PAB
Pesquisa Agropecuária Brasileira

ISSN 1678-3921

Journal homepage: www.embrapa.br/pab

For manuscript submission and journal contents, access: www.scielo.br/pab

Genetics/ Original Article

Estimation of genetic parameters and selection pressure in canary seed

Abstract – The objective of this work was to estimate the heritability parameters and selection gains in canary seed populations under different selection pressures. The base germplasm was composed of genotypes called "original" and genotypes subjected to the mutation process with sodium azide, to create genetic variability in the population. The selection was carried out based on the cycle of canary seed plants. The plants were marked in the field and collected for subsequent evaluation and categorization. A Bayesian inference model was used to determine the precision degree of the estimates and the genetic effects. Based on the data matrix obtained, the heritability parameters were estimated for the variables panicle length, number of grains per panicle, grain mass per panicle and panicle index. The response to selection was estimated based on selection pressures, varying between 1% (the highest intensity) and 90% (the lowest intensity). Narrow-sense heritability values for the variables panicle length, number of grains per panicle, weight of grains per panicle, and birdseed panicle index were 0.28, 0.33, 0.25, and 0.37, respectively. Based on the results presented for heritability values and selection gains for canary seed, it is possible to obtain improved lines from rigorous selection pressures.

Index terms: *Phalaris canariensis*, Bayesian inference, grain yield, heritability, plant breeding.

Estimativas de parâmetros genéticos e pressão de seleção em populações de alpiste

Resumo – O objetivo deste trabalho foi estimar os parâmetros de herdabilidade e ganhos de seleção em populações de alpiste submetidas a diferentes pressões de seleção. O germoplasma-base foi composto por genótipos denominados "originais" e genótipos submetidos ao processo de mutação com azida sódica, para criar variabilidade genética na população. A seleção foi realizada com base no ciclo das plantas. As plantas foram marcadas em campo e coletadas para posterior avaliação e categorização. Utilizou-se um modelo de inferência bayesiana, para determinar o grau de precisão das estimativas e os efeitos genéticos. Com base na matriz de dados obtida, estimaram-se os parâmetros de herdabilidade para as variáveis comprimento da panícula, número de grãos por panícula, massa de grãos por panícula e índice de panícula. A resposta à seleção foi estimada com base nas pressões de seleção, que variaram entre 1% (maior intensidade) e 90% (menor intensidade). Valores de herdabilidade no sentido restrito para as variáveis comprimento da panícula, número de grãos por panícula, massa de grãos por panícula e índice de panícula de alpiste foram 0,28, 0,33, 0,25 e 0,37, respectivamente. Com nos resultados apresentados quanto à herdabilidade e aos ganhos de seleção, é possível obter linhagens melhoradas de alpiste a partir de pressões de seleção rigorosas.

Termos de Indexação: *Phalaris canariensis*, inferência bayesiana, rendimento de grãos, herdabilidade, melhoramento de plantas.

Willyan Júnior Adorian Bandeira,
Universidade Regional do Noroeste do Estado do Rio Grande do Sul, Ijuí, RS, Brazil.
E-mail: bandeira.wjab@gmail.com

Ivan Ricardo Carvalho✉,
Universidade Regional do Noroeste do Estado do Rio Grande do Sul, Ijuí, RS, Brazil.
E-mail: carvalhoirc@gmail.com

Leonardo Cesar Pradebon,
Universidade Federal de Santa Maria, Departamento de Fitotecnia, Santa Maria, RS, Brazil.
E-mail: leonardopradebon@gmail.com

Natália Hinterholz Sausen,
Universidade Regional do Noroeste do Estado do Rio Grande do Sul, Ijuí, RS, Brazil.
E-mail: natalia.sausen@sou.unijui.edu.br

Jaqueline Piesanti Sangiovo,
Universidade Regional do Noroeste do Estado do Rio Grande do Sul, Ijuí, RS, Brazil.
E-mail: jaqueline.sangiovo@sou.unijui.edu.br

Gabriel Mathias Weimer Bruinsma,
Universidade Regional do Noroeste do Estado do Rio Grande do Sul, Ijuí, RS, Brazil.
E-mail: gmwbruinsma@hotmail.com

Murilo Vieira Loro
Universidade Federal de Santa Maria, Departamento de Fitotecnia, Santa Maria, RS, Brazil.
E-mail: muriloloro@gmail.com

✉ Corresponding author

Received
July 1, 2024

Accepted
January 14, 2025

How to cite
BANDEIRA, W.J.A.; CARVALHO, I.R.; PRADEBON, L.C.; SAUSEN, N.H.; SANGIOVO, J.P.; BRUINSMA, G.M.W.; LORO, M.V. Estimation of genetic parameters and selection pressure in canary seed. **Pesquisa Agropecuária Brasileira**, v.60, e03781, 2025. DOI: https://doi.org/10.1590/S1678-3921.pab2025.v60.03781.

Introduction

Canary seed (*Phalaris canariensis* L.) is an annual grass, that is cultivated in temperate regions and considered a true cereal, whose structures are similar to other species of the same family (Poaceae), such as wheat and oat (Rikal et al., 2023). The primary market for canary seed has been the bird food industry (Abdel-Aal, 2021). However, hairless (glabrous) canary seed genotypes, devoid of trichomes that are toxic to humans, were recently approved for human consumption in the United States of America and Canada (Patterson et al., 2018). This could promote the emergence of a niche market to this cereal within the food sector. Its grains contain, on average, 60% starch, 20% crude protein, 8% oil, 7% digestible fiber, and 2% mineral material, in addition to high levels of methionine, cysteine, and tryptophan in the amino acid composition (Abdel-Aal, 2021).

