

Genetic parameters and selection of sugarcane for borer resistance in the advanced selection stage

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Abstract: This study aimed to investigate genetic parameters and selection strategies for sugarcane resistance to borer and determine the effects of selection for borer resistance on yield traits. The infestation index by borer (IIB) and yield traits were assessed over 3 years in 35 sugarcane clones planted in four locations in southeastern Brazil. There was no genotype \times environment (year or location) interaction for borer resistance. Consequently, selection may be performed at only one location and year or by the mean of clones in several locations and/or years. The borer population affected the genotypic variance for borer resistance but when genotypic variance was significant, heritability was elevated and suitable genetic gain was achieved. Selection for borer resistance reduced the genetic gains for tons of cane per hectare, theoretical recoverable sugar, and tons of sugar per hectare; however, satisfactory selection gains for both borer resistance and yield were achieved using selection index.

Keywords: *Saccharum spp.*, *Diatraea saccharalis*, genotype \times environment interaction.

INTRODUCTION


Brazil is the world's largest sugarcane producer. The sugarcane crop area in the country covers nearly 8.38 million hectares and sugarcane production during the 2019/20 agricultural year is estimated at 622.3 million tons. It is estimated that sugar production will reach 31.8 million tons and ethanol production 30.3 billion liters (CONAB 2019)

The sugarcane stalk borer *Diatraea saccharalis* Fab. (Lepidoptera: Crambidae) is one of the major pests of sugarcane in Brazil and causes severe yield losses across the country (Francischini et al. 2017). The larvae open galleries in the stalks, reducing sugar content and stalk weight. In addition, it enables the entrance of fungus that causes red rot disease, which reduces both sugar yield and quality (Tomaz et al. 2017). This pest is managed using biological control with larval endoparasitoid *Cotesia flavipes* and egg parasitoid *Trichogramma galloi*. However, the use of chemical insecticides has increased (Simões et al. 2015, Valente et al. 2018).

The use of sugarcane varieties resistant to this pest is an important tool for Integrated Pest Management (IPM), enabling reduced environmental impacts, production costs, and yield losses (Milligan et al. 2003). Currently, transgenic sugarcane varieties resistant to *D. saccharalis* containing genes from *Bacillus*

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thuringiensis bacteria (*Bt*) have been released in Brazil (MAPA 2019). However, there is the possibility of the rapid evolution of sugarcane borer resistance to *Bt* proteins under large-scale field use (Girón-Pérez et al. 2014, Cristofolletti et al. 2018). The development of sugarcane genotypes resistant to the borer through conventional breeding could enable more durable resistance and could be performed in sugarcane breeding programs with no access to transgenic technologies.

Several resistance mechanisms against the sugarcane borer have been reported in sugarcane genotypes, including a low preference for oviposition, high mortality of early-instar larvae, the difficulty of larvae entering the stalks, and lower larvae development within the stalks (Pimentel et al. 2017, Tomaz et al. 2017). In addition, differences among genotypes are often reported in field trials for several resistance traits, such as the percentage of bored internodes or internodes with exit holes, percentage of bored stalks, pupation success, estimates of adults produced per area/year/variety, and the damage rating (Bessin et al. 1990, White 1993, White et al. 2011, Milligan et al. 2003, Nibouche and Tibere 2008, Nikpay 2016). Among these traits, the percentage of bored internodes (or infestation index) is the most effective trait for the prediction of yield losses (Milligan et al. 2003) and it is often assessed in sugarcane populations as an indication of the resistance level of the genotypes.

