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Inheritance of the Resistance to *Acanthoscelides obtectus* (Say.) in a Heterogeneous Inbred Families Population of Common Bean (*Phaseolus vulgaris* L.)

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Abstract: The bean weevil *Acanthoscelides obtectus* is one of the world's main pests of stored beans. The heterogeneous inbred family (HIF) population of near-isogenic lines (NILs) could be an exceptional strategy to study the inheritance of the resistance against *A. obtectus*. We developed a HIF population of 148 NILs of R-bufa-80-12. The objectives of this research were as follows: (1) to study and understand the genetics of the attack resistance to *A. obtectus* in a HIF population and (2) to identify the best lines to provide weevil resistance. The pure lines of the HIF population showed a great variability for all the analyzed traits. The traits studied in this research have a normal distribution showing continuous variation, so they are considered to be quantitatively inherited. The heritabilities for resistance traits were low and very low, ranging from 0.09 to 0.17. The heritability for 100 seed weight was the highest, with a significant value of 0.90. The best lines of the HIF population for resistance to *A. obtectus* comprised Line-45, Line-129, Line-124, Line-142 and Line-47. In general, these lines presented lower preference of adults, and lower consumption in grams and in percentages. However, lines 45 and 129 are the most interesting from a commercial point of view because they combine resistance and seed weight.

Keywords: bean weevil; common bean; HIF population; NILs; inheritance; weevil resistance

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1. Introduction

Common bean production is affected by biotic and abiotic factors. Some of the main biotic constraints involve post-harvest losses. These are caused by the bruchid species *Acanthoscelides obtectus* Say and *Zabrotes subfasciatus* Boheman. The common bean weevil, *A. obtectus*, is a devastating insect pest capable of causing severe common bean crop losses in many regions of the world [1,2]. It is a neotropical, multivoltine pest, distributed across the five continents and mainly in Latin America and Africa, and its place of origin is Central America [3]. Many species of the *Acanthoscelides* genus are found around the world. Since the middle of the 1980s, *A. obtectus* has expanded its distribution in cooler countries such as Russia [4].

There are many ways to control or reduce the damage of the bean weevil, from physical methods such as freezing, use of chemical products, farming practices or the use of natural enemies to methods such as the use of predatory mites including *Blattisocius tarsalis*, *Amblyseius swirskii* and the larval parasitoids *Anisopteromalus calandrae* and *Lariophagus distinguendus*. Nevertheless, the most effective control strategy is the use of resistant genotypes. Some of these practices have a negative impact on the quality of the seeds and the environment [5,6], but the development of resistant bean lines to *A. obtectus* attacks would be very cheap, and safe for humans and the environment [7].

Several steps must be carried out to develop resistant varieties. The first of these is to seek sources of resistance, highlighting that the available sources of resistance to weevil attack are scarce. Some reports mention that wild bean Mexican genotypes have been identified as highly resistant to this plague, such as the accession, G12952 [8] and QUES [9], and some Tepary beans (*Phaseolus acutifolius*), such as G40199 [10], T-amarillo and T-negro, which showed antixenosis, resistance and tolerance to *A. obtectus* infestation and demonstrated that both could be used for common bean breeding [7]. On the other hand, the Turkish common bean varieties Akdag, Akman-98, Noyanbey-98 and Kirikkale were found to be more resistant against *A. obtectus* attacks among 13 genotypes. Noyanbey-98 and Akman-98, with higher protein ratios, were found to be resistant against *A. obtectus*. Protein content, thicker seed testa, a low infection rate, and adult emergence are important parameters for resistance of genotypes [11]. The second step is to know the inheritance of the traits related to resistance. It will allow us to design the best selection program to improve resistance against weevil attacks. Consequently, little is known about the inheritance and mechanisms responsible for resistance or tolerance to *A. obtectus* in common beans. Only three QTL mapping reports [5,12,13], and two inheritance studies have been reported in biparental crosses, comprising a segregation 15S: 1R by Kornegay and Cardona [8] and 3R: 1S by Jiménez-Galindo et al. [14]. In the first study of QTLs, the authors found three QTLs to have resistance against *A. obtectus* on chromosomes Pv04 and Pv06. One of the QTLs on Pv04, named AO4.1SA, was previously reported as the arcelin, phytohemagglutinin and a-amylase (APA) resistance locus. The other two QTLs with resistance against *A. obtectus* are new [12]. In the second study of the QTL analysis using 157 RILs and 2,234,769 SNPs, the findings indicated a quantitative inheritance of the bruchid resistance trait controlled by polygenes. In addition, authors located a new quantitative trait locus on chromosome 6. Moreover, this locus was further delimited to an interval value of 122.3 kb between SSR markers I6–4 and I6–16. This region comprised five genes, with Phvul.006G003700 being among them, which encodes a bifunctional inhibitor and may be a potential candidate gene for bruchid resistance [5]. In the third study, Bornowski et al. [13] found loci and candidate genes underlying biotic stress resistance including resistance to bruchids, common bacterial blight, Fusarium wilt and the bean common mosaic necrosis virus. In the case of the inheritance of resistance to *A. obtectus*, two biparental crosses have been reported by Kornegay and Cardona [8]. Two recessive complementary and independent genes were suggested to be responsible for the number of days to adult emergence of *A. obtectus* in two F_2: A36 × G12952 and Pijao × G12952 with the segregation ratio of 15 [susceptible (short period to adult emergence)]:1 [resistant (long period)], and the resistance was found to be in cotyledons. Furthermore, in two biparental populations studied by Jiménez-Galindo et al. [14], a major gene was suggested to be responsible for the number of adults of the first generation in two F_2: P-saltillo × T-amarillo and T-amarillo × T-cafe with the segregation ratio of 3 [resistant lines (with zero adults of the first generation)]:1[susceptible line (with one or more first-generation adults)] (R:S). In contrast to the research reported by Kornegay and Cardona [8], in the last study we analyzed, resistance was found in the testa of resistant lines.

