], IAC 171 [Vermelho de Minas], IAC 622 [G2858], IAC 427 [Safira], IAC 606 [Apetito Branco], IAC 921 [Batista Brilhante (CB)], IAC 911 [Goytacazes], IAC 525 [Type Baetão], IAC 587 [Vermelho Desconhecido], IAC 1081 [CF-840743], Ento A, IAC 621 [A-449], IAC 634 [AND-277 (MA)], IAC 570 [MD-806], IAC 251 [Costa Rica], IAC 610 [Oito e Nove], IAC 584 [ARC-2], IAC 2 [Sanilac], IAC 583 [ARC-1], and IAC 818 [RAZ-59]	5.8±2.7 (9.6–0)	R
2	IAC 89 [Venezuela-350], IAC 633 [RG 1342 CH-60 (MA)], IAC 28 [Uberabinha], IAC 582 [IAPAR-44], IAC 172 [IPA-2], IAC 576 [EMP-81], IAC 465 [Porrillo Sintético], IAC 208 [44/71-85], IAC 385 [IAC Carioca Tybatã], IAC 937 [Contender], IAC 152 [STO ROSS], IAC 707 [IAC-Una], IAC 655 [A-55], IAC 835 [Bolinha CB] , IAC 211 [Retinto Santa Rosa], IAC 415 [73 VUL-3205], IAC 1081 [CF-840743], IAC 125 [Chumbinho-63], IAC 575 [RAI-76], IAC 215 [Pirata-1], IAC 677 [DOR-482], Ento B, IAC 559 [Iraí], IAC 602 [R.Bac.], IAC 203 [Rosado-14 (mulatinho)], IAC 186 [Coco Blanchi], IAC 627 [Amendoim], IAC 17 [Rosinha], IAC 1116 [PI 417660], IAC 625 [mar/02], IAC 159 [Aete-2], IAC 225 [México-309], IAC 249 [Preto Uberabinha], and IAC 681 [Xan-112]	7.4±2.55 (12.8–3.4)	S
	IAC 445 [B. Porrillo-70], IAC 586 [ARC-4], IAC 35 [ECU-208], IAC 816 [RAZ-49], and IAC 610 [Oito e Nove]	0.8±0.92 (2.2–0)	R
3	IAC 550 [Caeté (preta)], IAC 73 [Rosinha], IAC 316 [Mamoninha], IAC 546 [Gordo Branco], IAC 385 [México-488], IAC 239 [México-435], IAC 638 [TO], IAC 90 [B. Turrialba], IAC 835 [Bolinha CB] , IAC 578 [Tarumã], IAC 566 [Pijão], IAC 56 [ECU-311], IAC 1103 [PR-733639], IAC 679 [Turrialba-1], IAC 1062 [PR-733612], IAC 558 [Mulata Gorda], IAC 637 [TU], IAC 373 [México-498], IAC 107 [Guatemala], IAC 236 [Preto-208], IAC 112 [Type Baetão], IAC 832 [Pérola], IAC 567 [IAPAR-65], IAC 685 [G-5207], and IAC 254 [Quarenteno]	10.7±1.8 (14.6–7.8)	S
	IAC 481 [Carioca MG], IAC 492 [G11796], IAC 585 [ARC-3], and IAC 819 [RAZ-55]	4.2±2.83 (6–0)	R
4	IAC 49 [Carioca-80], IAC 569 [IAPAR-72], IAC 354 [Preto-146], IAC 646 [Mex-279], IAC 616 [A-443 (R.Nem.)], IAC 696 [RAPÉ], IAC 186 [Coco Blanchi], IAC 32 [Rosinha-127], IAC 600 [G4000], IAC 673 [MAM-38], IAC 835 [Bolinha CB] , IAC 462 [Branco Graúdo], IAC 605 [LP-88-175], IAC 672 [IAPAR-81], IAC 73 [Type Rosinha], IAC 654 [A-21], IAC 589 [Sangre-Toro], IAC 592 [Cal-153], IAC 389 [Small White 59 Preto], IAC 603 [R.Bac.], IAC 863 [Pirapora (CB)], and IAC 649 [A-211]	10.7±2.16 (13.6–5.8)	S
5	IAC 72 [Alemão], IAC 325 [Rosinha G2], IAC 676 [DOR-476], IAC 599 [AFR-188], IAC 835 [Bolinha CB] , IAC 350 [Preto-167], IAC 15 [Type Rosinha], IAC 598 [EMP-408], IAC 1052 [A-285], IAC 571 [A-300], IAC 24 [Rosinha-145-1-1], IAC 71 [Vermelhinho], IAC 398 [Cornell-49242], IAC 643 [PI-207262], IAC 25 [Leg. Floresta-5], IAC 249 [Preto Uberabinha], IAC 619 [Flor de Mayo], IAC 708 [IAC-Maravilha], IAC 590 [Real Mexican-34], IAC 368 [Porrillo-1], IAC 827 [Carioca Comum], IAC 636 [G916], IAC 160 [Uberabinha], and IAC 608 [Pompador]	16.5±1.28 (18.8±14.8)	S
	IAC 653 [Michelite], IAC 196 [HIBC], IAC 222 [Venezuela-42-5-1], IAC 650 [Mex-222], IAC 348 [Preto do Pocrone], IAC 680 [Durango-222], IAC 497 [Terra Velha], IAC 626 [FEB-29], IAC 684 [AND-279], IAC 74 [Enxofre (Diacol Mina Pent)], IAC 675 [DOR-391], IAC 349 [Pato de Minas], IAC 593 [EMP-407], IAC 620 [Pan-72], IAC 296 [Mulatinho], IAC 121 [Type Rosinha], IAC 617 [Bat-332], IAC 681 [Xan-112], IAC 604 [IAPAR-14], IAC 443 [Canário-101], IAC 572 [Jamapa], IAC 837 [IAC Carioca Eté], IAC 149 [Type Baetão], IAC 99 [México-115], IAC 416 [Rosado-13], IAC 138 [Leg. Rosinha], IAC 439 [B-Puebla-40], and IAC 559 [Iraí]	11.7±2.26 (14.6–7.4)	R