The study of genetic parameters in the populations is essential to determining the appropriate selection strategies when breeding for quantitative traits, such as borer resistance (White et al. 2001, Milligan et al. 2003). These parameters include genotypic variance, heritability, genotype × environment (location and year) interactions, and genetic correlation among traits. These parameters have been extensively studied in Brazil for several sugarcane traits, such as tons of cane per hectare (TCH) (Veríssimo et al. 2012), tons of Brix per hectare (TBH) (Bastos et al. 2007, Veríssimo et al. 2012), and tons of sugar per hectare (TSH) (Silveira et al. 2012). However, only a few studies regarding the genetic parameters for the resistance of sugarcane to borers, such as *D. saccharalis* and spotted borer *Chilo sacchariphagus* (Lepidoptera: Pyralidae), have been reported (White et al. 2001, Milligan et al. 2003, Nibouche and Tibere 2008, Tomaz et al. 2019). In addition, there is a need for studies regarding selection for borer resistance, in addition, to yield traits, because selection only for borer resistance may result in genotypes with unfavorable traits and lower sugar yield (White et al. 2006, White et al. 2011).

The lack of knowledge regarding genetic parameters of Brazilian sugarcane populations and selection strategies hinders the selection of resistance genotypes by Brazilian sugarcane breeding programs. Therefore, the goals of this study were to estimate genetic parameters (genotypic variance, heritability), assess the influence of the genotype × environment interaction in borer resistance, determine the effects of selection for borer resistance on yield traits, and compare selection strategies for borer resistance at several locations, across years, and for borer resistance in addition to yield traits.

MATERIAL AND METHODS

Plant material and experimental design

The genotypes used in this study compose the advanced stage or experimental stage of the sugarcane breeding program of the Universidade Federal de Viçosa, in partnership with RIDESA (Inter-university Network for the Development of Sugarcane Industry) (Gazaffi et al. 2016). The experiments were conducted on farms of RIDESA's partner mills in four locations: Iturama, Itapagipe, Ituiutaba, and Tupaciguara counties, Minas Gerais state, southeastern Brazil. Planting of sugarcane clones was conducted between April–May 2013. Soil fertilization, crop management, and harvest were performed according to procedures established and adopted by the growers. Each experiment was composed of two commercial sugarcane varieties (checks) and the genotypes selected in the previous selection stage (T3) by RIDESA's sugarcane breeding program. The experimental information on the number of genotypes, blocks, and plot sizes for each experiment are summarized in Table 1. The total number of genotypes used in all experiments was 35. The genotypes were not planted in all locations because of the lack of propagation material and restricted field area. However, most genotypes were repeated in at least two locations.

Data collection

For assessment of borer damage, 20 whole stalks per plot were randomly selected and harvested. Stalks were split longitudinally and the number of total internodes and bored internodes were recorded to calculate the infestation index (IIB) by borer with the formula:

Table 1. Number of genotypes and blocks, plot size, and years of assessment in the experimental net for sugarcane resistance to the borer

Locations	Genotypes	Blocks	Plots	Assessments	Checks
Itapagipe	18	4	4 rows (19 x 1.5 m)	2015, 2016	RB867515, RB966928
Iturama	18	5	5 rows (5 x 1.5 m)	2015, 2016, 2017	RB867515, CTC9
Ituiutaba	24	4	4 rows (19 x 1.5 m)	2015	RB867515, CTC9
Tupaciguara	24	5	5 rows (5 x 1.5 m)	2016, 2017	RB867515, RB855453
Genotypes (number of locations)					
RB855453 (1)	RB057246 (1)	RB047025 (2)	RB057249 (3)	RB047212 (3)	RB867515 (4)
RB966928 (1)	RB047413 (1)	RB047137 (2)	RB047016 (3)	RB047227 (3)	RB047002 (4)
RB047086 (1)	RB057230 (1)	RB057243 (2)	RB047018 (3)	RB047258 (3)	RB047226 (4)
RB047210 (1)	RB057235 (1)	RB057267 (2)	RB047055 (3)	RB057270 (3)	RB047248 (4)
RB047228 (1)	RB057237 (1)	RB047412 (2)	RB047050 (3)	RB057231 (3)	RB047409 (4)
RB057008 (1)	CTC9 (2)	RB057169 (2)	RB047201 (3)	RB057145 (4)	

$IIB = \left(\frac{\text{number of bored internodes}}{\text{total number of internodes}} \right) \times 100$ (White et al. 2011). The assessments of borer damage were performed in July 2015, July 2016, and July 2017, respectively, for the first, second, and third ratoon crops.