The bean weevil is highly adaptive, and its infection starts in the field and continues during storage, where it causes the biggest damage. Its preference host is *P. vulgaris*, but it also infects *P. lunatus* and other grain legumes. Larvae burrow into the seed to feed and metamorphose from larva to adult within the seed. Adults cause no direct damage to the common beans in storage because their consumption is imperceptible [7,15]; however, females can lay up to 60 eggs and these progenies will feed off the seeds causing the most significant damage [15].

Common bean (*Phaseolus vulgaris* L.) is a staple food in many developing regions, mainly in Latin America and Africa. This legume does not require any industrial processing to be consumed. Its grain is used as auto consumption and the spare grain is used as a cash source. The area of common bean harvested in 2021, globally, exceeded 36.6 million hectares, with a total production of 29.02 million tons [16]. In Mexico, common bean is the second most important crop by sown area after maize (*Zea mays* L.), with more than 1,615,875 hectares with a production of 1,157,643 tons in 2021 and an average yield of 0.716 kg per hectare [17]. Nutritionists characterize beans as an exceptional food resource because of their high protein content and its combination of carbohydrates, dietary fiber and minerals (particularly iron and zinc) [18]. This legume also contains thiamine and some neuroprotective and anticancer properties [19]. However, to take care of the nutritional and nutraceutical properties of the common bean, excellent storage care is required. Storage plagues damage the grains, reducing the quality and quantity of the already low production. Pests causing post-harvest loss may surpass 20% in underdeveloped and tropical nations due to insufficient management measures and environmental factors that allow pests to reproduce quickly [20]. Some studies have reported losses around the 7–40% mark [21]. This equates to a loss of 1.59 to 9.12 million tons according to the global common bean production in 2013 [7] of 1.59 to 11.6 million tons in 2021 [16]. However, other authors have reported losses in the range of 20 to 100% in stored common beans [22,23].

The use of resistant varieties is an important alternative within an integrated pest control, but the degree of resistance in commercial common bean cultivars is low; therefore, it is important to look for new sources of resistance to the weevil that hold possible commercial value. In this sense, the Rosa Bufa (R-bufa) genotype is interesting as it showed tolerance to drought when was evaluated with PEG-6000 [24] as well as in field experiments [25], where it also stands out for its precocity. The effect of moisture restriction on morphological and physiological characteristics of the grain in R-bufa is known [26], and the humidity restriction and high night temperature significantly and synchronously accelerates leaves and pod senescence in cv. R-bufa while, in contrast to the leaves of cv. OTI, the loss of green color began several days earlier than in pods [27]. In addition, heterogeneous inbred families (HIFs) within R-bufa that segregate for resistance to *A. obtectus* were identified, and it is an ideal material to study the inheritance of resistance to bean weevils as well as a means to develop resistant material that can be easily marketed. The advantage of HIF populations is that they are near-homozygous in the genome, except in the region studied by [28].

The objective of this research was to study the inheritance of resistance to *Acanthoscelides obtectus* in a HIF population of R-bufa-80-12 common bean and to identify the best lines of the HIF population generated to provide weevil resistance in common bean breeding for commercial genotypes that could reduce pesticide applications to control *A. obtectus* in stored and field beans, which is a very cheap and safe way for controlling this pest.