^a Overall mean±standard deviation considering all genotypes within a group. Values in parenthesis indicate the extreme values (amplitude) for the genotypes in the group.

^b Genotypes were classified according to their resistance level based on the 95% confidence interval (95% CI) for the *Z. subfasciatus* adults emerged from the susceptible standard cultivar Bolinha within each set. HS (highly susceptible)=values above the 95% CI; S (susceptible)=values within the 95% CI; R (resistant)=values below the lower limit of the 95% CI.

Z. subfasciatus, and the genotype IAC 457, which was considered resistant to *Z. subfasciatus*, was classified as highly susceptible to *A. obtectus*. These results corroborate data already available for the tested insect species (Guzmán-Maldonado *et al* 1996, Hartweck *et al* 1997) and the widely available literature showing that plant resistance to insects is species specific (Lara 1991, Panda & Khush 1995, Smith 2005). Differences in bean resistance to *A. obtectus* and *Z. subfasciatus* were related to the carbohydrate and protein fractions of *P. vulgaris* (Gatehouse *et al* 1987). While the carbohydrate fraction of a bean strain severely affected the development of *A. obtectus*, but not of *Z. subfasciatus*, the protein fraction of the same strain affected the development of *Z. subfasciatus* but had little or no effect on *A. obtectus* (Gatehouse *et al* 1987). These results indicate that the basis for resistance to these two pests in the strain tested was different and associated to multiple resistance mechanisms (Minney *et al* 1990). Thus, it is also possible to infer that genotypes such as IAC 525, IAC 556, IAC 584, IAC 615, IAC 749, and IAC 816, which were resistant to both *A. obtectus* and *Z. subfasciatus* in the present work, possess more than one resistance mechanism.