Because of the likely genotype \times location interaction for yield traits (Veríssimo et al. 2012, Silveira et al. 2012), the study of selection for borer resistance in addition to that of yield traits was performed at only one location. For this study, the theoretical recoverable sugar (TRS), TCH, and TSH were assessed in the experiment in Iturama during the agricultural years of 2015, 2016, and 2017. The number of stalks per meter and the mean weight of the stalks were assessed for TCH determination. Ten stalks per plot were weighed to estimate the mean weight of the stalks. Then, the stalks were taken to the lab of the sugar and alcohol industry for the determination of TRS. The TCH was estimated by the formula:

$$TCH = \frac{\text{number of stalks per meter} \times \text{mean weight of stalk} \times 10000}{1.5}$$

The TRS was estimated according to standard procedures used by the mills (Consecana 2006).

Data analysis

Genetic parameters and comparison of selection scenarios for borer resistance

The data for the infestation index were analyzed together using mixed models with the software Selegen-Restricted Maximum Likelihood (REML)/Best Linear Unbiased Predictors (BLUP) (Resende 2016). The data on the infestation index by *D. saccharalis* were analyzed considering four selection scenarios: single experiments, one location over 3 years, three locations in 1 year, and four locations over 3 years. The genetic parameters were estimated using the REML method. The significance of the effects (i.e., genotypic variance, genotype \times location interaction) was analyzed by deviance analysis (Likelihood Ratio Test) and the genotypic values were estimated by the BLUP (Resende 2016).

The genotypic values within every single experiment were estimated using the model:

$$y = Xr + Zg + e$$

where, y is the vector of phenotypic data, r is the vector of fixed block effects, g is the random effect of genotypes, and e is the vector of error. The capital letters represent the incidence matrix for the referred effects in the model described above and follow the models described below.

The genotypic values in one location (Iturama) over three years (2015, 2016, and 2017) were estimated by using the model:

$$y = Xm + Zg + Wp + Ti + e$$

where, y is the vector of phenotypic data, m is the vector of fixed effects of the year-block combination, g is the vector of random effects of genotypes, p is the vector of random effects of the environment or plot, i is the vector of the random interaction of genotype \times year and e is the vector of error.

The genotypic values in three locations (Iturama, Ituiutaba, and Itapagipe) and one year (2015) were estimated by using the model:

$$y = Xr + Zg + Wi + e$$

where, y is the vector of phenotypic data, r is the vector of fixed block effects, g is the vector of random effects of genotypes, i is the vector of the random interaction of genotype \times location, and e is the vector of error.

The genotypic values for selection in four locations over 3 years (Iturama, Itapagipe, and Ituiutaba in 2015, Iturama, Itapagipe, and Tupaciguara in 2016, and Iturama and Tupaciguara in 2017) were estimated by the model:

$$y = Xf + Zg + Qgl + Tgm + Wgml + Sp + e$$

where, y is the vector of phenotypic data, f is the vector of fixed effects of the block-location-year combination, g is the vector of random effects of genotypes, gl is the vector of the random effects of interaction of genotype \times location, gm is the vector of the random effects of interaction of genotype \times year, gml is the vector of the random effects of triple interaction of genotype \times location \times year, p is the vector of the random effects of plots within locations, and e is the vector of error.

Effect of selection for borer resistance in yield traits and use of selection index

The data for TRS, TCH, IIB, and TSH in the experiment of Iturama (2015, 2016, and 2017) were used to assess the effects of selection for borer resistance on yield traits and use of the selection index. The genotypic values for each trait were estimated using the model $y = Xm + Zg + Wp + Ti + e$, as previously described.