2. Materials and Methods

2.1. Plant Materials

2.1.1. Selection of the Parent from the HIF Population

The HIF method was used to develop the HIF population that is currently under study by [29]. In 2016, 21 seeds of R-bufa were sown in the greenhouses of the Misión Biológica de Galicia—CSIC (Pontevedra, Spain). The seeds of each plant were harvested individually. An evaluation of resistance to *A. obtectus* was carried out in the offspring of the following four families: R-bufa-80-2, R-bufa-80-4, R-bufa-80-12 and R-bufa-60.

For the evaluation of resistance, a bioassay was carried out in 2017 in the laboratories of the Misión Biológica de Galicia—CSIC. Each seed was placed in an individual pot with 5 females and 5 males of *A. obtectus*. The number of first-generation adults that emerged was recorded. The seed was considered resistant (R) if no adult emerged and susceptible (S) if 1 or more adults had emerged. The results of the different families comprised R-bufa 80-2: 7 R, 0 S; R-bufa-80-4: 6 R, 1 S; R-bufa-80-12: 5 R, 2 S; and R-bufa-60: 10 R, 0 S. With these results, the R-bufa-80-12 family was chosen as a parent from the HIF population because it showed the greatest variability for resistance/susceptibility to *A. obtectus*.

2.1.2. HIF Population Development

The variety R-bufa-80-12 was used to develop the HIF population. R-bufa-80 and T-amarillo were used as a susceptible and resistant control, respectively (Table 1).

In 2018, the seven seeds of offspring from the R-bufa-80-12 family were sown in Bachiniva, Chihuahua (Mexico). In total, 148 seeds were harvested; they were the origin of the 148 lines of the HIF population. In 2019, the 148 seeds were sown again to increase the number of seeds and for the establishment of the 148 lines. A scheme of the development process of the HIF population is shown in Figure 1.