Most part of existent canary seed genotypes come from Canada and Argentina, adapting to the temperate climate typical of these regions. Therefore, to adapt to the Brazilian subtropical climate, it is necessary the selection of this species genotypes. For that, it is essential to use the existing natural genetic variability (Carvalho et al., 2016), besides seeking ways to expand it by obtaining new gene constitutions to get more productive genotypes capable of expressing agronomic traits of interest, stable to the environment variations, and tolerant to biotic and abiotic stresses (Quadros et al., 2022). The selection of superior individuals within the species, by variability arising from mutations that occurred naturally in the environment, is the most common way. Nevertheless, other strategies to create genetic variability should be used to increase the probability of selecting promising genotypes.

Induced mutation with specific mutagens could generate individuals with desirable characteristics that could be exploited later (El-Degwy, 2013; Dewi et al., 2020). Furthermore, chemical mutagens are easy to use (Awan et al., 2021), generating results in a short period of time. In plants, ethyl methanesulfonate and sodium azide are widely used because they are highly efficient in causing mutation points in the genome (Kharkwa, 2012), which produces high effects on the phenotypic variability of all types of traits (Dewi et al., 2020). These mutations increase the probability of obtaining plants, which shows acclimatization to the cultivation environment (Channaoui et al., 2019) and better expression of traits related to grain productivity. However, using induced mutation as the only method to bring together all these characteristics in a new genotype is a difficult task, and it is only a complementary way of doing so.

The expansion of genetic variability should be accompanied by a rigorous analysis that allows to understand its magnitude, which makes it possible to visualize the probability of success in the selection of promising genotypes. In order to estimate the possible selection gains, variance components and genetic parameters should be obtained in such a way that the residual effect on the results be reduced, for more accurate inferences. Therefore, Bayesian inference allows of the reduction of the residual effect in parameter estimates (Silva et al., 2020). The efficiency of this method was proven in studies carried out to understand the genotype x environment interaction and selection gains, for instance, in sweet potato (Valadares et al., 2023), white oat (Azevedo et al., 2022), and wheat (Azevedo et al., 2023).

There are some studies that evaluate the genetic identity of canary seed and the effect of genotypes on its nutritional qualities (Kannan et al., 2017; Malunga et al., 2024), but none of them address the genetic parameters in a way that results in possible genetic gains for the species. This entails the need to identify genetic parameters and selection strategies that favor the obtention of superior genotypes.

The objective of this work was to estimate the heritability parameters and selection gains of canary seed populations under different selection pressures.

Materials and Methods

The present study was carried out in the experimental field of the program for genetic improvement of grain lines, located at the Universidade Regional do Noroeste do Estado do Rio Grande do Sul (Unijuí), in the municipality of Ijuí (28º23'15"S, 53º56'39"W, at 295 m altitude), from May to September 2023. The climate classification for the region, according to the Köppen-Geiger's classification, is Cfa (humid subtropical) (Setzer, 1966).

The soil is classified as a Latossolo Vermelho distroférrico típico, according to the Brazilian Soil Classification System (Santos et al., 2018), i.e., Oxisol, with a deep and well-drained profile. Soil analysis showed the following physicochemical attributes: 430 g kg^{-1} clay; 5.5 pH in water; 5.7 SMP index; 3.5 mg dm^{-3} P; 119 mg dm^{-3} K; 0.7% organic matter; 0.0 cmol$_c$ dm^{-3} Al; 3.6 cmol$_c$ dm^{-3} Ca; 1.5 cmol$_c$ dm^{-3} Mg; 2.4 Ca/Mg ratio; 6.2 cmol$_c$ dm^{-3} H+Al; 11.6 cmol$_c$ dm^{-3} CTC$_{pH7.0}$; 5.4 cmol$_c$ dm^{-3} effective CTC; 46.7% base saturation; 0.0% Al saturation; 4.2 mg dm^{-3} Cu; 3.1 mg dm^{-3} Zn; 5.6 mg dm^{-3} Mn; 2.2 mg dm^{-3} S.

The base germplasm used in the experiment was composed of pure lines of genotypes from Argentina and Canada, which were mixed to obtain 10 kg of canary seed. Out of this total, 5 kg were subjected to the mutation process with sodium azide, using the method proposed by Pharel (1994), aiming at the increase of genetic variability within the canary seed population. The other 5 kg remained original. The mutant seed showed 50% heterozygosity, and 50% homozygosity, while the original populations showed 100% heterozygosity (Borém & Miranda, 2009).

The experiment was carried out in the field, using an augmented design of blocks, with 5 experimental units of 500 m^2 each, composed of 25 m long lines spaced at 0.17 cm apart. The blocks were divided into two sub-blocks, where the original seed and mutants were sown separately in each of them. Sowing was carried out in the first fortnight of May, with 50 seed per linear meter sowing density for all populations. Fertilization equivalent to 300 kg ha^{-1} N-P-K formula 05-20-20 was applied at sowing and, subsequently, the equivalent of 100 kg ha^{-1} urea (45% N) was broadcasting on coverage at the full tillering plant stage. The selection was carried out based on the plant cycle, when plants were marked in the field to obtain populations with a similar cycle and, at the end of the cycle, they were collected for subsequent evaluation.

Grains from each selected plant were homogenized form a population with a similar cycle. The following traits were evaluated: days to flowering (DF, days); days to maturation (DM, days); panicle length (PL, cm); number of grains per panicle (NGP, units); grain weight per panicle (GWP, g); and panicle index (PI), which consists of the ratio between the number of grains and the length of the panicle. The climatic variables – minimum air temperature (Tmin, ºC), maximum air temperature (Tmax, ºC), mean air temperature (Tmean, ºC), and precipitation (Prec, mm) – were obtained using data from the NASA Power (2023).