The direct and indirect genetic gains were estimated by the following formulas:

$$GG_i\% = (X_{si} - X_{oi}) \times 100 / X_{oi}$$

$$GG_{j(i)}\% = (X_{sj(i)} - X_{oj}) \times 100 / X_{oj}$$

Where, GG_i is the genetic gain for trait i by direct selection for the trait i ; X_{si} is mean of individuals selected for trait i ; X_{oi} is the grand mean of the population for trait i ; $GG_{j(i)}$ is the indirect genetic gain for character j , by selection for the trait i ; $X_{sj(i)}$ is the mean of trait j in the individuals selected for the trait i ; and X_{oj} is the grand mean of the population for trait j .

The additive index was simultaneously used to select the genotypes for IIB, TCH, and TRS. The genotypic values predicted by BLUP were used to create the selection index.

The index coefficients for the genotypes were estimated by the formula:

$$I = (p \times TCH) \times (GV \times TCH) + (p \times TRS) \times (GV \times TRS) + (p \times IIB) \times (GV \times TCIIBH)$$

Where: p = economic weight (genetic standard deviation) and GV = genotypic value of the trait (Pedrozo et al. 2009). The efficiency of the selection index was obtained using the coincidence coefficient of selected genotypes by the index with the genotypes selected for TSH, which is the main sugar yield trait (Pedrozo et al. 2009).

RESULTS AND DISCUSSION

Genetic parameters and comparison of selection scenarios for borer resistance

The mean infestation by borer varied among years (11.54, 4.14, and 6.75% of bored internodes, respectively, in 2015, 2016, and 2017), which was likely related to environmental factors. The natural infestation pressure by the borer had a significant effect on the assessment of genetic variability in the population for borer resistance and on the experimental precision. For instance, the genetic variance was not significant in 2016 in the experiment in Iturama, when the infestation index by borer (IIB) was low (6.37%), but it was significant in 2015 and 2017, where infestation indexes were higher (13.85 and 9.22%, respectively) (Table 2). To overcome this issue, the sugarcane breeding program of the USDA (United States Department of Agriculture) commonly enhances borer pressure with an adjacent planting of maize (*Zea mays* L.), which is artificially inoculated with borer larvae and insecticides are applied to control natural enemies of the borer

Table 2. Genetic parameters for infestation index by *D. saccharalis* in individual experiments and three selection scenarios

Estimates	First year (2015)			Second year (2016)			Third year (2017)	
	Itapagipe	Iturama	Ituiutaba	Itapagipe	Iturama	Tupaciguara	Iturama	Tupaciguara
σ_g^2	2.22	4.93*	13.88**	0.02	0.97	1.15*	4.50**	0.06
σ^2	8.95	17.62	15.72	1.94	9.91	5.1	9.53	5.19
σ_p^2	11.17	22.55	29.6	1.96	10.87	6.25	14.03	5.25
h_{gm}^2	0.5	0.58	0.78	0.04	0.33	0.53	0.7	0.05
Ac	0.71	0.76	0.88	0.19	0.57	0.73	0.84	0.19
CV	0.38	0.3	0.31	0.98	0.49	0.49	0.33	0.53
Mean	7.91	13.85	12.85	1.42	6.37	4.62	9.22	4.27
GG(%)	ND	-14.52	-28.82	ND	ND	-23.10	-16.79	ND

	One location ¹ , 3 years ²	Three locations ³ , 1 year ⁴	Four locations ⁵ , 3 years
σ_g^2	2.18*	5.86**	1.80**
σ_{gy}^2	1.28	-	0.47
σ_{gl}^2	-	1.87	0.63
σ_{gyl}^2	-	-	0.77
σ^2	12.2	14.6	9.18
σ_p^2	15.82	22.34	14.69
h_{gm}^2	0.63	0.74	0.80
Ac	0.77	0.86	0.89
r_{gy}	0.63	-	0.79
r_{gl}	-	0.76	0.74
r_{gyl}	-	-	0.49
Mean	9.81	11.82	7.63
GG(%)	-8.89	-16.82	-14.17