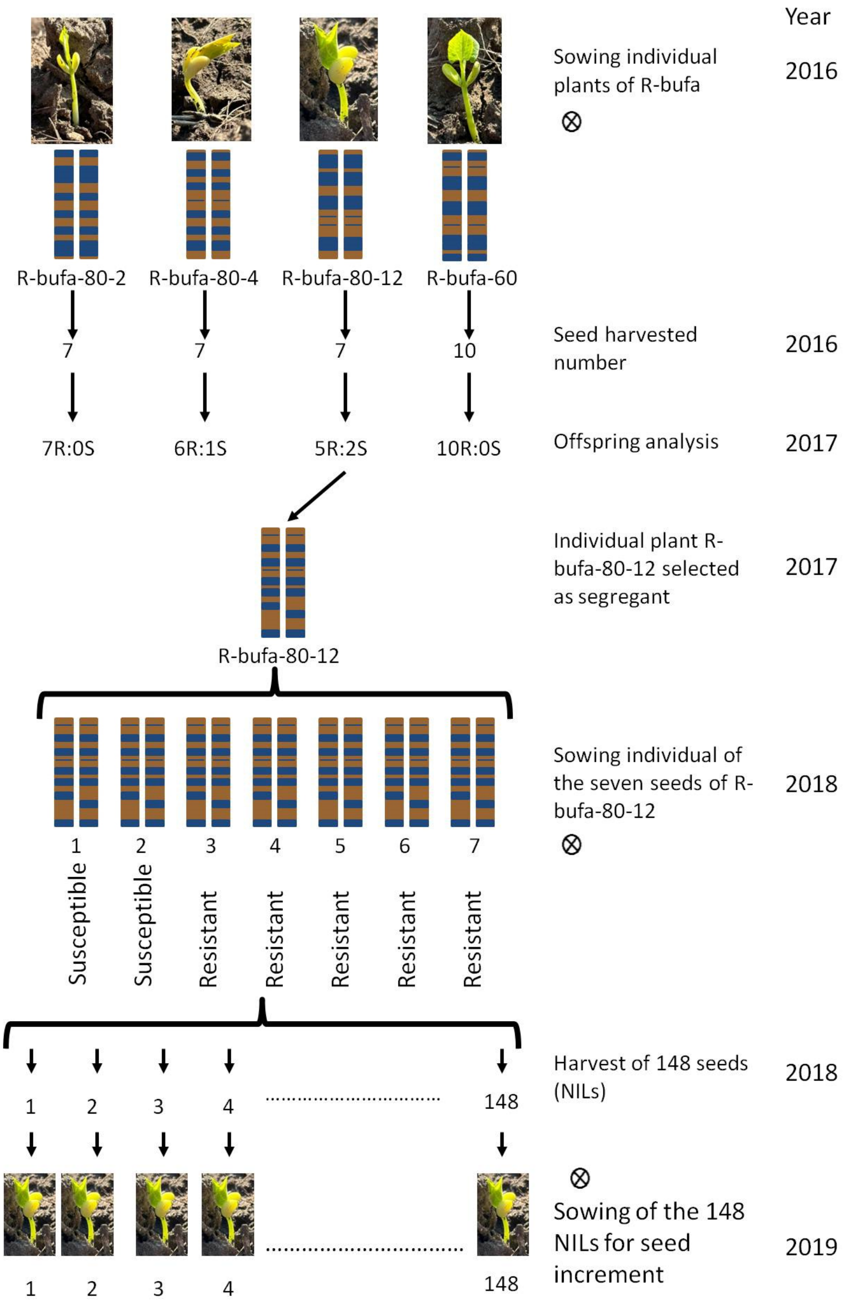

Figure 1. Scheme of obtaining 148 NILs of R-bufa-80-12 genotype.

Table 1. Characteristics of two common bean genotypes, the parental and the family genotype, used to create the HIF population analyzed for resistance to *A. obtectus* and the resistant control T-amarillo genotype.

Genotype	Species	Growth Habit	Resistance Level [1]
R-bufa-80	*P. vulgaris*	II	Susceptible
R-bufa-80-12	*P. vulgaris*	II	Segregant
T-amarillo	*P. acutifolius*	III	Resistant

[1] The resistance of T-amarillo is shown in Jiménez et al. [7] and Jiménez-Galindo et al. [14]. Growth habit type II: indeterminate growth habit; vegetative terminal bud on main stem and branches; node and leaf production occur after flowering commences. Both main stem and branches are strong and upright. Growth habit type III: indeterminate growth habit. Branches relatively weak and open, semi-prostrate or twining. Pod load largely concentrated in the basal part of the plant. The maximum yield is realized in monoculture [30].

2.2. Experimental Design

The 148 lines of the HIF population along with R-bufa-80, parents of the HIF population, and T-amarillo, were used as a resistant control [7,14] and were evaluated in two bioassays for resistance to *A. obtectus*. The seeds used from the lines and the parent and control were harvested in 2019 in Bachiniva, Chihuahua. The adults of *A. obtectus* used in this experiment were recollected in 2019 in the same location. The genotypes were evaluated using a 15 × 10 simple lattice design with two replications. Both experiments started on 12 April 2021 and ended on 11 February 2022. The 150 accessions (148 HIF population, 1 parent and 1 control) were evaluated in plastic bottles of 5 cm in diameter and 5 cm in height, with 10 seeds per repetition and genotype. The bottles were left open inside a warehouse highly infested with *A. obtectus*. Four aleatory samples of 1 m^2 size were taken to determine the level of infestation. On average, 367 adults were found per square meter. The adults of *A. obtectus* were kept in contact with the seeds of the pure lines for 10 months. The following variables were measured: (1) weight of 100 seeds, obtained with the following formula: weight of 100 seeds = 100 × initial weight of 10 seeds ÷ 10; (2) consumption in grams, obtained by subtracting the final seed weight from the initial weight; (3) consumption in percent, obtained with the following formula: consumption % = (initial weight − final weight) × 100 ÷ initial weight; and (4) preference (number of adults in a bottle), determined by accounting the number of adults per repetition at the end of the experiments.

2.3. Statistical Analysis

An analysis of variance and a comparison of means were carried out for the 148 seeds of the HIF population plus the original variety and the resistant control for all traits. Genotypes were considered as fixed effects while bioassays, replicates, blocks and all interactions were considered random factors [31]. The distribution of all resistance characteristics and the weight of 100 seeds were analyzed using the univariate procedure (PROC UNIVARIATE) of SAS 9.4 [31]. Heritabilities (h^2) across environments were estimated for each trait on a family mean basis as described by Holland et al. [32]. Genetic and phenotypic correlations between traits were calculated following Holland's instructions [33]. All previous analyses were performed with SAS software 9.4 [31].

