ADRIANO CIRINO TOMAZ

GENETIC PARAMETERS AND STRATEGIES FOR SELECTING SUGARCANE GENOTYPES FOR BORER RESISTANCE

Tese apresentada à Universidade Federal de Viçosa, como parte das exigências do Programa de Pós-Graduação em Fitotecnia para obtenção do título de Doctor Scientiae.

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A meus pais João e Cleusa e à minha irmã Adriana, com os quais aprendi tudo de importante,

DEDICO.

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Contents

RESUMO

TOMAZ, Adriano Cirino, D.Sc. Universidade Federal de Viçosa, abril de 2018. **Parâmetros genéticos e estratégias de seleção de genótipos de cana-de-açúcar para resistência à broca-da-cana**. Orientador: Márcio Henrique Pereira Barbosa. Coorientadores: Luiz Alexandre Peternelli e Marcos Deon Vilela de Resende.

A broca-da-cana Diatraea saccharalis (Lepidoptera: Crambidae) é uma das principais pragas da cana-de-açúcar no Brasil e vem sendo controlada principalmente por controle biológico e químico. Não há variedades de cana-de-açúcar resistentes à broca-da-cana no Brasil. A falta de estudos sobre parâmetros genéticos nas populações brasileiras de melhoramento e sobre métodos de seleção dificulta o desenvolvimento de variedades resistentes por programas de melhoramento genético convencionais. Assim, o objetivo deste estudo foi estimar parâmetros genéticos e comparar estratégias de seleção de cana-de-açúcar para resistência à broca-da-cana em diferentes fases de seleção. O estudo foi divido em duas partes, sendo que na primeira parte foi avaliada uma população na fase T1 (população de sementes verdadeiras) e uma na fase T2 (primeira geração de seleção clonal). Na segunda parte do estudo, foi utilizada uma população em fase experimental (FE). Os objetivos do experimento T1 foram: estimar variância genotípica entre famílias de irmãos completos, herdabilidade individual e em nível de médias de famílias, efeitos genéticos aditivo e e não-aditivo; comparar seleção massal, seleção de famílias e seleção de genitores. Os objetivos do experimento T2 foram: estimar herdabilidade em nível de média de clones e variância genotípica entre clones; e confirmar a eficiência na seleção de famílias na fase T1. O experimento T1 foi conduzido no delineamento em blocos casualizados com 46 famílias de irmãos-completos e quatro repetições por família, sendo implementado no ano de 2014 no município de Iturama-MG. No ano de 2015, foi feita a avaliação do índice de infestação por broca (IIB) em 10 plantas por parcela, totalizando 40 plantas por família. No ano de 2016, foram selecionados 32 individuos das três famílias mais resistentes e 32 individuos das três famílias mais suscetíveis para compor o experimento T2, plantado no município de Capinópolis-MG. Este experimento foi conduzido no delineamento em blocos casualizados com cinco repetições e 64 clones. O IIB foi avaliado em 2017. No experimento T1, a herdabilidade para média de famílias ($h^2 = 0.77$) foi maior do que herdabilidade individual ($h^2 = 0.16$), indicando que seleção de famílias é mais eficiente do que a seleção individual (massal). A variância genotípica entre média de famílias foi significativa, indicando a possibilidade de seleção de famílias para resistência à broca.

O efeito genético aditivo é mais importante do que o efeito de dominância. Assim, a seleção de genitores pode ser feita com base em seus efeitos genéticos aditivos. No exerimento T2 a variância genotípica entre indivíduos dentro da mesma família foi significativa, indicando haver grande variabilidade dentro de famílias de irmãos-completos. Deste modo, a seleção pela média de famílias na fase T1 deve ser seguida da seleção de clones na fase T2, onde é possível avaliar os clones em experimentos com repetições e com herdabilidade moderada ($h^2 = 0.61$). O objetivo da segunda parte do trabalho foi avaliar os efeitos das interações genótipo x ambiente (locais, anos) na seleção para resistência à broca; o efeito da seleção para a resistência à broca em componentes de produção (toneladas de cana por hectare (TCH), açúcares teoricamente recuperáveis (ATR) e toneladas de POL por hectare (TPH)); e avaliar o uso de índice de seleção para selecionar clones para resistência à broca conjuntamente com componentes de produção. O IIB foi avaliado em uma população em fase experimental (FE) com 35 clones, plantados em quatro locais em experimentos com quatro ou cinco repetições e com 18 ou 24 clones por local. O IIB foi avaliado nos anos de 2015, 2016 e 2017. Não houve interações entre genótipo x ano, genótipo x local e genótipo x local x ano para resistência à broca. A herdabilidade individual nos experimentos onde houve variância genotípica signitficativa foi de moderada a elevada ($0.53 < h^2 < 0.78$), assim como as herdabilidades para seleção em vários anos e um local ($h^2 = 0.63$), vários locais e um ano ($h^2 = 0.74$), e vários ano e vários locais ($h^2 = 0.80$). Assim, a seleção pode ser feita em apenas um local e ano ou pela média dos genótipos vários locais e anos. A seleção para resistência à broca reduziu os ganhos genéticos para TCH, ATR e TPH, justificando o uso de índice de seleção, no qual é possível obter ganhos satisfatórios para todas as características. Em geral, podemos concluir que a seleção em T1 permite selecionar famílias e genitores mais promissores para resistência à broca. No entanto, esta deve ser seguida da seleção de clones no T2, devido à alta variabilidade genética dentro de famílias. Para seleção em estágios mais avançado de seleção, esta pode ser feita em apenas um ano e local ou pela média dos clones nos vários ambientes. O uso de índice de seleção combinando os caracteres IIB, TCH e ATR permite a seleção de genótipos com considerável resistência à broca e alta produtividade.

Palavras-chave: Diatraea saccharalis, Saccharum spp., herdabilidade.

ABSTRACT

TOMAZ, Adriano Cirino, D.Sc. Universidade Federal de Viçosa, April, 2018. **Genetic parameters and strategies for selecting sugarcane genotypes for borer resistance.** Adviser: Márcio Henrique Pereira Barbosa. Co-advisers: Luiz Alexandre Peternelli and Marcos Deon Vilela de Resende.

The sugarcane borer Diatraea saccharalis (Lepidoptera: Crambidae) is one of the most important pests in sugarcane crops in Brazil and it has been controlled mainly by the use of both biological and chemical control. There is no sugarcane varieties resistant to this pest in Brazil. The lack of knowledge about genetic parameters in Brazilian sugarcane breeding populations and about selection strategies hinders the development of resistant varieties by conventional breeding programs. Therefore, the purpose of this study was to estimate genetic parameters and to compare strategies for selecting sugarcane genotypes for borer resistance. This study was divided in two parts: In the first part, a T1 (originated from true seed) and a T2 (first clonal selection stage) populations were used. In the second part of the study, a population in an experimental stage was used. The T1 experiment aimed to: estimate individual heritability, heritability at family mean level, genotypic variance among families, additive and non-additive genetic effects; and compare individual, family and parents selection. The T2 experiment aimed to: estimate heritability at clone means level and genotypic variance among clones; and assess the efficiency of family selection at T1 stage. T1 experiment was carried out in a randomized block design with 46 full-sib families and four replicates per family. This experiment was established in the year of 2014, at Iturama municipally, Minas Gerais state. In the year of 2015, the infestation index by borer (IIB) was assessed in ten plants per plot, totaling 40 plants per family. In 2016, 32 individuals from the three most resistant and 32 individuals from the three most susceptible families were selected in T1 experiment, to compose de T2 experiment, conducted at Capinópolis municipality, Minas Gerais state. This experiment was carried out in a randomized block design, with five replicates and 64 clones. The IIB was assessed in the year of 2017. In T1 experiment, the heritability at family means level ($h^2 = 0.77$) was higher than individual heritability ($h^2 = 0.16$). It indicates that family selection is more effective than individual or mass selection. There was difference among family means ($18.41 < IIB < 30.41\%$), indicating the possibility of selecting families for borer resistance. The additive genetic effect is more important than non-additive effects so parents can be selected only through their genetic additive