σ_g^2 = Genetic variance, σ^2 = Residual variance, σ_p^2 = Phenotypic variance, h_{gm}^2 = Heritability of genotypic mean, Ac = Accuracy of selection by genotypic mean, CV = Coefficient of residual variance, GG = Genetic gain, considering 20% of genotypes selected, σ_{gy}^2 = Variance of genotype × year interaction, σ_{gl}^2 = Variance of genotype × location interaction, σ_{gyl}^2 = Variance of genotype × year × location triple interaction, r_{gy} = Genotypic correlation between years, r_{gl} = Genotypic correlation between locations, r_{gyl} = Genotypic correlation among locations and years, ND = Non-determined. * Significant at $P < 0.05$ and ** Significant at $P < 0.01$, according to deviance analysis. ¹ Iturama, ² 2015, 2016, and 2017, ³ Iturama, Itapagipe, and Ituiutaba, ⁴ 2015, ⁵ Iturama, Itapagipe, and Ituiutaba in 2015, Iturama, Itapagipe, and Tupaciguara in 2016, and Iturama and Tupaciguara in 2017.

(White et al. 2001). However, an artificial infestation is not recommended in experiments located in field areas of mills because of the risk of infesting commercial crop areas. In this case, selection for borer resistance must be performed in locations and years with high natural infestations.

The individual analysis of the experiments demonstrated that the genotypic variance was significant in four of eight experiments, indicating a difference among genotypes in borer resistance (Table 2). The genetic gain of selection (~20% of genotypes selected) varied from 14.42 to 28.82, which is considered to be high.

In the analysis of the IIB in the three studied selection scenarios, the genotypic variances for genotype × year, genotype × location, and genotype × year × location interactions were not significant (Table 2). In addition, the genotypic correlations between years, locations, and year × location combinations were high, indicating a high consistency in genotype classification among environments (years or locations). White et al. (2001) examined the resistance of sugarcane families to *D. saccharalis* and found no significant family × year interaction. Previous studies also indicated no significant genotype × location interaction in sugarcane resistance to *D. saccharalis* (Milligan et al. 2003) and the spotted borer *C. sacchariphagus* (Nibouche and Tibere 2008). However, our h appeared to be the first to consider the genotype × location × year triple interaction. In all studied selection scenarios, the genotypic variance was significant, which fosters the achievement of genetic gains for borer resistance (Table 2).

The broad-sense heritability for IIB in individual experiments where the genotypic variance was significant or in the studied selection scenarios were moderate to high and relatively similar ($0.53 < h^2 < 0.78$). These heritabilities were close to that reported by Milligan et al. (2003) for the infestation index by *D. saccharalis* ($h^2 = 0.62$) and to the value

found by Nibouche and Tibere (2008) for the infestation index by the spotted borer *C. sacchariphagus* ($h^2 = 0.80$). The high heritabilities enabled the acquisition of satisfactory genetic gains by selecting for borer resistance ($28.82\% < GG < 8.89\%$) (Table 2).

The coincidence of genotypes selected for borer resistance was high among the individual experiments (Table 3) and selection scenarios (Table 4). For instance, the genotypes RB047050, RB047226, RB047055, RB047212, RB047201, and RB047258, which were selected considering the most complete selection scenario (four locations and 3 years) were selected in most of the situations, confirming high consistence among the experiments.

The accuracy of predicting genotypic values for the genotype in single experiments was high ($Ac > 0.70$) (Table 3). On the other hand, the accuracy of predicting genotypic values for the IIB in several locations depended on the number of locations where the clone was present. The accuracies for the genotype present at only one location were relatively low ($Ac < 0.70$), whereas the accuracies for the genotype present in at least two locations were high ($Ac > 0.70$) (Table 4).