Arcelin, a toxic protein to several insects including *Z. subfasciatus* (Cardona *et al* 1990, Pereira *et al* 1995, Wanderley *et al* 1997, Barbosa *et al* 1999, 2000a, b, 2002, Mazzonetto & Vendramim 2002, Baldin & Pereira 2010), but with little or no effect on *A. obtectus* (Guzmán-Maldonado *et al* 1996, Hartweck *et al* 1997), is also available in the genotypes IAC 583, IAC 584, IAC 816, IAC 818, and IAC 819, all of them classified as resistant to *Z. subfasciatus*. This may explain the differences in resistance observed for the two species studied here. Arcelin production in *P. vulgaris* is mediated by eight known variants, termed Arc-1 to Arc-8 (Acosta-Gallegos *et al* 1998, Lioi *et al* 2003, Zaugg *et al* 2013), and these variants belong to the lectin family, which also includes phytohemagglutinins and α -amylase inhibitors.

The lack of correlation we reported among bean morphological traits and bean susceptibility to *A. obtectus* and *Z. subfasciatus* has also been reported by Guzmán-Maldonado *et al* (1996). However, these authors were able to demonstrate a negative correlation between the lectin content (a chemical characteristic) in the seed and the oviposition and adult emergence of *Z. subfasciatus*. Although an association between the host bean origin and resistance to a pest has been demonstrated for the pathogen *Colletotrichum lindemuthianum* (Chiorato *et al* 2006), we were not able to establish such correlation in our study. Pathogen-host associations are more specific than herbivore-host associations, and this is most likely the reason why there has not been an apparent co-evolution between *P. vulgaris* and *A. obtectus* or between *P. vulgaris* and *Z. subfasciatus*, in contrast to that observed between *P. vulgaris* and *C. lindemuthianum*.

Thus, it appears that the botanical traits analyzed in the current study in regards to the flower, pod, seed, and plant phenology were not good indicators of genotype resistance to *A. obtectus* and *Z. subfasciatus*. In fact, it was not expected that characteristics such as flower wing color or bracteole shape, for instance, would be directly related to resistance to the tested Bruchinae species. However, it could be possible to a single gene to have multiple phenotypic effects, encoding both a given morpho-agronomic characteristic and a seed beetle resistance trait, or that resistance genes may be linked to other genes conferring those characteristics.

Among the morphological characters used in the present work, the TSW was the one to indirectly provide information about the origin of genotypes. Genotypes with TSW values greater than 41 g are usually of Andean origin, while those with TSW values lower than 41 g are of Mesoamerican origin (Gepts 1984, Gepts & Bliss 1986). According to Hancock (2004), these are the two main centers of origin of beans. As found for both species, *A. obtectus* and *Z. subfasciatus*, the scatter plots of resistance to the insects did not form clusters similar to the genotype TSWs, showing the lack of correlation between these characteristics and indicating that resistance to *A. obtectus* and *Z. subfasciatus* is not related to the genotype center of origin.

Both *A. obtectus* and *Z. subfasciatus* are originally from Central and South Americas (Bondar 1936, Athié & Paula 2002, Hill 2002) and may have coevolved with common bean. There are wild genotypes and improved materials among the genotypes we tested, whose hybridization levels were not determined. The patterns of the protein phaseolin in cultivated beans are similar to those from wild common beans and landraces from Middle America and the Andean region of South America, supporting the theory that these two regions are the primary areas of bean domestication (Gepts *et al* 1986). However, phaseolin does not have detrimental effects on seed beetles. Nevertheless, Guzmán-Maldonado *et al* (1996) did not find correlation between seed protein content and resistance to *A. obtectus* and *Z. subfasciatus*. When principal component analysis was used to explain the genetic variability among bean accessions, the three components that explained 83% of the variation did not include any physical or chemical seed trait (CIAT 1979 apud Graham & Ranalli 1997).

Based on our results, we can conclude that there is no correlation between the morpho-agronomic traits of the 50 and 202 bean genotypes tested and their resistance to the seed beetles *A. obtectus* and *Z. subfasciatus*, respectively. This indicates that bioassays, even being time-consuming and labor-intensive, are essential to characterize resistant varieties. The causes for bean genotype resistance to *A. obtectus* and *Z. subfasciatus* are likely independent and not related to the genotype center of origin.

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