effects. The results of T2 experiment indicated that there is high genetic variance of clones within families (6.63 < IIB < 17.57%). Thus, the selection of families at T1 stage must be followed by clone selection at T2 stage, where the individuals can be assessed in replicated experiments and higher heritability at clone means level can be achieved ($h^2 = 0.61$). The second part of this study aimed to: estimate variance components and heritability; assess the effect of genotype x environment (location, year) interaction in borer resistance; to compare selection strategies; to assess the effect of selection for borer resistance in productivity components (Tons of cane per hectare (TCH), Theoretically recoverable sugar (TRS) and Tons of sugar per hectare (TSH)); and to study the possibility of using selection index for selecting sugarcane genotypes for borer resistance and yield components. A population at an experimental stage with 35 clones, planted in four locations in experiments with 18 or 24 clones and four or five replicates was used. The IIB was assessed in the years of 2015, 2016 and 2017. There was no genotype x year, genotype x location nor genotype x year x location interaction for borer resistance. The heritability in single experiments was moderate or elevated ($0.53 < h^2 < 0.78$) as well as heritabilities for selection in one location and several years ($h^2 = 0.63$), several locations and one year ($h^2 = 0.74$), and several locations and years ($h^2 = 0.80$). Therefore, selection for borer resistance may be performed at only one location and year or by the clones' means in several locations and years. The selection for borer resistance reduced the genetic gains for TCH, TRS and TSH, justifying the use of selection index, which made it possible to obtain satisfactory genetic gains for IIB, TRS and TCH. We can conclude that selection at T1 stage enables selection of families and parents for borer resistance. However, this selection must be followed by clone selection at T2 stage, due to high genetic variability within families. In more advanced selection stages, the clones can be selected either in one location and year or by their means in several years and locations, as there is no genotype x environment interaction. The use o selection index combining IIB, TCH and TRS enables selecting sugarcane for borer resistance in addition to stalk and sugar productivity.

Keywords: Diatraea saccharalis, Saccharum spp., heritability.

GENERAL INTRODUCTION

Brazil is the largest sugarcane producer in the world and this crop is essential to the country´s agribusiness. The increase of world´s demand for ethanol produced from renewable sources, in addition to the large cultivable areas and favorable edaphoclimatic conditions make Brazil the most promising country to the exportation of this commodity. The estimated sugarcane production for 2017/2018 crop season is 635.6 million of tons, harvested in a cultivated area of about 8.74 million hectares (CONAB, 2017).

According to Barbosa et al. (2012), in the year of 1970, the total recoverable sugar productivity (TRS) in Brazil was in average, 3712 Kg/ha, and in 2011, it reached 9148 kg/ha. However, the estimated TRS for 2017/18 crop season is 10147 kg/ha in the Central-South region of Brazil (CONAB, 2017). This increase in productivity is due to the use of new technologies, both in agriculture and in the industry. It is estimated that crop breeding contributes to nearly 50% of this productivity gain (Barbosa et al., 2012).

In addition to increasing yield, crop breeding is an important tool to overcome biotic and abiotic stresses that hinders the sugarcane genotypes to achieve their maximum genetic potential. Insect pests constitute an important biotic stress among the various limiting factors that affect sugarcane production (Dinardo-Miranda, 2008). In general, insect pests have been projected to account for more than 10% of yield loss in sugarcane worldwide. The use of resistant varieties is the most cost effective and appropriate means for managing pests and diseases (Milligan et al., 2003).

The sugarcane stalk borer Diatraea saccharalis Fabr. (Lepidoptera: Crambidae) is the major pest of sugarcane in Brazil. This pest is controlled specially by the use of the parasitoid Cotesia flavipes (Hymenoptera: Braconidae) and chemical insecticides. However, the development of resistant sugarcane varieties to D. saccharalis is very important to the sugarcane sector owing the reduction of yield losses and production costs. Currently in Brazil, there are some efforts to develop sugarcane varieties resistant to D. saccharalis through biotechnology, specially by inserting "Bt genes", derived from Bacillus thuringiensis bacteria, into commercial varieties (Cristofoletti et al., 2018). However, the whole process from selecting effective Bt genes against the borer up to the release of commercial transgenic variety takes a long time, it is a very expensive process and it demands a large amount of resources and more advanced

Technologies, which are often not available for conventional breeding programs. In addition, some studies have shown the possibility of rapid evolution of sugarcane borer resistance to Bt proteins in large-scale field use (Girón-Perez et al., 2014).

There are some reports of releasing sugarcane clones resistant to D. saccharalis in other countries, mainly in United States of America (White et al., 1993b; 1998; 2011). Kimbeng et al. (2006) demostrated that borer resistance can be increased in segregating sugarcane population by selecting and crossing among the most resistant parents and then focusing selection on progeny within those crossess. Some sugarcane genotypes present genes that confer some resistant traits to D. saccharalis. There are some reports of sugarcane genotypes which causes higher mortality of early-instar larvae feeding on leaves (Coburn & Hensley, 1972; Tomaz et al., 2017), preventing or delaying larval penetration into the stalk (White et al., 1993; Tomaz et al., 2017) and reducing larval development within the stalk (Tomaz et al., 2017). In addition, there is often difference among sugarcane genotypes for several damage measures under field conditions such as percentage of bored internodes or internodes with exit holes, percentage of stalks bored, pupation success, estimates of adults produced per area/year/variety and damage rating (Bessin et al., 1990; Nibouche & Tibere, 2008; Milligan et al., 2003; White et al., 1993a, 2011). It reinforces the possibility of selecting sugarcane genotypes for borer resistance in breeding populations.

Sugarcane breeding programs usually starts by evaluating large numbers of seedlings derived from true seed, obtained from programmed cross-breeding. The first selection stage (T1 stage) is the only one to be planted with true seed as subsequent stages are planted using vegetative propagation. In T1 stage, mass or individual selection is routinely applied. This selection may be effective for traits with high heritability as Brix and resistance to diseases. Although, this type of selection can be inefficient fo traits with low heritability due the lack of replication of each individual (Brasileiro et al., 2016). However, family selection, when followed by individual clone selection, is superior in terms of genetic gain than either family or individual clone selection alone as selection within families with higher genotypic values can increase the probability of selecting superior clones (Barbosa et al., 2005; Brasileiro et al., 2017).

Family selection is particularly useful for traits with low heritability because, unlike clones, families can be evaluated using replicated plots and across years and sites, thereby improving estimates of family means (Kimbeng & Cox, 2003). In

addition, the availability of family data makes it possible to estimate the breeding value of parents, by using the Best Linear Unbiased Predictors (BLUP), which enables to plan better cross combinations. The BLUP allows data from a diverse range of mating designs, and combine all information from families, parents, individuals and environment into a single breeding value for each trait and genotype (Kimbeng & Cox, 2003; Barbosa et al., 2004).