Overall, because of the non-significant effect of genotype \times environment (location or year) interaction in the sugarcane resistance to borer, the genotypes could be selected for borer resistance in a single experiment or by means of experiments in several locations. The selection in a single location in 1 year is advantageous because of the cost effectiveness of the borer damage assessment because it is a field based and labor-intensive task, as highlighted by Milligan et al. (2003). However, the genotypes that advance to the experimental stages of a sugarcane breeding program are often not planted in all locations of the experimental network because of technical issues, such as the lack of propagation material or field area. The selection in a single location could exclude several genotypes from selection for borer resistance. In this case, the genotypes could be selected by means of an infestation index in all assessed locations. This practice could enable

Table 3. Genotypic values of sugarcane genotypes for infestation index by borer (IIB%) in individual experiments

Rank	Iturama (2015)		Ituiutaba (2015)		Tupaciguara (2016)	
	Clone	IIB (%)	Clone	IIB (%)	Clone	IIB (%)
1	RB047055	11.26	RB047201	7.64	RB047258	3.28
2	RB047248	11.99	RB047212	9.12	RB047212	3.49
3	RB047226	12.04	RB047409	9.41	RB047050	3.53
4	RB047050	12.06	RB047018	9.76	RB047409	3.71
5	RB047002	12.29	RB047002	9.79	RB047055	3.78
6	RB047258	12.50	RB047226	10.12	RB047413	4.03
7	RB047201	12.76	RB047258	10.30	RB047412	4.15
8	RB047025	13.10	RB047412	10.56	RB057230	4.18
9	RB047409	13.65	RB047050	10.85	RB057231	4.46
10	RB057145	14.06	RB867515	11.33	RB047226	4.47
11	RB057267	14.11	RB047228	11.52	RB057270	4.51
12	RB057270	14.79	RB047227	11.76	RB855453	4.67
13	CTC9	14.80	RB047086	12.48	RB057169	4.73
14	RB867515	15.15	RB057243	12.49	RB057235	4.79
15	RB047249	15.47	RB057246	12.68	RB047016	4.79
16	RB057231	16.17	RB047248	14.15	RB047002	4.96
17	RB047016	16.45	CTC9	14.17	RB057237	5.00
18	RB057243	16.64	RB047016	15.36	RB047018	5.04
19	$Ac = 0.74$		RB057169	15.50	RB867515	5.04
20			RB057231	16.15	RB047227	5.04
21			RB047137	17.42	RB047248	5.38
22			RB057145	18.12	RB057243	5.58
23			RB047249	18.23	RB057145	5.96
24			RB057008	19.40	RB047249	6.44
			$Ac = 0.86$		$Ac = 0.71$	

u + g = Genotypic values (BLUP's) for infestation index by borer. Ac = Accuracy for genotypic value prediction. Bold letters represent the genotypes selected for borer resistance in the 3 year – four location selection scenario. Ac = Accuracy.

accurate prediction of the resistance of all the genotypes to the sugarcane borer, especially the genotypes assessed in more than one location.

Effects of the selection for borer resistance on yield traits and use of the selection index

The yield traits assessed to select sugarcane genotypes usually present a significant genotype × location interaction (Bastos et al. 2007, Silveira et al. 2012). Therefore, the study of the effect of selection for borer resistance in yield traits and the use of the selection index was performed at only one location. The TCH, TRS, and TSH were analyzed based on data from the experiment in Iturama during 2015, 2016, and 2017. The analyses showed that there was no genotype × year interaction for any trait and genotypic variance was significant for all traits (Table 5). Therefore, genetic gains of selection could be obtained for all traits.