3. Results

3.1. Mean, Ranks and Heritabilities of the HIF Population

Significant differences were found for almost all the variables studied between the control of T-amarillo and the line that gave rise to the HIF population (R-bufa-80), except for the variable of preference and the number of adults in the bottle at the end of the experiments. The population showed wide variability for the traits studied, from 16.9 to 29.5 g for 100 seed weights, from no consumption up to 0.763 g or 29.5% of the initial weight, and 1.25–9.72 for preference, when including the number of adults in the bottle at the end of the experiments. The heritabilities for resistance traits were low and very low, ranging from 0.09 to 0.17 and were not significant. The heritability for 100 seed weights was the highest, with a significant value of 0.90 (Table 2).

Table 2. Mean, range, least significant difference (LSD) and heritability (h^2) of the HIF population for resistance to *A. obtectus* for 100 seed weights and resistance traits.

	Seed Trait	**Resistance Traits**		
	100 Seed Weights (g)	**Consumption (g)**	**Consumption (%)**	**Preference (n)**
NILs				
Mean	24.5	0.284	11.5	4.60
Range	16.9–29.5	−0.060–0.763	−2.5–29.5	1.25–9.72
LSD	2.00	0.353	14.03	4.49
h^2	0.90 ± 0.02	0.17 ± 0.14	0.16 ± 0.14	0.09 ± 0.12
Parent and control				
R-bufa-80	23.5 ^{a}	0.479 ^{a}	18.5 ^{a}	8.25 ^{a}
T-amarillo	14.2 ^{b}	0.020 ^{b}	1.4 ^{b}	4.00 ^{a}
LSD	1.8	0.273	11.3	4.36

The heritabilities (h^2) for each trait were estimated according to Holland et al. [32]. Means followed by the same letter are not significantly different ($p < 0.05$).

3.2. Genetic and Phenotypic Correlations

Positive and significant genetic correlations were found between consumption in grams and percentage of consumption (0.94). Low, positive and significant phenotypic correlations were also found between 100 seed weights and consumption (g) (0.15), and between preference (n) and consumption (g and %) (0.20). Finally, a significant positive correlation between consumption (g) and consumption (%) (0.99) was found (Table 3).

Table 3. Genetic (below) and phenotypic (above) correlation coefficients between agronomic traits and resistance to *A. obtectus*.

	100 Seed Weight (g)	**Preference (n)**	**Consumption (g)**	**Consumption (%)**
100 seed weight (g)		0.06	0.15 *	0.06
Preference (n)	0.30		0.20 *	0.20 *
Consumption (g)	0.45	2.9		0.99 *
Consumption (%)	0.12	2.7	0.94 *	

* Correlation coefficients that exceed twice their standard error.

3.3. Distributions Analysis

The pure lines (NILs) of the HIF population showed a great variability for all the traits analyzed, as visualized in the ranges of all traits (Table 2). All traits studied in this research have a normal distribution showing continuous variation, so they are considered to be quantitatively inherited (Figure 2). However, variability was found for the traits studied, which allows selecting lines with a high level of resistance within the R-bufa-80-12 HIF population.

3.4. Mean Comparison of the Five Best and the Five Worst Lines for Resistance to *A. obtectus*

The means of all the lines of the HIF population for all the traits studied are shown in Table S1. The best lines within the HIF population for resistance to *A. obtectus* were Line-47, Line-124, Line-129, Line-45 and Line-142. These lines presented consumption in grams (< 0.08 g) and consumption in percent (4.0%) of the seed. These lines were compared with the lines that had the worst response for resistance to *A. obtectus*: Line-102, Line-3, Line-62, Line-98 and Line-63 with a consumption of >0.6 g and a consumption of >25.0%. T-amarillo showed a consumption of 0.022 g and 1.5%. R-bufa-80 showed a consumption of 0.357 g and 15% (Figure 3).