Family experiments can also been used to study the importance of additive and non-additive genetic effects. When the non-additive genetic effects are important for determinate trait, specially dominance effects, there is a possibility of increasing genetic gain by exploring heterosis, through selection of crossings with high specific combining ability (SCA). When there is a predominance of genetic additive effects, the genitors can be selected based on their performance or their general combining ability (GCA) or their per se performance (Bastos et al., 2003). White el al. (2001) reported that additive genetic variance is more important than dominance to sugarcane resistance to D. saccharalis. However, for sugarcane resistance to African borer, both additive and non-additive genetic effects may be present (Zhou, 2015).

In South Africa, family experiments have been used to study the genetic inheritance and control, selection strategies and to identify superior families and parents for sugarcane resistance to African sugarcane borer Eldanna saccharina (Lepidoptera: Pyralidae) (Zhou, 2015, 2016; Zhou & Mokwele, 2017). In Brazil, family studies have been focused mainly to select families and parents for yield traits, especially ton of stalk per hectare (Barbosa et al., 2004, 2005). However, no family studies about D. saccharalis resistance have been performed. Such studies could enable determination of selecting strategies in addition to identify promising clones, families and parents for D. saccharalis resistance.

The sugarcane resistance to borer is known to have a quantitative genetic control (Viator & Henderson, 1970). For this type of trait, the study of heritability is essential to show which portion of phenotypic variance is due to genetic causes. Thus, selection for traits with low heritability in a population is unlikely to be successful as the environmental effect may not permit identification of the superior genotypes. Milligan et al. (2003) and Nibouche & Tibere (2008) found heritabilities of 0.62 and 0.80, for infestation index by D. saccharalis and spotted borer Chilo sacchariphagus (Lepidoptera: Pyralidae) for clone means, respectively. For family means, heritabilities of 0.76 and between 0.51-0.56 for infestation index by

D. saccharalis and African borer E. saccharina, respectively, have been reported (White et al., 2001; Zhou, 2015, 2016). In general, these values are moderate to elevated and indicate that selection for borer resistance based on infestation index can be effective.

Quantitative traits can be subjected to high environmental effects so the importance of genotype x environment (location and/or year) interactions are essential to determine appropriate selection strategies. In case of significant genotype x environment interactions, the genotypes should be selected based either on their stability and/or adaptability to different environments or for a specific environment. In the absence of genotype x environment interaction, the genotypes can be selected by their means in several environments or selection in only one environment is enough. In sugarcane, genotype x environment interaction is common for most traits such 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, previous studies have shown no family x year interactions for sugarcane resistance to D. saccharalis (White et al., 2001) nor genotype x location interaction for sugarcane resistance to D. saccharalis and C. sacchariphagus (Milligan et al., 2003, Nibouche & Tibere, 2008). The studies about stability/adaptability of the clones are performed in the experimental stage, when is possible to assess the performance of the clones in several locations and for several years.

The selection of genotypes based in one or few traits may be inappropriate as negative genetic correlations among traits of interest may be observed. An alternative in this case is the use of selection index, where genotypes are selected for a combination of traits. In sugarcane, selection index has been used to select genotypes for yield traits as number of stalks per meter, average stalk mass and Brix (Pedrozo et al., 2009). In addition, Milligan et al. (2003) developed a selection index to select sugarcane genotypes for borer resistance using five damage measures. However, selection only for borer resistance may result in genotypes with unfavorable traits and lower sugar yield (White et al., 2006, 2011). The use of selection index to select for borer resistance in addition to yield traits have not been reported.

The lack of knowledge about genetic parameters of Brazilian sugarcane populations and about selection strategies hinders the selection of resistance genotypes by Brazilian sugarcane breeding programs. Therefore, this study

aimed to estimate genetic parameters and to compare selection strategies in three stages of sugarcane breeding programs, in addition to identify superior famílies, genitors and clones for borer resistance.

This thesis was written in two chapters:

In the first chapter, a T1 (originated from true seed) and a T2 (first clonal selection stage) populations were used to estimate genetic parameters, compare selecting strategies and to identifiy superior families, parents and clones for borer resistance.

The T1 experiment aimed to:

1) Estimate individual heritability and heritabilty at family means level, genotypic variance among families, additive and non-additive genetic effects;
2) Compare family, parents and individual selection;
3) Identify promising parents and families for resistance to borer.

The T2 experiment aimed to:

1) Estimate heritability at clone means level and genotypic variance among clones within families;
2) Assess the efficiency of family selection at T1 stage;
3) Identify superior clones.

In the chapter two, the study aimed to estimate genetic parameters and compare selection strategies in the last selection stage (experimental stage or FE). The second part of this study aimed to:

1) Assess the effect of genotype x environment (location, year) interaction in borer resistance;
2) Identify superior clones for borer resistance;
3) Assess the effect of selection for borer resistance in productivity components (Tons of cane per hectare (TCH), Theoretically recoverable sugar (TRS) and Tons of sugar per hectare (TSH));
4) Study the use of selection index to identify genotypes that combine satisfactory borer resistance and stalk and sugar yield.

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CHAPTER 1: GENETIC PARAMETERS AND SELECTION OF SUGARCANE FOR BORER RESISTANCE IN EARLY-SELECTION STAGE

ABSTRACT

The sugarcane stalk borer Diatraea saccharalis Fab. (Lepidoptera: Crambidae) is one of the major pests in sugarcane in Brazil. However, there is no sugarcane varieties resistant to this pest in the country. Selection for borer resistance in early stages of a sugarcane breeding programs could increase the resistance of sugarcane clones in the following selection stages. However, there is no study about genetic parameters and selection strategies for sugarcane borer resistance in early selection stages in Brazil. In this study, a T1 (originated from true seed) population was used to estimate heritabilities at family means level and individual heritability, genotypic variance among families, additive and non-additive genetic effects; to compare individual, family or parents selection; and to identify promising parents and families for resistance to borer. Then, a T2 (first clonal selection stage) population was used to estimate heritability at clone means level and genotypic variance among clones; to assess the efficiency of family selection at T1 stage; and to identify superior clones for borer resistance. T1 experiment was conducted in randomized block design with four replicates and 46 full-sib families (T1) and the infestation index by borer (IIB) was assessed in two stalks of 10 plants per plot, totaling 40 individuals per family. In the following year, 32 individuals from the three most resistant family and 32 individuals from the three most susceptible families were selected to compose the first clonal selection stage (T2). This experiment was carried out in a randomized block design with five replicates and 64 clones. In the following year, the IIB was assessed in four stalks per plot. In T1 experiment, the heritability at family means level ($h^2 = 0.77$) was higher than individual heritability ($h^2 = 0.16$), so family selection is more effective than individual selection at T1 stage. The families RB027060 x RB957506, RB876030 x RB928064, RB988137 x RB951541, RB966928 x RB855156 and RB987649 x RB867515 were the most resistant families to borer. The additive genetic effect was more important for borer resistance than non-additive effects so the parents may be selected through their additive effects for borer resistance. The genotypes RB987649, RB988137, RB928064, RB966928 were the most promising parents for borer resistance (considering the accuracy higher than 0.70). In T2 experiment, the heritability at clone means level was moderate ($h^2 = 0.61$), indicating the possibility of selecting resistant clones. As genotypic variance among clones within families was significant, the selection of families at T1 stage must be followed by a

clone selection at T2 stage, to identify the superior clones within the selected families. The most resistant clones 56, 61, 47, and 54 were derived from a resistant family RB876030 x RB928064. We can conclude that family experiments enable selection of more promising families and parents for borer resistance. However, due the high genotypic variance within families, the family selection at T1 stage must be followed by a clone selection at T2 stage.

Key-words: Saccharum spp., Diatraea saccharalis, full-sib families.