To determine the degree of precision and genetic effects, a Bayesian inference model was used based on the Monte Carlo algorithm with Markov chains (MCMC). The model assumptions were verified as described by Azevedo et al. (2022), for which the normality of errors and homogeneity of variances were verified for the fixed effect (block), and for the random effect (genotypes). With the assumptions met, the approximate model used was

$$y = X_\beta + Z_1\delta_1 + Z_2\delta_2 + e,$$

in which: y is considered the vector of phenotypic values; X and β are, respectively, the incidence matrix and the corresponding vector of systematic effects (general average); Z_1 and Z_2 are the random effects incidence matrices, δ_1 is the vector of block effects; δ_2 is the vector of genetic values; and e is the residual vector. In the present study, 1,000,000 iterations were used a priori, for which the first 100 iterations were discarded as burn-in, in which the Markov chains' convergence was verified through the Geweke's diagnostic. Then the parameters were calculated as follows: low-95% CI (confidence interval lower than 95% probability); up-95% CI (confidence interval higher than 95% probability); and significance of the probabilistic model using the Monte Carlo method with Markov chains (pMCMC).

Based on the data matrix obtained, the heritability parameters were estimated in the broadest sense: ($H^2=\sigma_P/\sigma_G$), in which σ_P consists of phenotypic variance and σ_G consists of genotypic variance. Narrow-sense heritability was calculated as follows:

$$h_a^2 = \sigma_a^2 / \sigma_a^2 + \sigma_d^2 + \sigma_e^2,$$

in which: σ^2_a is the additive genetic variance, σ^2_d is the genetic variance of dominance; and σ^2_e is the environmental genetic variance. Thus, the response to selection was estimated by the formula

$$R = h_a^2(i)(\sqrt{\sigma P}),$$

in which: R is the response to selection (selection gain); h^2_a is the heritability in the strict sense; i is the selection intensity (which varies according to selection pressure); and σ_P is the phenotypic variance. The pressures and intensities (i) corresponding selection parameters are, respectively: 1.00%, 2.665; 5.00%, 2.063; 10.00%, 1.775; 20.00%, 1.400; 30.00%, 1.160; 50.00%, 0.800. From this, genetic gain was inferred, to define the optimal selection pressure to be used for canary seed cultivation. Analyses were carried out with the functions of the packages MCMCglmm version 2.35 (Hadfield, 2010), and metan (multi-environment trials analysis) version 1.18.0 (Olivoto & Lúcio, 2020), using the package EstimateBreed (Bandeira et al., 2025) version 1.0.1' of the R software (R Core Team, 2023).

Results and Discussion

Analysis of the meteorological data, during the canary seed cycle, shows that changes in air temperature and precipitation values are directly related to the cycle length of each mutant and original population (Table 1). According to Baier et al. (1988), the ideal temperatures for crop development are 9 to 10ºC during the germination period, 15 to 16ºC during the flowering period and 18 to 20ºC during the maturation period. Therefore, the average temperature was close to optimum for all populations. Accumulated precipitation required for the plant cycle varied between 410 and 720 mm among populations; this difference is directly related to the cycle duration of the genotypes of each population. In this scenario, populations 1 and 10 showed the lowest and highest accumulated precipitation, respectively. May et al. (2022) reported that an amount of 350 mm of precipitation is sufficient for the birdseed cycle, based on normal precipitation data occurring over 30 years in Canada, and the highest crop yield occurred with precipitation values above 500 mm.

Table 1. Average values of mean air temperature (Tmean), minimum air temperature (Tmin), maximum air temperature (Tmax), and accumulated precipitation during the crop cycle of original and mutant populations of canary seed (*Phalaris canariensis*).

Population(1)	Tmean (ºC)	Tmin (ºC)	Tmax (ºC)	Precipitation (mm)
Original				
1	15.8	10.8	22.1	410
2	15.8	10.7	22.0	454
3	16.0	11.0	22.2	529
4	16.3	11.3	22.5	638
5	16.5	11.4	22.7	655
Mutant				
6	15.8	10.7	22.0	454
7	16.0	10.9	22.2	488
8	16.6	11.4	22.7	660
9	16.6	11.4	22.7	660
10	16.6	11.4	22.8	720

(1)Original, canary seed not subjected to induced mutation; and mutant, canary seed subjected to induced mutation with sodium azide.

The variance component estimates were significant for all variables in all populations (pMCMC<0.05), making them viable for interpreting genetic parameters obtained *a posteriori* (Table 2). Notwithstanding, among several Bayesian inference methods, the Markov chain Monte Carlo (MCMC) simulation can be applied to generate a chain of successive iterations, updating the estimates by probability starting from the initial parameter (a priori) (Silva et al., 2020).

The number of days to flowering showed a range between 80 and 118 days, in which populations 1, 7, and 8 were earlier with 80, 90, and 95 days, respectively, while populations 4, 5, and 6 were the latest with 116, 118, and 116 days, respectively (Table 3). Thereafter, physiological maturity was inferred to be 100, 104, and 107 days for populations 7, 1, and 8, while populations 4, 5, and 6 required 128, 134, and 131 days to maturity, respectively.

According to Cogliatti et al. (2011), the duration of the cycle is related to the response of canary seed genotypes to air temperature. These authors reported the averages of 1,644 and 1,802 of growing degree days (GDD), measured in Celsius degrees until maturity. Taking into account that the average air temperature was 16.2ºC (Cogliatti et al., 2011) and that, in a study by May et al. (2022) the average minimum temperature of 2ºC was recorded during the cycle, it can be inferred that these results would lead to daily accumulations of 14.2ºC, which would tend to a minimum cycle ranging between 116 and 127 days, similarly observed in present study.