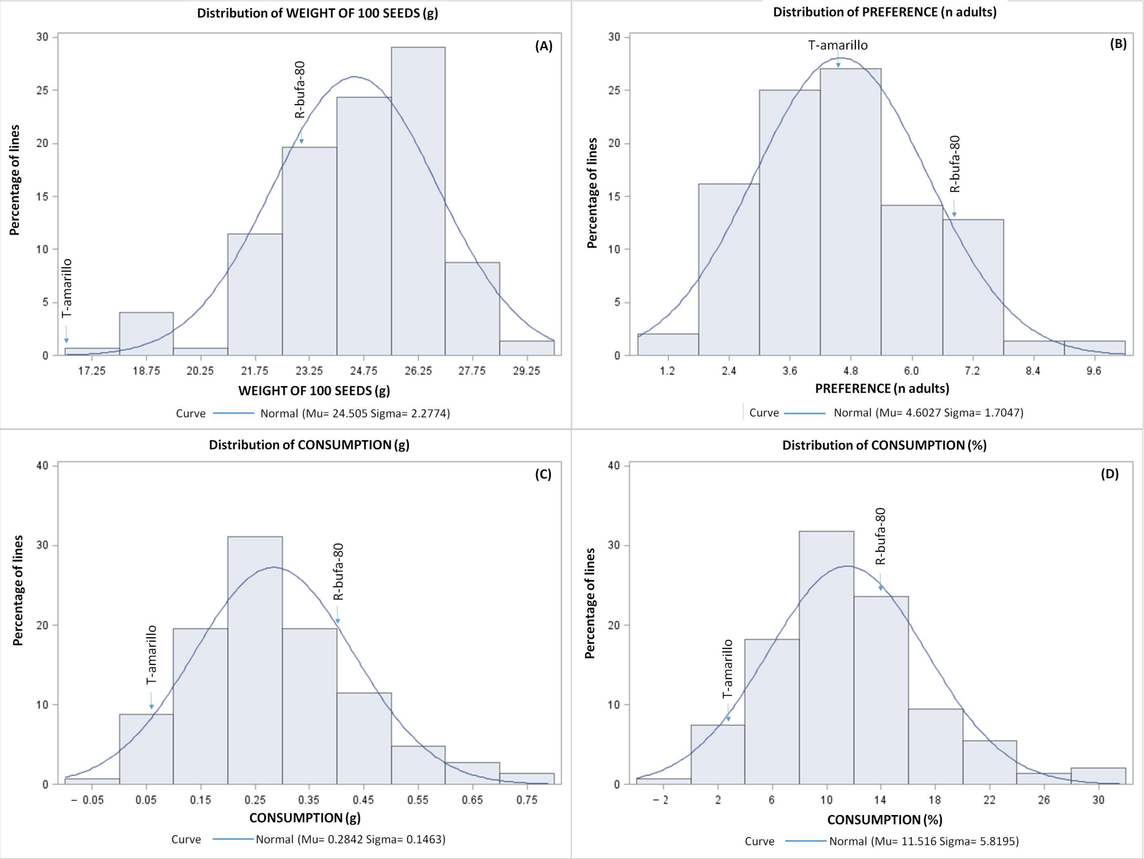

Figure 2. (**A**) Distribution analysis for 100 seed weights. (**B**) Preference (n adults per repetition at the end of experiments). (**C**) Consumption in grams. (**D**) Consumption in percent of 148 NILs of the HIF population.