1. INTRODUCTION

The sugarcane stalk borer Diatraea saccharalis Fab. (Lepidoptera: Crambidae) is one of the major pests of sugarcane in Brazil (Dinardo-Miranda et al., 2008). This pest is controlled specially by use of the parasitoid Cotesia flavipes (Hymenoptera: Braconidae) and chemical insecticides. The use of sugarcane varieties resistant to this pest could act as an important tool to Integrated Management of this pest, reducing the costs with Cotesia releases and insecticide spraying. There are some efforts to develop sugarcane varieties resistant to D. saccharalis through biotechnology, specially by inserting Bt genes, derived from Bacillus thuringiensis bacteria, into commercial varieties (Cristofoletti et al., 2018). However, there is a possibility of rapid evolution of sugarcane borer resistance to Bt proteins in large-scale field use (Girón-Perez et al., 2014).

The registration of sugarcane genotypes resistant to borer through common breeding United States of America indicates the possibility of developing sugarcane genotypes resistant to D. saccharailis through conventional breeding (White et al., 1993; 1998; 2011). Kimbeng et al. (2006) demonstrated that borer resistance can be increased in segregating sugarcane population by selecting and crossing among the most resistant parents and then focusing selection on progeny within those crossess. Previous studies have demonstrated that some sugarcane genotypes in Brazil have genes that confers some degree of resistance to D. saccharalis. This resistance is achieved due to the presence of some leaf component which causes higher mortality of early-stage larvae, some barrier on the stalk surface that hinder or delay larvae penetration within the stalks or some trait within the stalks that reduce larval feeding and/or affect larval performance (Dinardo-Miranda et al., 2012; Tomaz et al., 2017; Pimentel et al., 2017). These resistance genes are likely to provide resistance more durable than that conferred

by Bt genes. Thus, it is possible to increase the resistant of sugarcane varieties to borer by selecting and recombining genotypes with resistance traits.

Sugarcane breeding programs usually starts by evaluating large numbers of seedlings derived from true seed, obtained from programmed cross-breeding. The first selection stage (T1 stage) is the only one to be planted with true seed as subsequent stages are planted using vegetative propagation. The selection for borer resistance at T1 stage could increase the frequency of favorable alleles, increasing the resistance of the population for the following selection stages. Individual (mass) selection is inefficient at this stage for traits with low heritability as borer resistance due the lack of replication for each individual (Brasileiro et al., 2016). Family selection is particularly useful for traits with low heritability because, unlike clones, families can be evaluated using replicated plots and across years and sites, thereby improving estimates of family means (Kimbeng & Cox, 2003). Family selection, when followed by individual clone selection, is superior in terms of genetic gain than either family or individual clone selection alone (Brasileiro et al., 2016). The availability of family data makes it possible to estimate the breeding value of parents using the Best Linear Unbiased Predictors (BLUP) and it enables planning better cross combinations. The BLUP allows data from a diverse range of mating designs, parent, family and individual data to be combined into a single breeding value for each trait and genotype (Kimbeng & Cox, 2003; Barbosa et al., 2004).

Family experiments can also been used to study the importance of additive and non-additive genetic effects. This information is very useful for designing the best breeding strategies. When the non-additive genetic effects are important for determinate trait, there is the possibility of increasing genetic gain by exploring heterosis, through selection of crossings with high specific combining ability (SCA). When there is a predominance of genetic additive effects, the genitors can be selected based on their per se performance or their general combining ability (SCA) (Bastos et al., 2003). White el al. (2001) reported that additive genetic variance is more important than dominance to sugarcane resistance to D. saccharalis. However, for sugarcane resistance to African borer, both additive and non-additive genetic effects may be present (Zhou, 2015).

Family experiments have been used to study the genetic inheritance, selection strategies and to identify superior families and parents for sugarcane resistance to African sugarcane borer Eldanna saccharina (Lepidoptera: Pyralidae) (Zhou, 2015,

2016; Zhou & Mokwele, 2017). In Brazil, family studies have been focused mainly to select families and parents for yield traits, especially ton of stalk per hectare (Barbosa et al., 2004, 2005). However, no family studies about D. saccharalis resistance have been performed. Such studies could enable determination of selecting strategies in addition to identify promising clones, families and parents for D. saccharalis resistance.

In this study, a T1 (originated from true seed) and a T2 (first clonal selection stage) populations were used to estimate genetic parameters, to compare selection strategies and to identify superior parents, families and clones for borer resistance. The purposes of the T1 experiment were to estimate heritabilities at family means level and individual hertability, genotypic variance among families, additive and dominance genetic effects; to compare individual, family or parents selection; and to identify promising parents and families for resistance to borer. The T2 experiment aimed to estimate heritability for clone means and genotypic variance among clones; to assess the efficiency of family selection at T1 stage; and to identify superior clones for borer resistance.

2. MATERIAL AND METHODS

2.1 Selection of sugarcane for borer resistance at seedling stage (T1)

2.1.1 Plant material and experimental design

Seedlings were germinated in March/2014 from true seeds in a glasshouse at the research station “Centro de pesquisa e melhoramento da cana-de-açúcar” (CECA) located at Oratórios county, Minas Gerais state. This station belongs to the sugarcane breeding program of UFV (Universidade Federal de Viçosa) in partnership with RIDESA (Inter-university Network for the Development of Sugarcane Industry (Barbosa et al., 2012). The seedlings were then transplanted to a field area of a partner mill, located in Iturama county, Minas Gerais state, in December/2014.

The sugarcane families were divided in two experiments in the same area and containing 24 families each. Two families (943 and 1046) were planted in both experiments to be used as controls. The plots were composed by a single row (14.5m) containing 25 plants (stools) of each family. Spacing between rows was 1.5m while spacing between stools within a row was 0.6 m. The plants were fertilized with 400

kg/ha of 04-30-16 (N-P-K). The trial was conducted in a randomized block design with 46 full-sib families (Table 1) with four replicates per family.

Table 1. Families and parents used in experiment for estimate genetic parameters and compare selection strategies for borer resistance.

Experiment 1			Experiment 2		
Family	**Female**	**Male**	**Family**	**Female**	**Male**
925	RB987933	RB931556	359	RB027060	RB961003
931	RB867515	SP83-2847	378	RB867515	RB855156
940	RB027046	RB008133	393	RB876030	RB928064
943	RB977543	RB008296	404	RB928064	RB961003
944	RB975184	RB008004	407	RB928064	RB04820
950	RB965902	SP83-5073	416	RB931556	RB937570
953	TUC71-7	SP83-5073	455	RB961003	RB027060
963	RB008041	RB92579	464	RB966928	RB855156
967	SP83-2847	RB987935	490	RB988137	RB99395
976	SP77-5181	RB867515	491	RB988137	RB951541
987	SP83-2847	RB975201	498	RB99382	RB92579
988	RB987649	RB867515	532	RB988137	RB937510
989	RB867515	RB987649	550	RB047121	RB965902
1000	RB027060	RB957506	557	RB979505	SP85-3877
1003	RB997751	RB988082	904	RB947520	RB928064
1016	RB99395	RB92579	906	RB951541	RB937570
1027	RB92579	RB986419	928	RB975201	RB966928
1028	RB935907	RB947663	930	RB987935	SP83-2847
1032	RB92579	RB008041	**943**	RB977543	RB008296
1035	RB957751	RB928064	958	SP83-5073	RB92579
1036	RB957751	RB027042	972	RB867515	RB008296
1040	RB867515	RB965518	1013	RB855453	RB965902
1045	RB92579	RB835054	1042	RB998132	RB998025
1046	RB835054	RB92579	**1046**	RB835054	RB92579

2.1.2 Data collection

The assessment of borer damage was performed in July/2015. Ten stools per plot were randomly selected for assessment of borer damage. Two stalks per stools (individuals) were harvested and the number of total internodes and bored internodes per stalk were recorded to calculate the percentage of bored internode per plant. The estimation of infestation index per stool were calculated by using the mean of both plants. Each family was represented by nearly 40 individuals (4 plots x 10 individuals/plot). However, in some plots less plants were assessed as the death of some seedlings reduced the number of plantas.