Broad-sense heritability (H^2) values, which considers the total genetic effect, varied between 0.38 and 0.57 for panicle length (Table 3). Taking into account that the classification of heritabilities considers magnitudes between 0.01 and 0.15 as low, 0.16 to 0.50 as medium, and greater than 0.51 as high (Resende et al., 1995; Paludeto et al., 2017), it is possible to infer (from heritability values) the magnitude of the environmental effect on the expression of the

Table 2. Variance components of traits estimated by Bayesian inference for ten populations of canary seed (*Phalaris canariensis*) regarding the evaluated variables.

Population(1)	Traits(2)	Post.mean(3)	<95% CI(4)	>95% CI(4)	DIC(5)	pMCMC(6)
Original						
1	PL	3.572	3.374	3.779	86.287	0.0001
	NGP	61.780	56.630	67.320	328.234	0.0001
	GWP	0.113	0.098	0.128	-280.441	0.0001
	PI	17.680	16.340	18.960	226.021	0.0001
2	PL	3.605	3.463	3.739	21.081	0.0001
	NGP	52.900	48.950	57.160	582.442	0.0001
	GWP	0.081	0.072	0.090	-370.278	0.0001
	PI	14.990	13.740	16.160	275.313	0.0001
3	PL	3.650	3.534	3.769	5.989	0.0001
	NGP	72.000	67.310	76.400	353.213	0.0001
	GWP	0.078	0.070	0.086	-395.513	0.0001
	PI	19.850	18.690	20.960	292.416	0.0001
4	PL	4.031	3.896	4.160	37.338	0.0001
	NGP	70.800	65.830	75.830	640.570	0.0001
	GWP	0.065	0.059	0.072	-434.766	0.0001
	PI	17.780	16.610	19.010	297.105	0.0001
5	PL	3.569	3.455	3.676	39.553	0.0001
	NGP	65.220	60.680	69.770	611.617	0.0001
	GWP	0.070	0.063	0.076	-425.998	0.0001
	PI	18.420	17.230	19.640	-67.990	0.0001
Mutant						
6	PL	3.651	3.547	3.756	3.634	0.0001
	NGP	56.110	52.250	60.270	335.233	0.0001
	GWP	0.063	0.058	0.069	-449.858	0.0001
	PI	15.540	14.470	16.650	315.658	0.0001
7	PL	3.471	3.345	3.584	0.557	0.0001
	NGP	67.890	63.890	71.980	57.991	0.0001
	GWP	0.066	0.059	0.073	-423.754	0.0001
	PI	19.710	18.570	20.810	267.755	0.0001
8	PL	3.277	3.136	3.421	-17.165	0.0001
	NGP	33.750	31.490	35.970	359.418	0.0001
	GWP	0.033	0.030	0.036	-510.571	0.0001
	PI	10.293	9.727	10.900	152.508	0.0001
9	PL	3.780	3.632	3.928	-3.909	0.0001
	NGP	66.220	60.490	71.930	323.130	0.0001
	GWP	0.772	0.069	0.086	-288.037	0.0001
	PI	17.570	16.180	19.010	204.857	0.0001
10	PL	3.580	3.446	3.711	-45.648	0.0001
	NGP	54.770	50.930	59.230	505.576	0.0001
	GWP	0.055	0.049	0.061	-437.476	0.0001
	PI	15.690	14.460	17.020	158.254	0.0001

(1)Original, canary seed not subjected to induced mutation; and mutant, canary seed subjected to induced mutation with sodium azide. (2)Traits: PL, panicle length; NGP, number of grains per panicle; GWP, grain weight per panicle; and PI, panicle index. (3)Mean of the posterior distribution. (4)Confidence interval (CI): <95% CI, below 95% probability; >95% CI, greater than 95% probability. (5)DIC: deviance information criterion. (6)pMCMC: significance of the probabilistic model using the Monte Carlo method with Markov Chains.

components of interest. In this context, population 5 obtained the lowest value (0.38), while populations 3, 7, and 9 obtained 0.51, and population 10 obtained 0.57. A positive phenotypic relationship was reported between plant height and productivity of canary seed (Cogliatti et al., 2011), which, nevertheless, highlights that this association is undesirable, due to the tendency of tall plants to become lodging, similarly to what was observed for wheat and barley prior to the introduction of dwarfism genes (Chandler & Harding, 2013).

There was an amplitude between 0.35 and 0.67 in H^2, for the number of grains per panicle (Table 3), in which the values 0.35, 0.36, 0.37, and 0.38 – classified as medium – were observed for populations 2, 5, 8, and 4, respectively. These values suggest that the environmental effect was about 75% for these populations. High heritabilities were obtained for populations 1 (0.62) and 7 (0.67), which can partly be explained by their precocity. Regarding grain weight per panicle, the broad-sense heritability was similar for all populations, remaining close to 0.50. For the panicle index character, the highest H^2 was obtained by population 5 (0.74), while the lowest value was obtained by population 6 (0.42).

The values related to the additive genetic portion, determined by narrow-sense heritability (h^2) (Table 3), varied between 0.19 and 0.28 for panicle length. Thus, it can be inferred that the effect of the environment is important for the expression of canary seed yield components, in which less variation was observed, in comparison with the heritability in the broad-sense. Population 5 showed the lowest h^2 value (0.19), while the highest values were observed in populations 8 and 10, with 0.27 and 0.28, respectively.