Table 4. Genotypic values of sugarcane genotypes for infestation index by borer (IIB) in three selection scenarios

Rank	Four locations ¹ , 3 years ²				Three locations ³ , 1 year ⁴			One location ⁵ , 3 years ²	
	Clone	IIB (%)	n	Ac	Clone	IIB (%)	Ac	Clone	IIB (%)
1	RB047201	5.56	3	0.80	RB047201	8.92	0.86	RB047055	7.72
2	RB047212	6.01	3	0.79	RB047212	9.47	0.81	RB047201	8.20
3	RB047055	6.31	3	0.82	RB047226	9.49	0.86	RB047409	8.77
4	RB047258	6.60	3	0.81	RB047018	9.62	0.81	RB047050	8.82
5	RB047226	6.63	4	0.84	RB047050	9.91	0.82	RB047226	8.98
6	RB047050	6.70	3	0.81	RB047055	9.93	0.82	RB047002	9.12
7	RB047409	6.83	4	0.84	RB047258	9.97	0.82	RB047258	9.22
8	RB047018	6.86	3	0.79	RB047002	10.25	0.86	RB057145	9.47
9	RB047002	6.98	4	0.84	RB047412	10.34	0.70	RB047025	9.55
10	RB047412	7.06	2	0.73	RB047227	10.42	0.81	RB057267	9.59
11	RB047210	7.11	1	0.64	RB047210	10.43	0.70	RB867515	9.65
12	RB047228	7.14	1	0.54	RB047248	10.82	0.86	CTC9	10.04
13	RB047413	7.20	1	0.66	RB047409	10.88	0.86	RB047016	11.02
14	RB057230	7.26	1	0.66	RB047228	10.97	0.70	RB047248	11.21
15	RB047227	7.26	3	0.79	RB047086	11.61	0.70	RB057270	11.23
16	RB855453	7.37	1	0.66	RB047025	11.73	0.82	RB057231	11.29
17	RB047025	7.45	2	0.78	RB057267	11.73	0.82	RB057249	11.36
18	RB867515	7.46	4	0.84	RB057246	11.74	0.70	RB057243	11.42
19	RB057267	7.46	2	0.78	RB966928	11.86	0.70		
20	RB047086	7.51	1	0.54	RB867515	12.41	0.86		
21	RB057246	7.59	1	0.54	CTC9	13.04	0.82		
22	RB057235	7.61	1	0.66	RB057243	13.28	0.86		
23	RB966928	7.72	1	0.64	RB047137	13.51	0.81		
24	CTC9	8.05	2	0.75	RB057169	13.60	0.70		
25	RB047248	8.26	4	0.84	RB057270	13.90	0.82		
26	RB057237	8.31	1	0.66	RB057145	14.16	0.86		
27	RB057243	8.40	2	0.84	RB047016	14.58	0.82		
28	RB057169	8.55	2	0.73	RB057231	14.73	0.82		
29	RB047016	8.72	3	0.81	RB057249	15.15	0.82		
30	RB057145	8.75	4	0.84	RB057008	16.18	0.70		
31	RB057231	8.81	3	0.81					
32	RB047137	8.81	2	0.71					
33	RB057270	8.91	3	0.82					
34	RB057249	9.78	3	0.81					
35	RB057008	10.19	1	0.54					

Ac = Accuracy for genotypic value prediction. ¹ Iturama, Itapagipe, and Ituiutaba in 2015, Iturama, Itapagipe, and Tupaciguara in 2016, and Iturama and Tupaciguara in 2017. ² 2015, 2016, 2017. ³ Iturama, Itapagipe, and Ituiutaba. ⁴ 2015. ⁵ Iturama. Bold letters represent the genotypes selected for borer resistance in the 3 year – four location selection scenario. *n is the number of experiments in which the clone was present.

Even though the selection of the sugarcane genotypes for infestation index provided considerable genetic gains for borer resistance, the indirect genetic gain in TRS, TCH, and especially TSH were much lower than would be obtained by direct selection for each trait, with some even exhibiting negative values (Table 5). The selection for only borer resistance may result in genotypes with unfavorable traits and lower sugar yield (White et al. 2006, White et al. 2011). Therefore, the use of the selection index was justified.