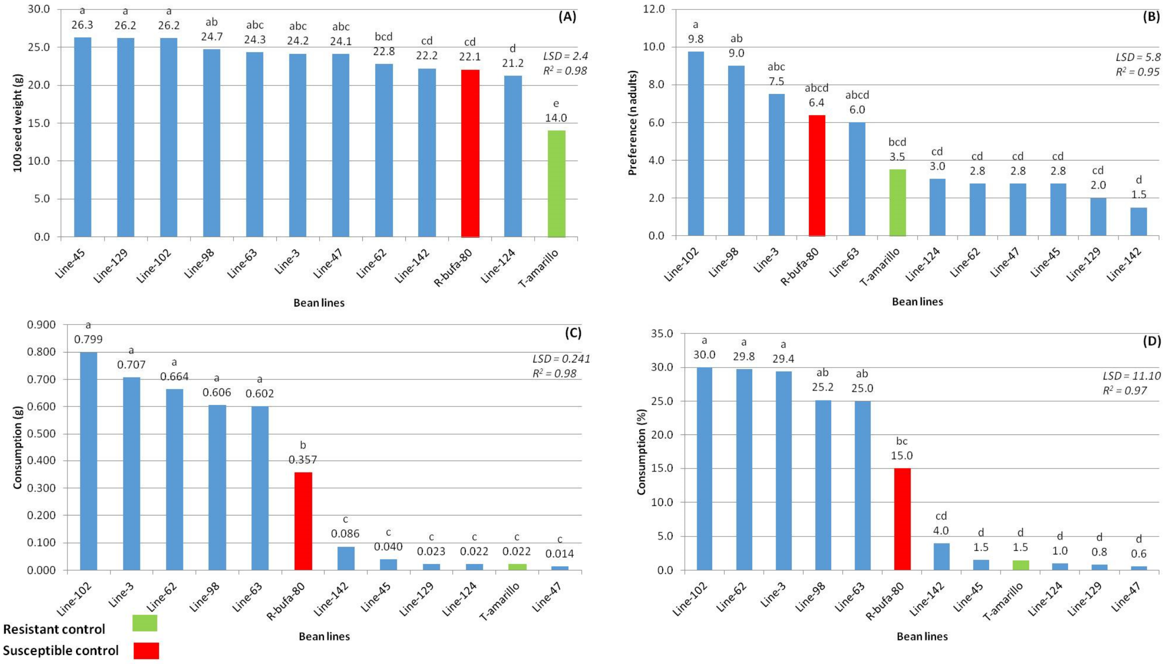

Figure 3. Means and LSD for (**A**) 100 seed weights, (**B**) preference (n adults), (**C**) consumption in grams and (**D**) consumption in percent of 10 contrasting NILs of the HIF population (R-bufa-80 and T-amarillo genotypes). The values are means of four replicates, two per bioassay. Means followed by the same letter are not significantly different ($p < 0.05$).

4. Discussion

Tepary beans from Mexico are a great source of resistance against *A. obtectus* to improve the harvest of the common bean [14]. Also, some ancient common beans from Mexico could be excellent sources of resistance to *A. obtectus*, as is the case of the R-bufa genotype.

In the case of the inheritance of resistance to *A. obtectus*, two biparental crosses were reported by Kornegay and Cardona [8], and in two biparental populations were reported by Jiménez-Galindo et al. [14]. In the first study, two recessive complementary and independent genes were suggested to be responsible for the number of days to adult emergence of *A. obtectus* in two F_2: A36 × G12952 and Pijao × G12952 with the segregation ratio of 15 [susceptible (short period to adult emergence)]:1 [resistant (long period)] with the resistance being found in cotyledons. In the second study, a Mendelian gene was suggested to be responsible for the number of adults of the first generation in two F_2: P-saltillo × T-amarillo and T-amarillo × T-cafe with the segregation ratio of 3 [resistant lines (with cero adults of the first generation)]:1[susceptible line (with one or more first-generation adults)]. Contrary to research reported by Kornegay and Cardona [8] in their study, the resistance was found in the testa of resistant lines. Our research is in accordance with Li et al. [5] and Minney [34] and Kamfwa [12], who found that a quantitative inheritance of the weevil resistance trait was controlled by polygenes, which were determining the percentage of seeds damaged by bruchids. Our results of quantitative inheritance of seed weights agree with Kamfwa [12]. It should be noted that weevil tolerance-related traits, i.e., days to adult emergence, explored by Kornegay and Cardona [8] were different from the number of adults studied by Jiménez-Galindo et al. [14]. Our results regarding preference, consumption in grams and consumption in percent were of quantitative inheritance, which is consistent with previous studies reported by Li et al. [5] and Minney [34]. However, the results do not agree with the study of Jiménez-Galindo et al. [14], who found a major gene in two F_2 populations.

There are no reports of HIF populations in common beans, but they have been used in other species such as maize [28,35], rice (*Oriza sativa* L.) [36] or Arabidopsis (*Arabidopsis thaliana* L.) [37], mainly to validate QTL of various characters. In this case, the traits studied in this HIF population are quantitatively inherited, as we can see in Figure 2, where it evident that all traits studied have a normal distribution and therefore are of quantitative inheritance. The advantage of these populations is that they are near-homozygous within their genome, except in the region under study by [28].

Knowing the heritability of traits is important in choosing the most appropriate selection program to improve it [38]. In this study, the HIF population of NILs showed a heritability of 0.90 for the variable of weights of 100 seeds. Our results agree with White et al. [39], who found a heritability of 0.57 to 0.80 for the same trait. In this research, the heritabilities for the resistance traits to *A. obtectus* were very low for preference with a heritability of 0.09, low for consumption (in percent) with a heritability of 0.17 and for consumption (in grams) with a heritability of 0.17. These heritabilities did not differ significantly from zero. The heritability of other pest-tolerance-related traits such as tolerance and antixenosis in beans to leafhoppers, are often reported to be low and quantitatively inherited (Galwey and Evans [40] and Kornegay and Temple [41]). A reason for such low heritability is due to pest variability. Another possible reason which could be responsible for our results indicating that heritability was low for weevils could also be the bean population and pest variability used within this study. Gonzales et al. [42] also reported low heritability for antixenosis in common beans to leafhoppers. The heritability values for these traits indicate that while seed weight would be an easy trait to improve using simple phenotypic selection programs, such as mass selection, improving insect resistance is more complex. The following three sources of variation are involved in the calculation of heritability: the variation between lines, bioassay × line interaction and residual error. For consumption (both in g and %), the sum of squares (SS) of the source of variation between lines represents 32% of the total variation while the residual error represents 40%. For the preference trait the difference is greater, representing the residual error at 44% and the lines at 29% of the total SS. The residual error was high because, besides the components that we cannot control for any character in the resistance traits, we had to include variability due to the presence of insects. On the other hand, the genetic variation of a HIF population is less than that of a diverse panel of lines in which several defense mechanisms can be combined. Therefore, one possibility to breed resistant traits is to reduce the residual error, which is a challenge when working with pests. Another alternative could be to perform association analysis between molecular markers and resistance characters to assess the use of marker-assisted selection programs or even genomic selection [43].