The h^2 ranged between 0.17 and 0.33 for the number of grains per panicle (Table 3). The lowest heritability values were shown by populations 2, 4, 5 and 9, while the largest heritable portions occurred in populations 1 and 7, with 0.31 and 0.33, respectively. Narrow-sense heritability values showed the same values in all populations for grain weight per plant (0.25). As for the panicle index, the variation of heritability varied between 0.21 and 0.37, for which populations 5 and 10 showed greater values, with h^2 of 0.37 and 0.30, respectively. The value of narrow-sense heritability directly reflects the selection gains, a context in which reduced values imply more rigorous selection pressures (fewer number of individuals selected) to be successful.

As it is an autogamous plant, canary seed benefits from narrow-sense heritability, which can be carried over to the next generation. Due to this characteristic, after achieving sufficient genetic variability, breeding programs can direct selection strategies with methods developed for self-pollinating plants, such as the pedigree method (Oliveira et al., 2015).

Estimates based on narrow-sense heritability values show that rigorous selection pressures resulted in the highest values of selection gain, across all agronomic

Table 3. Days to flowering (DF), days to physiological maturity (DM), broad-sense heritabilities (H^2) and narrow-sense heritabilities (h^2) in different traits[(1)] of original and mutant populations of canary seed (*Phalaris canariensis*).

Population[(2)]	DF	DM	H^2				h^2			
			PL	NGP	GWP	PI	PL	NGP	GWP	PI
Original										
1	80	104	0.48	0.62	0.51	0.53	0.24	0.31	0.25	0.27
2	104	111	0.49	0.35	0.51	0.48	0.24	0.17	0.25	0.24
3	111	118	0.51	0.47	0.50	0.50	0.26	0.24	0.25	0.25
4	116	128	0.44	0.38	0.50	0.45	0.22	0.19	0.25	0.22
5	118	134	0.38	0.36	0.50	0.74	0.19	0.18	0.25	0.37
Mutant										
6	116	131	0.46	0.54	0.50	0.42	0.23	0.27	0.25	0.21
7	90	100	0.51	0.67	0.50	0.49	0.25	0.33	0.25	0.24
8	95	107	0.54	0.37	0.50	0.49	0.27	0.19	0.25	0.24
9	114	125	0.51	0.47	0.50	0.46	0.26	0.23	0.25	0.23
10	114	125	0.57	0.41	0.50	0.59	0.28	0.20	0.25	0.30

(1)Traits: PL, panicle length; NGP, number of grains per panicle; GWP, grain weight per panicle; and PI, panicle index. (2)Original, canary seed not subjected to induced mutation; and mutant, canary seed subjected to induced mutation with sodium azide.

traits of interest (Table 4 and Table 5). Selection pressures from 1% to 4% can be applied, if the interest is to obtain panicle length increments greater than 0.30 cm for all populations. It is necessary to consider that the selection of panicle length should not penalize the number of grains per plant at the same time that it should not favor lodging. Plants with unbalanced height and panicle length are more prone to lodging. The reduction of grain yield promoted by plant lodging varies between 8% and 34% (Berry et al., 2004), and between 43% and 61% (Acreche & Slafer, 2011).

A greater variation was observed in genetic gains for the number of grains per panicle among the populations evaluated (Table 4), and it was more pronounced in populations 1, 6, and 7, which withstood selection pressures of up to 10%, while maintaining a gain of 10 grains per panicle. However, the identification of an optimal selection pressure should consider the entire genetic basis present. Therefore, it is possible to obtain genetic progress for this character with 3% selection pressures. This greater tolerance to more stringent selection pressure is directly related to the heritability values previously discussed. The reduced selection gain values for the grain weight per plant are related to the low heritability in the restricted sense for the trait, in addition to the fact that the production of light grains is an intrinsic characteristic of canary seed. This also shows that mutation induction was not effective to create variability for this trait.

There was no direct influence of selection gains on the panicle length and number of grains per panicle, and on the panicle index character (Table 5). This is an indication that gains for panicle length are not related to the greater number of grains, a fact that is proven when the greatest selection gain for the panicle index was obtained by population 5, which means

Table 4. Response to selection of canary seed (*Phalaris canariensis* L.) populations for panicle length and number of grains per panicle based on selection pressures between 1% (highest intensity) and 90% (lowest intensity).

Population(1)	Selection pressures												
	1%	2%	3%	4%	5%	10%	20%	40%	50%	60%	70%	80%	90%
Original	Panicle length												
1	0.45	0.40	0.37	0.36	0.34	0.29	0.23	0.16	0.13	0.11	0.08	0.06	0.03
2	0.46	0.41	0.38	0.37	0.35	0.30	0.24	0.16	0.14	0.11	0.08	0.06	0.03
3	0.48	0.44	0.40	0.39	0.37	0.31	0.25	0.17	0.14	0.11	0.09	0.06	0.04
4	0.42	0.38	0.35	0.33	0.32	0.27	0.22	0.15	0.12	0.10	0.08	0.05	0.03
5	0.36	0.32	0.30	0.29	0.28	0.23	0.19	0.13	0.11	0.08	0.07	0.05	0.03
Mutant													
6	0.43	0.39	0.36	0.35	0.33	0.28	0.23	0.16	0.13	0.10	0.08	0.06	0.03
7	0.48	0.43	0.40	0.38	0.37	0.31	0.25	0.17	0.14	0.11	0.09	0.06	0.04
8	0.50	0.46	0.42	0.40	0.39	0.33	0.26	0.18	0.15	0.12	0.09	0.07	0.04
9	0.48	0.43	0.40	0.38	0.37	0.31	0.25	0.17	0.14	0.11	0.09	0.06	0.04
10	0.53	0.48	0.45	0.42	0.41	0.35	0.27	0.19	0.16	0.13	0.10	0.07	0.04
Original	Number of grains per panicle												
1	20.21	18.26	16.99	16.17	15.57	13.17	10.48	7.26	5.99	4.79	3.74	2.62	1.50
2	11.25	10.16	9.46	9.00	8.66	7.33	5.83	4.04	3.33	2.67	2.08	1.46	0.83
3	15.45	13.96	12.99	12.36	11.90	10.07	8.01	5.55	4.58	3.66	2.86	2.00	1.14
4	12.49	11.29	10.50	10.00	9.63	8.14	6.48	4.49	3.70	2.96	2.31	1.62	0.93
5	11.68	10.56	9.82	9.35	9.00	7.61	6.06	4.20	3.46	2.77	2.16	1.51	0.87
Mutant													
6	17.46	15.78	14.68	13.97	13.45	11.38	9.05	6.27	5.17	4.14	3.23	2.26	1.29
7	21.75	19.66	18.29	17.40	16.76	14.18	11.28	7.81	6.45	5.16	4.03	2.82	1.61
8	12.06	10.90	10.14	9.65	9.29	7.86	6.25	4.33	3.57	2.86	2.23	1.56	0.89
9	15.14	13.68	12.73	12.11	11.66	9.87	7.85	5.44	4.49	3.59	2.80	1.96	1.12
10	13.21	11.94	11.10	10.57	10.17	8.61	6.85	4.74	3.91	3.13	2.45	1.71	0.98