2.1.3 Data analysis

The data of infestation index were analyzed by using the Selegen-REML/BLUP software (Statistic system and computerized genetic selection by linear mixed models

(Resende, 2016). The first model was used to estimate genetic parameters for family selection:

(1) $y = Xr + Zg + Wj + \varepsilon$; where y is the vector of data, r is the vector of fixed effect of replicates, g is the vector of random effect of genotypes, j is the vector of random effect of plots and ε is the vector of residual or random error.

The broad-sense heritability at family means level was calculated by the following formula:

(a) $h^2_{fm} = \sigma^2_f / (\sigma^2_f + \sigma^2_b/r + \sigma^2/gr)$

Where σ^2_f is the genotypic variance among full-lib progenies equivalent to ½ of genetic additive variance + ¼ of genetic dominance variance and ignoring epistasis, σ^2_b is the variance among blocks, σ^2 is the residual variance, r is the number of blocks and g is the number of families. The accuracy of selecting by family means was calculated as $Ac = \sqrt{h^2_{fm}}$.

The second model was used to estimate genetic parameters for parent and individual selection:

(2) $y = Xr + Za + Wj + Td + \varepsilon$; where y is the vector of data, r is the fixed effect of blocks, a is the vector of random additive genetic effects, j is the vector of random plot effects, d is the vector of random dominance genetic effects (for full-lib progenies) and ε is the vector of residuals or random error. The capital letters are the incidence matrices to the referred effects (Resende, 2006).

The narrow-sense and broad-sense heritabilities at plant level were calculated respectively by the following formulas:

(b) $h^2_a = \sigma^2_a / \sigma^2_p$

(c) $h^2_g = \sigma^2_a + \sigma^2_d / \sigma^2_p$;

Where σ^2_a is the additive genetic variance, σ^2_d is the dominance effect and σ^2_p is phenotypic variance.

The variance components were estimated by REML (restricted maximum likelihood) procedure and the significance of the effects were tested by using the deviance analysis by Likelihood ratio test (LRT). The genotypic values of families and additive genetic effects of the parents were estimated by using Best linear unbiased predictors (BLUP) (Resende, 2006).

2.2 Selection of sugarcane for borer resistance at first clonal stage (T2)

2.2.1 Plant material and experimental design

In April/2016, superiror individuals from the T1 population were selected by experient sugarcane breeders of RIDESA, folowing the parameters of routine individual selection, based on their general vigor. To compose the first clonal stage (T2), 32 indviduals were selected from the three most resistant families and 32 individuals were selected from the three most susceptible families, to compose a resistant and a susceptible group, respectively. The T2 population, composed by 64 individuals, was then planted in the field of the research station (CEPET) of UFV (Federal University of Viçosa), located at Capinópolis county, Minas Gerais state.

Each plot was composed by a single row (1 m) and spacing between plots was 1.0 m. The plants were fertilized with 400 kg/ha of 04-30-16 (N-P-K). The trial was conducted in a randomized block design with five replicates per clone.

2.2.2 Data collection

The assessment of sugarcane damage was performed in July/2017. Four stalks per plot were harvested and the number of total internodes and bored internodes per stalk were recorded to calculate the percentage of bored internode per plot.

2.2.3 Data analysis

The data of infestation index were analyzed by using the Selegen-REML/BLUP (Statistic system and computed genetic selection by way of linear mixed models) software (Resende, 2015). The model used to estimate genetic parameters for clonal selection:

(1) $y = Xr + Zf + Wb + Sc + \varepsilon$; where y is the vector of data, r is the vector of fixed effect of location, f is the vector of full-sib families (random), b is the vector of the random effects of blocks, c is the vector of clones within families (random), and ε is the vector of residual or error (random). The capital letters are the incidence matrices to the referred effects (Resende, 2015).

The variance components were estimated by REML (restricted maximum likelihood) procedure and the significance of the effects were tested by using the

deviance analysis. The genotypic values of clones were estimated by using Best linear unbiased predictors (BLUP) (Resende, 2006). The broad-sense heritability at clone means level was calculated by the formula:

(1) $h^2_{gm} = \sigma^2_f + \sigma^2_{c/f} / (\sigma^2_f + \sigma^2_{c/f} + \sigma^2/r)$

Where σ^2_f is the genotypic variance among full-lib progenies equivalent to ½ of genetic additive variance + ¼ of genetic dominance variance and ignoring epistasis, σ^2_p is the phenotypic variance, $\sigma^2_{c/f}$ is genetic variance among clones within families equivalent to ½ of genetic additive variance + ¾ of genetic dominance variance + epistatic effects (Resende, 2015).

3. RESULTS AND DISCUSSION

3.1 Selection of sugarcane for borer resistance at seedling stage (T1)

The genotypic variance for family effect was significant ($P < 0.01$), indicating that there is difference among family means. The broad-sense heritability at family means level was high ($h^2_{fm} = 0.77$) as well as the accuracy of families selection (Ac = 0.88) (Table 2). This heritability was close to that found for infestation index by D. saccharalis ($h^2 = 0.76$) and African borer E. saccharina ($h^2 = 0.51$-0.56) (White et al. 2001; Zhou, 2015, 2016). The high heritability at family means level indicates that selecting more resistant families may be effective. On the other hand, the individual heritability was low (Table 2). Therefore, selection of individuals within family or individual selection is less effective than family selection at T1 stage. Similar results were found for sugarcane resistance to D. saccharalis and African sugarcane borer (White et al, 2001, Zhou & Mokwele, 2015).

The genotypic values for family means (u + g) ranged from 18.41 to 30.41% of bored internodes, evidencing the difference among families (Table 3). In addition, the predicted genetic gain of selecting the 10 most resistant families (selection intensity ~ 20%) was -17.5%. The families RB027060 x RB957506, RB876030 x RB928064, RB988137 x RB951541, RB966928 x RB855156 and RB987649 x RB867515 were the most resistant families to borer. The accuracy of predicting genotypic values for family means ranged from 0.73 to 0.86, depending on the number of individuals per family (Table 3), which can be considered as elevated accuracies.

The variance due to additive genetic effect was highly significant ($P < 0.01$) while the variance of dominance on non-additive effects was not significant (Table 2).

Therefore, genetic additive effect or general combining ability (GCA) is more important to borer resistance than dominance effect or specific combining ability (SCA) and exploration of heterosis would not increase the genetic gain (Bastos et al., 2003). White et al. (2001) also observed that additive genetic effect is more important than dominance effect to sugarcane resistance to D. saccharalis. However, previous studies have suggested the presence of additive and non-additive genetic effects of sugarcane resistance to African borer (Zhou & Mokwele, 2015; Zhou, 2015).

Table 2: Variance componentes (REML), means and heritabilities for sugarcane borer resistance at seedling stage (T1).