The use of selection index using IIB, TRS, and TCH enabled the acquisition of high genetic gains for all traits, providing values close to those that would be obtained by direct selection for each trait (Table 5). In addition, there was a high coincidence between the genotypes selected by the selection index and the genotypes selected for TSH (coincidence coefficient = 83.33%), which is the main trait targeted in sugarcane breeding and reflects the yield of the main product of the sugarcane crop. We highlighted the consistency of the selection index by the fact that the control variety RB867515, which is known to have high borer resistance level (Ferreira et al. 2018) and high TBH (Bastos et al. 2007, Silveira et al. 2012), was selected using the designed selection index.

Indeed, as the genotypes used in this study composed the most advanced stage of RIDESA's breeding program, they underwent several selection steps and had favorable agronomic traits, which created potential varieties could be

Table 5. Genetic parameters, genotypic values, and direct and indirect genetic gains by direct selection for each trait, selection for borer resistance, and selection using the selection index for tons of cane per hectare (TCH), theoretical recoverable sugar (TRS), infestation index by borer (IIB), and tons of sugar per hectare (TSH)

Estimates	TCH	TRS	IIB	TSH
σ_g^2	160.43**	35.61**	2.01**	5.00**
σ_{gy}^2	35.58	7.20	0.68	0.82
σ^2	233.06	54.05	13.36	7.16
σ_p^2	444.37	97.74	16.66	13.06
h_{gm}^2	0.82	0.83	0.57	0.85
r_{gy}	0.82	0.83	0.77	0.86
Mean	131.55	139.98	9.88	18.43
GG by direct selection for the trait (%)	10.57	4.18	-11.31	12.64
Indirect GG by selection for infestation index (%)	1.44	-0.07	-11.31	1.39
Indirect GG by selection using selection index (%)	8.37	2.67	-8.23	11.78

Rank of genotypes according to selection index	Genotypic values			
	TCH	TRS	IIB	TSH
CTC9*	148.76*	151.58*	10.03	22.95*
RB047055*	128.01	146.33*	8.00*	18.79
RB047409*	148.34*	140.71	8.89*	20.95*
RB047002*	134.70	148.13*	9.18*	20.02*
RB867515*	149.93*	140.24	9.64	21.12*
RB047201*	145.62*	135.31	8.64*	19.79*
RB057145	138.21*	142.37*	9.61	19.74*
RB047050	123.04	137.13	8.74*	16.81
RB047016	130.74	142.78*	11.19	18.69
RB047258	127.00	135.11	9.29	17.18
RB057249	130.98	141.65	11.28	18.53
RB047025	113.87	141.47	9.64	15.96
RB057243	124.34	143.75*	11.35	17.90
RB057267	120.73	137.83	9.86	16.50
RB047248	141.89*	132.89	10.99	18.75
RB047226	120.95	131.69	9.10*	15.77
RB057270	117.91	137.38	10.94	16.07
RB057231	122.89	133.27	11.41	16.26

σ_g^2 = Genotypic variance, σ_{gy}^2 = Variance of genotype \times year interaction, σ^2 = Residual variance, σ_p^2 = Phenotypic variance, h_{gm}^2 = Heritability for genotypic mean, r_{gy} = Genotypic correlation among years, GG = genetic gain, considering an ~20% of genotypes selected, ** Significant at $P < 0.01$, according to deviance analysis. * Genotypes selected by direct selection for the respective trait.

recommended to the growers. The most resistant of these genotypes could be readily recommended for locations with higher borer pressure if they combine borer resistance with other favorable agronomic traits, such as high sugar yield.

CONCLUSIONS

The borer population influences both genotypic variance and heritability; thus, it is necessary to select sugarcane clones for borer resistance in areas with high natural borer infestation to achieve suitable genetic gains.

The genotypes could be selected either in a single location and single year or through genotypic means in several locations, years, or location and year combinations.

Selection for borer resistance reduces the genetic gains for TCH, TRS, and TSH. However, the use of the selection index combining IIB with TCH and TRS may enable the selection of genotypes with considerable both borer resistance and sugar yield.

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