(1)Original, canary seed not subjected to induced mutation; and mutant, canary seed subjected to induced mutation with sodium azide.

Table 5. Response to selection of canary seed (*Phalaris canariensis*) populations for grain weight per panicle and panicle index based on selection pressures between 1% (highest intensity) and 90% (lowest intensity).

Population(1)	Selection pressures												
	1%	2%	3%	4%	5%	10%	20%	40%	50%	60%	70%	80%	90%
Original	Grain weight per panicle												
1	0.03	0.03	0.03	0.02	0.02	0.02	0.02	0.01	0.01	0.01	0.01	-(2)	-
2	0.03	0.03	0.03	0.02	0.02	0.02	0.02	0.01	0.01	0.01	0.01	-	-
3	0.03	0.03	0.02	0.02	0.02	0.02	0.02	0.01	0.01	0.01	0.01	-	-
4	0.03	0.03	0.02	0.02	0.02	0.02	0.02	0.01	0.01	0.01	0.01	-	-
5	0.03	0.03	0.02	0.02	0.02	0.02	0.02	0.01	0.01	0.01	0.01	-	-
Mutant													
6	0.03	0.03	0.02	0.02	0.02	0.02	0.02	0.01	0.01	0.01	0.01	-	-
7	0.03	0.03	0.02	0.02	0.02	0.02	0.02	0.01	0.01	0.01	0.01	-	-
8	0.03	0.03	0.02	0.02	0.02	0.02	0.02	0.01	0.01	0.01	0.01	-	-
9	0.03	0.03	0.02	0.02	0.02	0.02	0.02	0.01	0.01	0.01	0.01	-	-
10	0.03	0.03	0.02	0.02	0.02	0.02	0.02	0.01	0.01	0.01	0.01	-	-
Original	Panicle index												
1	4.52	4.09	3.80	3.62	3.49	2.95	2.35	1.63	1.34	1.07	0.84	0.59	0.34
2	4.11	3.72	3.46	3.29	3.17	2.68	2.13	1.48	1.22	0.97	0.76	0.53	0.30
3	4.28	3.87	3.60	3.43	3.30	2.79	2.22	1.54	1.27	1.01	0.79	0.56	0.32
4	3.82	3.45	3.21	3.05	2.94	2.49	1.98	1.37	1.13	0.90	0.71	0.49	0.28
5	6.33	5.72	5.32	5.06	4.88	4.13	3.28	2.27	1.88	1.50	1.17	0.82	0.47
Mutant													
6	3.54	3.20	2.98	2.83	2.73	2.31	1.84	1.27	1.05	0.84	0.66	0.46	0.26
7	4.16	3.75	3.49	3.32	3.20	2.71	2.15	1.49	1.23	0.98	0.77	0.54	0.31
8	4.14	3.74	3.48	3.31	3.19	2.70	2.15	1.49	1.23	0.98	0.77	0.54	0.31
9	3.92	3.55	3.30	3.14	3.02	2.56	2.03	1.41	1.16	0.93	0.73	0.51	0.29
10	w5.06	4.57	4.25	4.05	3.90	3.30	2.62	1.82	1.50	1.20	0.94	0.66	0.37

(1)Original, canary seed not subjected to induced mutation; and mutant, canary seed subjected to induced mutation with sodium azide. (2)No response to selection.

that most structures that form the inflorescence and, subsequently, the grains, are not viable in the field. Selection should occur in a way that increases the primary components of performance in the foreground. Selection pressures between 3% and 4% are ideal for this trait and allows of panicle index values greater than 3.0 to be obtained in all populations.

The selection of plants with a compact panicle phenotype that maintain an acceptable number of grains is one of the ways for obtaining promising lineages that will result in higher grain yields in the field.

Conclusions

1. Heritability values and selection gains estimated for canary seed make it possible to obtain improved lines from rigorous selection pressures.

2. Indirect selection for canary seed yield is viable by using easily measurable characteristics, through rigorous selection pressures.

Acknowledgment

To Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), for financial support (307554/2021-0).

References

ABDEL-AAL, E.-S.M. Nutritional and functional attributes of hairless canary seed groats and components and their potential as functional ingredients. **Trends in Food Science & Technology**, v.111, p.680-687, 2021. DOI: https://doi.org/10.1016/j.tifs.2021.03.029.