Family selection	Parent selection
	σ^2_a = 37.03**
σ^2_f = 15.52**	σ^2_d = 0.35^{NS}
σ^2 = 211.47	σ^2 = 192.92
σ^2_p = 243.79	σ^2_p = 245.64
h^2_{fm} = 0.77	h^2_a = 0.15 ± 0.036
Ac_{fm} = 0.88	h^2_g = 0.16
Mean = 24.36	c^2_d = 0.01
	Mean = 24.27

σ^2_f = genotypic variance among full-sib families, σ^2 = residual variance or error (random), σ^2_p = phenotypic variance, h^2_{fm} = broad-sense heritability for family mean, Ac_{fm} = accuracy for selection by family means, σ^2_a = Additive genetic variance, σ^2_d = Dominance genetic variance or specific combining ability, h^2_a = narrow-sense heritability, h^2_g = broad-sense heritability for individuals within families, c_d^2 = determining coefficient of specific combining ability.

The genetic additive effects of parents (a) ranged from -10.52 to 6.94, evidencing the genetic variability of parentes to borer resistance (Table 2). The accuracy of estimating additive effects of parents ranged from 0.53 to 0.86 (Table 2). Parents represented in only one cross showed relatively low accuracies (< 0.70) while the genitors represented by two or more crosses showed accuracies higher than 0.70. However, due the difficulty of synchronization of flowering of genitors, this is not always possible in large sugarcane breeding programs. Therefore, we assume that for selection of parents for borer resistance through their additive effects, it must be represented in at least two crosses. Although, three or four crosses per genitor would provide better estimates of their additive values and it should be used when possible (Resende & Barbosa, 2005). Considering only the parents represented in at least two crosses the predicted genetic gain is -20.5%, which indicates that selecting most resistance parents for further crosses may enhance the resistance of breeding sugarcane population to borer. The genotypes RB987649, RB988137, RB928064, RB966928 were the most promising parents for borer resistance. Kimbeng et al. (2006) demonstrated

Table 3. Genotypic values for infestation index of borer (IIB) at seedling stage (T1).

Rank	Family selection				Parent selection			
	Family	IIB(%)	Accuracy	n	Parent	a	Accuracy	n cr.
1	1000	18.41	0.73	30	RB987649	-10.52	0.74	2
2	393	18.55	0.77	40	RB988137	-9.63	0.75	3
3	491	19.98	0.77	40	RB957506	-6.72	0.58	1
4	464	20.16	0.77	40	RB928064	-6.56	0.82	5
5	988	20.30	0.77	40	RB876030	-6.56	0.65	1
6	490	20.32	0.76	34	RB986419	-5.52	0.66	1
7	404	20.37	0.77	40	RB966928	-5.06	0.72	2
8	1027	20.73	0.77	40	RB008041	-4.57	0.74	2
9	532	20.94	0.76	36	RB027060	-4.29	0.74	3
10	1032	21.22	0.77	40	RB951541	-2.62	0.74	2
11	989	21.75	0.77	40	RB961003	-2.45	0.76	3
12	359	22.02	0.77	40	RB931556	-2.33	0.71	2
13	953	22.27	0.77	40	TUC-717	-2.23	0.63	1
14	925	22.28	0.77	40	RB979505	-2.17	0.56	1
15	557	22.68	0.77	40	SP85-3877	-2.17	0.56	1
16	963	22.89	0.77	40	RB855156	-1.80	0.75	2
17	407	22.93	0.77	40	RB987933	-1.43	0.60	1
18	904	23.17	0.77	40	RB937510	-1.33	0.62	1
19	416	23.52	0.77	40	SP83-5073	-0.71	0.80	3
20	906	23.81	0.77	40	RB937570	-0.60	0.71	2
21	1003	23.91	0.77	40	RB997751	0.02	0.56	1
22	455	24.00	0.77	40	RB988082	0.02	0.56	1
23	1028	24.30	0.77	40	RB04820	0.40	0.65	1
24	958	24.52	0.77	40	RB947663	0.43	0.56	1
25	928	24.75	0.77	40	RB935907	0.43	0.56	1
26	1035	25.03	0.77	40	RB947520	0.79	0.65	1
27	944	25.41	0.73	30	RB855453	0.91	0.62	1
28	1046	25.70	0.86	80	RB92579	0.97	0.85	8
29	1045	25.96	0.73	30	RB99395	1.05	0.76	2
30	950	26.08	0.77	40	RB977543	1.42	0.67	1
31	987	26.15	0.77	40	SP77-5181	1.51	0.66	1
32	930	26.41	0.77	40	RB008004	1.59	0.53	1
33	1016	26.57	0.77	40	RB975184	1.59	0.53	1
34	498	26.76	0.77	40	RB047121	2.02	0.62	1
35	976	26.90	0.77	40	RB965518	2.08	0.66	1
36	1013	26.94	0.77	40	RB987935	2.12	0.71	2
37	967	27.15	0.77	40	RB975201	2.54	0.74	2
38	1040	27.27	0.77	40	RB835054	2.70	0.78	2
39	1036	27.51	0.73	30	RB027042	2.77	0.57	1
40	943	27.61	0.86	80	RB99382	2.79	0.65	1
41	550	27.63	0.77	40	RB998132	3.79	0.56	1
42	378	28.07	0.77	40	RB998025	3.79	0.56	1
43	1042	28.27	0.77	40	SP83-2847	4.76	0.80	4
44	931	28.29	0.77	40	RB965902	5.32	0.77	3
45	972	30.39	0.77	40	RB957751	6.45	0.71	2
46	940	30.41	0.77	40	RB008296	6.48	0.75	2
47					RB867515	6.65	0.86	6
48					RB008133	6.94	0.56	1
49					RB027046	6.94	0.56	1

* a = additive genetic value; n = number of individuals assessed per family; n cr. = number of crosses envolving the genitor.

that borer resistance can be increased in segregating sugarcane population by selecting and crossing among the most resistant parents and then focusing selection on progeny within those crossess.

3.2 Selection of sugarcane for resistance to borer at first clonal stage (T2)

The genetic variance among clones within families was significant ($P < 0.01$)(Table 4). The genotypic values for clone means (u + g) ranged from 6.63 to 17.57 % of bored internodes, evidencing the diference among clones (Table 5). The heritability at clone means level was moderate ($h^2 = 0.61$), suggesting the high possibility of obtaing satisfactory genetic gains. The predicted genetic gain of selecting the 12 most resistant clones (selection intensity ~ 20%) is -28.96%.

Table 4: Variance componentes (REML), means and heritabilities for sugarcane borer resistance at first clonal stage (T2).

Selection of clones
$\sigma^2_f = 1.47^{NS}$
$\sigma^2_{c/f} = 9.13^{**}$
$\sigma^2 = 34.17$
$\sigma^2_P = 45.64$
$h^2_f = 0.03$
$h^2_{gm} = 0.61$
Ac = 0.78
Cve% = 49.45%
Mean = 11.82

σ^2_f = genotypic variance among full-lib progenies equivalent to ½ of genetic additive variance + ¼ of genetic dominance variance, ignoring epistasis; $\sigma^2_{c/f}$ = genetic variance among clones within families equivalent to ½ of genetic additive variance + ¾ of genetic dominance variance + epistatic effects; σ^2 = residual or error (random), σ^2_P = phenotypic variance, h^2_f = individual broad-sense heritability, $c^2_{c/f}$ = determining coefficient of clone within family effect, h^2_{gm} = broad-sense heritability for clone mean, Ac = accuracy of clone selection, CVe% = residual coefficient of variation.