Kornegay et al. [44] found that seed size is negatively correlated with adult weight but not with days to adult emergence. The correlation coefficients between seed size and number of eggs, number of adults, adult weight and life cycle were 0.64, 0.69, 0.63 and −0.42, respectively [45]. In this study, positive and significant phenotypic correlations were found between the weights of 100 seeds and consumption in grams (0.15). This means that, probably in some lines with larger seeds, the adults consume a greater amount of the grain due to the accessibility of food, and a greater number of adults emerge. However, the correlation coefficient is low although it is significant; this suggests that the weights of the seeds were not important to determine consumption. Also, we found positive and significant phenotypic correlations between preference (n) and consumption in grams (0.20), and percentage of consumption (0.20). The consumption by *A. obtectus* is highly correlated with the number of first-generation adults [7,14], and could also be attributed to beneficial thermal conditions in a range of 20–28 °C [46].

All the characters studied in this study have a continuous distribution, and are considered to be of quantitative inheritance. However, variability was found for the studied characters that allow selecting lines with a high level of resistance within the HIF population of R-bufa-80-12. The most promising lines from a commercial point of view are lines 45 and 129, since in addition to showing low consumption when attacked by the weevil, they also have one of the best weights (greater than 26 g), which are significantly higher than the weights of R-bufa-80 and the T-amarillo control. Other studies have also found normal distributions for resistance traits to *A. obtectus*. In fact, the F_2 that was reported by Kornegay and Cardona [8] showed a continuous, but skewed, distribution of variable days to adult emergence from a low to high quantity. The F_3 generation showed an overall decrease in the levels of resistance compared to the original evaluations. Kornegay and Cardona [8] found only a few F_2 individuals with the level of resistance of the G12952 genotype. In this study, many inbred lines such as Line-47, Line-124, Line-129, Line-45 and Line-142 (of the HIF population) with resistance were found.

The more resistant lines of the HIF population are a suitable material to common bean breeding for resistance to *A. obtectus*. This HIF population is also suitable for genetic genomics, proteomics and metabolomics studies to find new compounds, proteins and resistance genes to *A. obtectus*. Further investigation of sequencing analysis could identify candidate genes and genetic sequences for *A. obtectus* resistance.

5. Conclusions

All traits studied in this research with the HIF population of R-bufa-80-12 had a continuous distribution and therefore were of quantitative inheritance. Phenotypically, seed size is positively correlated with greater seed consumption. Likewise, the preference (*n* adults) is positively correlated with consumption in grams and in percentage. The lines of the HIF population present great variability with values significantly below and above the parental R-bufa-80 seeds for the characteristics of the weights of 100 seeds, preference (*n* adults), consumption in g and consumption in percent. The best lines of the HIF population for resistance to *A. obtectus* are Line-45, Line-129, Line-124, Line-142 and Line-47. In general, these lines presented lower preference of adults, and lower consumption in grams and in percentages. Line-45, Line-124, Line-129 and Line-47 presented similar consumption in % and in g as the resistant control (T-amarillo). However, lines 45 and 129 are the most interesting from a commercial point of view because they contain combined resistance and a large seed. The most susceptible lines for resistance to *A. obtectus* were Line-102, Line-3, Line-62, Line-98 and Line-63. These lines presented more preference, except for Line-62. They also showed high consumption in grams and in percentages.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/agronomy13102553/s1, Table S1. Means of parents and controls and all the lines of the HIF population for all the traits studied.

Author Contributions: A.Y.A.-R., G.C.-P. and J.C.J.-G. designed this study and discussed the results; J.C.J.-G. developed the HIF population; A.Y.A.-R., G.C.-P., R.A.M. and J.C.J.-G. carried out field experiments and performed statistical analysis of the data; A.Y.A.-R., G.C.-P., J.C.J.-G., N.R.-C., O.R.-V., J.J.F.-G. and R.A.M. drafted the initial manuscript. All authors have read and agreed to the published version of the manuscript.

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Data Availability Statement: The data sets and material generated and analyzed during this study are available from José Cruz Jiménez-Galindo upon reasonable request.

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