ACRECHE, M.M.; SLAFER, G.A. Lodging yield penalties as affected by breeding in Mediterranean wheats. **Field Crops**

Research, v.122, p.40-48, 2011. DOI: https://doi.org/10.1016/j.fcr.2011.02.004.

AWAN, F.S.; SADIA, B.; ALTAF, J.; HABIB, M.; HAMEED, K.; HUSSAIN, S. Genetic variability trough induced mutation. In: MAIA, R.; CAMPOS, M. de A. (Ed.). **Genetic variation**. London: IntechOpen, 2021. DOI: https://doi.org/10.5772/intechopen.95027.

AZEVEDO, C.F.; BARRETO, C.A.V.; NASCIMENTO, M.; CARVALHO, I.R.; KEHL, K.; CRUZ, C.D.; NASCIMENTO, A.C.C. Genotype-by-environment interaction of wheat using Bayesian factor analytic models and environmental covariates. **Euphytica**, v.219, art.95, 2023. DOI: https://doi.org/10.1007/s10681-023-03223-z.

AZEVEDO, C.F.; NASCIMENTO, M.; CARVALHO, I.R.; NASCIMENTO, A.C.C.; ALMEIDA, H.C.F. de; CRUZ, C.D.; SILVA, J.A.G. da. Updated knowledge in the estimation of genetics parameters: a Bayesian approach in white oat (*Avena sativa* L.). **Euphytica**, v.218, art.43, 2022. DOI: https://doi.org/10.1007/s10681-022-02995-0.

BAIER, A.C.; FLOSS, E.L.; AUDE, M.I.S. **As lavouras de inverno - 1**: aveia, centeio, triticale, colza, alpiste. Rio de Janeiro: Globo, 1988. v.1, 172p. (Coleção do Agricultor Sul; Publicações Globo Rural).

BANDEIRA, W. J. A.; CARVALHO, I. R.; LORO, M. V.; PRADEBON, L. C.; SILVA, J. A. G. EstimateBreed: Estimation of Environmental Variables and Genetic Parameters. Available at:<https://cran.r-project.org/web/packages/EstimateBreed/index.html>. Accessed on: Apr. 25 2025.

BERRY, P.M.; STERLING, M.; SPINK, J.H.; BAKER, C.J.; SYLVESTER-BRADLEY, R.; MOONEY, S.J.; TAMS, A.R.; ENNOS, A.R. Understanding and reducing lodging in cereals. **Advances in Agronomy**, v.84, p.217-271, 2004. DOI: https://doi.org/10.1016/S0065-2113(04)84005-7.

BORÉM, A.; MIRANDA, G.V. **Melhoramento de plantas**. 5.ed. rev. e ampl. Viçosa: Ed. da UFV, 2009. 529p.

CARVALHO, I.R.; NARDINO, M.; FERRARI, M.; PELEGRIN, A.J. de; DEMARI, G.H.; SZARESKI, V.J.; FOLLMANN, D.N.; BAHRY, C.A.; SOUZA, V.Q. de; OLIVEIRA, A.C. de; MAIA, L.C. Genetic variability among common black bean (*Phaseolus vulgaris* L.,) accessions in southern Brazil. **Australian Journal of Crop Science**, v.10, p.1474-1483, 2016. DOI: https://doi.org/10.21475/ajcs.2016.10.10.p7786.

CHANDLER, P. M.; HARDING, C. A. 'Overgrowth' mutants in barley and wheat: new alleles and phenotypes of the 'Green Revolution' Della gene. **Journal of Experimental Botany**, v.64, p.1605-1613, 2013. DOI: https://doi.org/10.1093/jxb/ert022.

CHANNAOUI, S.; LABHILILI, M.; MOUHIB, M.; MAZOUZ, H.; EL FECHTALI, M.; NABLOUSSI, A. Development and evaluation of diverse promising rapeseed (*Brassica napus* L.) mutants using physical and chemical mutagens. **Oilseed and Fats, Crops and Lipids**, v.26, art.35, 2019. DOI: https://doi.org/10.1051/ocl/2019031.

COGLIATTI, M.; BONGIORNO, F.; DALLA VALLE, H.; ROGERS, W.J. Canaryseed (*Phalaris canariensis* L.) accessions from nineteen countries show useful genetic variation for agronomic traits. **Canadian Journal of Plant Science**, v.91, p.37-48, 2011. DOI: https://doi.org/10.4141/CJPS09200.

DEWI, A.K.; DWIMAHYANI, I.; SOBRIZAL. Application of induced mutation technique to improve genetic variability of Indonesian traditional rice varieties. **IOP Conference Series: Earth and Environmental Science**, v.482, art.012016, 2020. DOI: https://doi.org/10.1088/1755-1315/482/1/012016.

EL-DEGWY, I.S. Mutation induced genetic variability in rice (*Oryza sativa* L.). **Egyptian Journal of Agronomy**, v.35, p.199-209, 2013. DOI: https://doi.org/10.21608/agro.2013.87.

HADFIELD, J.D. MCMC methods for multi-response generalized linear mixed models: the MCMCglmm R package. **Journal of Statistical Software**, v.33, p.1-22, 2010. DOI: https://doi.org/10.18637/jss.v033.i02.

KANNAN, U.; ALTAHER, A.F.; BÅGA, M.; HUCL, P.; CHIBBAR, R.N. Utilization of microsatellite markers to assess hybridity and genetic identity of canary seed (*Phalaris canariensis* L.) genotypes. **Canadian Journal of Plant Science**, v.97, p.835-841, 2017. DOI: https://doi.org/10.1139/cjps-2016-0129.