Our study agrees with the literature, which states that family selection, when followed by individual clone selection, is superior in terms of genetic gain than either family or individual clone selection alone as selection within families with higher genotypic values can increase the probability of selecting superior clones (Barbosa et al., 2005; Brasileiro et al., 2017). In our study, nearly 60% of the selected clones came from the more resistant families selected in the seedling stage. In addition, the most resistant clones 56, 61, 47, and 54 were derived from a resistant family RB876030 x RB928064. Indeed, the high variance within families for borer resistance enabled a high frequency of resistant clones within families with lower means and high

variance, which reinforces the idea that family selection at T1 stage must be followed by clone selection at T2 stage.

Table 5. Genotypic values for infestation index by borer (IIB) at T2 stage.

Rank	Family category (T1)	Family	Clone	IIB(%)
1	**res**	393	56	6.63
2	**res**	393	61	7.54
3	**res**	393	47	7.89
4	**res**	393	54	7.96
5	sus	972	34	8.08
6	**res**	393	65	8.23
7	**res**	393	45	8.31
8	**res**	393	53	8.32
9	sus	940	8	8.50
10	sus	972	33	8.72
11	sus	931	24	8.78
12	sus	931	28	8.82
13	**res**	393	59	8.97
14	sus	931	13	9.26
15	sus	972	35	9.54
16	**res**	393	68	9.79
17	**res**	393	52	9.97
18	sus	940	26	10.02
19	sus	940	25	10.08
20	**res**	393	46	10.10
21	**res**	393	62	10.21
22	**res**	393	48	10.26
23	sus	972	31	10.43
24	sus	940	20	10.71
25	**res**	491	50	10.94
26	**res**	393	60	11.09
27	sus	931	16	11.11
28	**res**	1000	7	11.16
29	**res**	1000	4	11.17
30	**res**	393	66	11.21
31	sus	940	18	11.29
32	sus	931	29	11.31
33	sus	940	11	11.33
34	sus	940	21	11.52
35	sus	931	27	11.58
36	**res**	393	51	11.59
37	sus	931	15	11.59
38	**res**	491	57	11.62
39	**res**	393	44	11.81
40	**res**	491	64	12.04
41	**res**	1000	5	12.09
42	sus	972	41	12.15
43	sus	931	17	12.35
44	**res**	1000	1	12.55
45	**res**	393	67	12.67
46	**res**	393	55	12.92
47	**res**	491	49	12.95
48	**res**	491	63	13.30
49	sus	972	42	13.31
50	**res**	1000	3	13.43
51	sus	940	19	13.49
52	sus	931	14	13.64
53	sus	972	30	13.91
54	**res**	1000	2	14.11
55	**res**	1000	6	14.37
56	sus	931	12	14.43
57	sus	972	40	14.54
58	sus	940	9	14.73
59	sus	940	22	15.05
60	sus	972	43	16.17
61	sus	972	39	16.41
62	sus	940	10	17.05
63	sus	940	23	17.19
64	**res**	491	58	17.57

* The codes res and sus mean that the clone was selected within a resistent ou susceptible family in T1 experiment, respectively.

Our results also shows the high genetic variability for borer resistance in Brazilian sugarcane populations. This genetic variability should be explored by the breeder to increase the resistance of the varieties. Overall, our data shows that sugarcane borer resistance has a very complex genetic control, with high genetic variance both among and within families.

4. CONCLUSIONS

- In T1 experiment, the heritability at family means level was higher than individual heritability so family selection is more effective than individual selection at T1 stage;

- The families RB027060 x RB957506, RB876030 x RB928064, RB988137 x RB951541, RB966928 x RB855156 and RB987649 x RB867515 were the most resistant families to borer;

- The additive genetic effect was more important for borer resistance than non-additive effects. Therefore, the parents may be selected through their additive effects for borer resistance;

- The genotypes RB987649, RB988137, RB928064, RB966928 were the most promising parents for borer resistance (considering the accuracy higher than 0.70);

- In T2 experiment, the heritability at clone means level was moderate (h^2 = 0.61), indicating the possibility of selecting clone for borer resistance.

- The genotypic variance among clones within families was significant so selection of families at T1 stage must be followed by a clone selection at T2 stage, to identify the superior clones within the selected families.

- The most resistant clones 56, 61, 47, and 54 were derived from a resistant family RB876030 x RB928064. We can conclude that family experiments enable selection of more promising families and parents for borer resistance.

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CHAPTER 2: GENETIC PARAMETERS AND SELECTION OF SUGARCANE FOR BORER RESISTANCE IN LATE SELECTION STAGE

ABSTRACT

The sugarcane stalk borer Diatraea saccharalis Fab. (Lepidoptera: Crambidae) is one of the major pests in sugarcane in Brazil. The absence of knowledge about genetic parameters and selection strategies for borer resistance in Brazil hinders the development of resistant varieties by Brazilian sugarcane breeding programs. Therefore, this study aimed to estimate genotypic variance among sugarcane clones, heritability and genotype x environment (year/location) interaction for borer resistance; the effects of selection for borer resistance in yield traits; to compare selection strategies for borer resistance through several locations and years and selection for borer resistance in addition to yield traits by using selection index were studied. A population at experimental stage with 35 clones was used for this study. The clones were planted in four locations (Iturama, Ituitaba, Itapagipe and Tupaciguara counties, Minas Gerais State) in experiments carried out in randomized block designs with four or five replications and 18 or 24 clones per location. The infestation index by borer (IIB) and yield traits were assessed in the years of 2015, 2016 and 2017. There were no genotype x year and genotype x location interactions neither genotype x year x location interactions for borer resistance. The heritability in single experiments, where genotypic variance was significant, was moderate or elevated ($0.53 < h^2 < 0.78$) as well as heritabilities for selection in one location and several years ($h^2 = 0.63$), several locations and one year ($h^2 = 0.74$), and several both locations and years ($h^2 = 0.80$). Therefore, selection for borer resistance may be performed at only one location and year or by the clones' means in several locations and years. The most resistant clones to borer were RB047050, RB047226, RB047055, RB047212, RB047201 and RB047258. The selection for borer resistance reduced the genetic gains for Tons of cane per hectare (TCH), Theoretically recoverable sugar (TRS) and Tons of sugar per hectare (TSH), justifying the use selection index. The genotypes CTC9, RB047055, RB047409, RB047002, RB867515 and RB047201were selected for both borer resistance and stalk and sugar productivity. We can conclude that sugarcane clones may be selected in a sigle experiment or by their means in several location and years for borer resistance. In addition, the use of selection index combining infestation index by borer with TCH and TRS may enable selection of genotypes with considerable borer resistance and elevated sugar and stalk yield.

Key-words: Saccharum spp., Diatraea saccharalis, genotype x environment interaction.

1. INTRODUCTION

The sugarcane stalk borer Diatraea saccharalis Fab. (Lepidoptera: Crambidae) is one of the major pests in sugarcane in Brazil causing severe yield losses across the country (Dinardo-Miranda et al., 2008). This pest is controlled specially by use of the parasitoid Cotesia flavipes and chemical insecticides. The development of resistant sugarcane varieties to D. saccharalis is very important to the sugarcane sector owing the reduction of yield losses and production costs. However, there is no commercial sugarcane varieties resistant to borer in Brazil.

There are some reports of releasing sugarcane clones resistant to D. saccharalis in other countries, mainly in United States of America (White et al., 1993, 1998, 2011). In Brazil some sugarcane genotypes present genes that confer some resistant traits to D. saccharalis, which indicates the possibility of developing sugarcane genotypes resistant to this pest. There are some reports of sugarcane genotypes which causes higher mortality of early-instar larvae feeding on leaves (Tomaz et al., 2017), preventing or delaying larval penetration into the stalk (Tomaz et al., 2017) and reducing larval development within the stalk (Tomaz et al., 2017, Dinardo-Miranda et al., 2012).