KHARKWA, M.C. A brief history of plant mutagenesis. In: SHU, Q.Y.; FORSTER, B.P.; NAKAGAWA, H. (Ed.). **Plant mutation breeding and biotechnology**. Wallingford: CABI, 2012. p.21-30.

MALUNGA, L.N.; THANDAPILLY, S.J.; HUCL, P.J.; AMES, N. Effects of genotype and growing year on nutritional composition and pasting properties of glabrous canary seed (*Phalaris canariensis* L.) groat flours. **Foods**, v.13, art.1786, 2024. DOI: https://doi.org/10.3390/foods13111786.

MAY, W.E.; TRAIN, J.C.; GREIDANUS, L. Response of annual canarygrass (*Phalaris canariensis* L.) to nitrogen fertilizer and fungicide applications. **Canadian Journal of Plant Science**, v.102, p.83-94, 2022. DOI: https://doi.org/10.1139/cjps-2020-0221.

NASA POWER. National Aeronautics and Space Administration Prediction of Worldwide Energy Resource. **POWER docs**. Available at: <https://power.larc.nasa.gov/docs/>. Access on: July 4 2023.

OLIVEIRA, H.S. de; RODRIGUES, R.; BENTO, C. dos S.; MEDEIROS, A.M.; SUDRÉ, C.P.; COUTO, M.F.; VIANA, A.P. Towards a new strategy to breed an autogamous plant: a case of study in *Capsicum baccatum* var. *pendulum*. **Scientia Horticulturae**, v.192, p.279-286, 2015. DOI: https://doi.org/10.1016/j.scienta.2015.06.017.

OLIVOTO, T.; LÚCIO, A.DAL'C. metan: an R package for multi-environment trial analysis. **Methods in Ecology and Evolution**, v.11, p.783-789, 2020. DOI: https://doi.org/10.1111/2041-210X.13384.

PALUDETO, J.G.Z.; ESTOPA, R.A.; TAMBARUSSI, E.V. Eficiência da seleção precoce em clones de *Eucalyptus grandis* W. Hill ex Maiden x *Eucalyptus urophylla* S. T. Blake. **Revista do Instituto Florestal**, v.29, p.169-179, 2017. DOI: https://doi.org/10.24278/2178-5031.201729203.

PATTERSON, C.A.; MALCOLMSON, L.; LUKIE, C.; YOUNG, G.; HUCL, P.; ABDEL-AAL, E. Glabrous canary seed: a novel food ingredient. **Cereal Foods Word**, v.63, p.194-200, 2018. DOI: https://doi.org/10.1094/CFW-63-5-0194.

PHAREL, P.G. **Tratamento de sementes de arroz (oryza sativa l.) com azida sódica em diferentes condições de ambiente**. 1994. 140p. Dissertação (Mestrado) - Universidade de São Paulo, Piracicaba.

QUADROS, V.; CARVALHO, I.R.; DEMARI, G.H.; SOUZA, V.Q. de; FERREIRA, L.L.; MOURA, N.B.; MARTINS, T. da S.; SILVA, J.A.G. da; LAUTENCHLEGER, F.; LORO, M.V. Parameters and genetic variability in black beans f5 families. **Functional Plant Breeding Journal**, v.4, art.9, 2022. DOI: https://doi.org/10.35418/2526-4117/v4n1a9.

R CORE TEAM. **R**: a language and environment for statistical computing. Vienna: R Foundation for Statistical Computing, 2023.

RESENDE, M.D.V. de; ARAÚJO, A.J. de; SAMPAIO, P. de T.B.; WIECHETECK, M.S.S. Acurácia seletiva, intervalos de confiança e variâncias de ganhos genéticos associados a 22 métodos de seleção em *Pinus caribaea* var. *hondurensis*. **Floresta**, v.25, p.3-16, 1995.

RIKAL, L.I.; FIGUEIREDO, A.K.; RICCOBENE, I.C. Physicochemical and functional properties of canaryseed (*Phalaris canariensis* L.) with and without spicules flour. **Cereal Chemistry**, v.100, p.904-913, 2023. DOI: https://doi.org/10.1002/cche.10669.

SANTOS, H.G. dos; JACOMINE, P.K.T.; ANJOS, L.H.C. dos; OLIVEIRA, V.A. de; LUMBRERAS, J.F.; COELHO, M.R.; ALMEIDA, J.A. de; ARAUJO FILHO, J.C. de; OLIVEIRA, J.B. de; CUNHA, T.J.F. **Brazilian soil classification system**. 5th ed. rev. and exp. Brasília: Embrapa, 2018. 335p.

SETZER, J. **Atlas climático ecológico do estado de São Paulo**. São Paulo: Comissão Interestadual da Bacia Paraná-Uruguai, 1966. 61p.

SILVA, F.A. da; VIANA, A.P.; CORRÊA, C.C.G.; CARVALHO, B.M.; SOUSA, C.M.B. de; AMARAL, B.D.; AMBRÓSIO, M.; GLÓRIA, L.S. Impact of Bayesian inference on the selection of *Psidium guajava*. **Scientific Reports**, v.10, art.1999, 2020. DOI: https://doi.org/10.1038/s41598-020-58850-6.

VALADARES, N.R.; FERNANDES, A.C.G.; RODRIGUES, C.H.O.; GUEDES, L.L.M.; MAGALHÃES, J.R.; ALVES, R.A.; ANDRADE JÚNIOR, V.C. de; AZEVEDO, A.M. Estimation of genetic parameters and selection gains for sweet potato using Bayesian inference with *a priori* information. **Acta Scientiarum. Agronomy**, v.45, e56160, 2023. DOI: https://doi.org/10.4025/actasciagron.v45i1.56160.