Several studies have demonstrated genetic variabily for several borer damage measures under field conditions such as percentage of bored internodes or internodes with exit holes, percentage of stalks bored, pupation success, estimates of adults produced per area/year/variety and damage rating (Bessin et al., 1990; Nibouche & Tibere, 2008; Milligan et al., 2003; White et al., 1993a, 2011). It reinforces the possibility of selecting sugarcane genotypes for borer resistance in breeding populations.

Viator & Henderson (1971) found borer resistance to be genetically quantitative. Quantitative traits can be subjected to high environmental effects so the importance of genotype x environment (location and year) interactions are essential to determine appropriate selection strategies. In sugarcane, genotype x environment interaction is common for most traits 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, previous studies showed no family x year (White et al., 2001) interactions for sugarcane resistance to D. saccharalis nor genotype x location interaction for sugarcane resistance to D. saccharalis and spotted

borer Chilo sacchariphagus (Lepidoptera: Pyralidae)(Milligan et al., 2003, Nibouche & Tibere, 2008). However, no studies considering the genotype x location x year triple interaction have been reported.

The selection of genotypes based in one or few traits may be inappropriate as negative genetic correlations among traits of interest may be observed. An alternative in this case is the use of selection index, were genotypes are selected by a combination of traits. In sugarcane, selection index has been used to select genotypes for yield traits as number of stalks per meter, average stalk mass and Brix (Pedrozo et al., 2009). In addition, Milligan et al. (2003) developed a selection index to select sugarcane genotypes for borer resistance by using five damage measures. However, selection only for borer resistance may result in genotypes with unfavorable traits and lower sugar yield (White et al., 2006, 2011). Although, the use of selection index to select for borer resistance in addition to yield traits have not been reported.

The lack of knowledge about genetic parameters of Brazilian sugarcane populations and selection strategies hinders the selection of resistance genotypes by Brazilian sugarcane breeding programs. Therefore, this study aimed to estimate genetic parameters (genotypic variance, heritability); to assess the influence of genotype x environment in borer resistance; the effects of selection for borer resistance in yield traits and compare selection strategies for borer resistance through several locations and years and selection for borer resistance in addition to yield traits.

2. MATERIAL AND METHODS

2.1 Plant material and experimental design

The genotypes used in this study compose the last stage or experimental stage of sugarcane breeding program of "Universidade Federal de Viçosa", in partnership with RIDESA (Inter-university Network for the Development of Sugarcane Industry)(Barbosa et al., 2012). The trials were carried out in farms of RIDESA's partner mills in four locations: Iturama, Itapagipe, Ituiutaba and Tupaciguara counties, Minas Gerais state. Planting was done between April-May/2013. The soil fertilization, crop management and harvest were performed according to procedures established by the growers themselves. Each trial was composed by two commercial sugarcane varieties (checks) and the genotypes selected in previous selection stage (T3) by RIDESA's sugarcane breeding program. The genotypes were not planted in all location

due the lack of propagation material and restricted field area. However, most genotypes were repeated in at least two locations. Additional experimental information as number of genotypes and blocks and plot size for each experiment are summarized in table 1. The total number of genotypes used in all experiments was 35.

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

Location	genotypes	blocks	plots	assessments	checks
Itapagipe	18	4	4 rows (19m x 1.5m)	2015, 2016	RB867515, RB966928
Iturama	18	5	5 rows (5m x 1.5m)	2015, 2016, 2017	RB867515, CTC-9
Ituiutaba	24	4	4 rows (19m x 1.5m)	2015	RB867515, CTC-9
Tupaciguara	24	5	5 rows (5m x 1.5m)	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)	CTC-9 (2)	RB057169 (2)	RB047201 (3)	RB057145 (4)	

2.2 Data collection

For assessment of borer damage, twenty plants per plot were harvested, longitudinally split and the number of total internodes and bored internodes were recorded to calculate the infestation index (II) by using the formula: (number of bored internodes / number of internodes)*100 (Viator & Henderson, 1971). The assessments of borer damage were performed in July/2015, July/2016 and July/2017, in the first, second and third ratoon crops, respectively.

Due the likely genotype x location interaction in yield traits, the study of selection for borer resistance in addition to yield traits was performed at only one location. For this study, the Theoretically recoverable sugar (TRS), tons of cane per hectare (TCH) and Tons of sugar per hectare (TSH) were assessed in the experiment of Iturama in the years of 2015, 2016 and 2017. All these traits were measured by following current methods employed by RIDESA´s sugarcane breeding programs.

2.3 Data analysis

2.3.1 Genetic parameters and comparison of selection sceneries for borer resistance

The data of infestation index were analyzed trough mixed models by using the software Selegen-REML/BLUP (Rezende, 2016). The data of infestation index by D. saccharalis were analyzed considering four selection sceneries: single experiments, one location in three years, three locations in one year and four locations in three years. The genetic parameters were estimated by Restricted Maximum Likelihood (REML). The significance of the effects (i.e. genotypic variance, genotype x location interaction) were analyzed by deviance analysis (Likelihood Ratio Test) and the genotypic values were estimated by Best Linear Unbiased Predictors (BLUP)(Resende, 2006).

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

1) $y = Xr + Zg + e$,

where, y is the vector of 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 are the incidence matrix for the referred effects (Rezende, 2006).

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

2) $y = Xm + Zg + Wp + Ti + e$,

where, y is the vector of data, m is the vector of fixed effects of combination year-block, g is the vector of random effects of genotypes, p is the vector of random effects of environment or plot, i is the vector of random interaction genotype x 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:

3) $y = Xr + Zg + Wi + e$,

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

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

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

where, y is the vector of data, f is the vector of fixed effects of combination block-location-year, g is the vector of random effects of genotypes, gl is the vector of random effects of interaction genotype x location, gm is the vector of random effects of interaction genotype x year, glm is the vector of random effects of triple interaction genotype x location x year, p is the vector of random effects of plots within locations and e is the random effects of residual.

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

The data of TRS, TCH, II and TSH in the experiment of Iturama (2015, 2016 and 2017) were used to assess the effect of selection for borer resistance in yield traits and use of selection index.

The genotypic values for each trait were estimated by using the model:

5) $y = Xm + Zg + Wp + Ti + e$, previously described.

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

1) $GG_i\ \% = (X_{Si} - X_{0i})*100/\ X_{0i}$
2) $GG_{j(i)}\% = (X_{Sj(i)} - X_{0(j)})*100/\ X_{0(j)}$

Where: GG_i = genetic gain in trait i by selection for trait i; X_{Si} = mean of individuals selected for the trait i; X_{0i} = grand mean of the population for the trait i; $GG_{j(i)}$ = indirect genetic gain in character j, by selection for the trait i; $X_{Sj(i)}$ = mean of trait j in the individuals selected for the trait i; $X_{0(j)}$ = grand mean of the population for the trait j.

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

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

3) $I = (p \times TCH) \times (VG \times TCH) + (p \times TRS) \times (VG \times TRS) + (p \times II) \times (VG \times II)$

Where: p = economic weight for the trait and VG = genotypic value for the trait (Pedrozo et al., 2009). The efficiency of selection index was obtained by 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).

3. RESULTS AND DISCUSSION

3.1 Genetic parameters and comparison of selection sceneries for borer resistance

The mean infestation by borer varied along the years (11.54, 4.14 and 6.75% of bored internodes in 2015, 2016 and 2017, respectively), which is likely to be related to environmental factors. The natural infestation pressure by borer has a significant effect in the assessment of genetic variability in the population for borer resistance and in the experimental precision. For instance, in the experiment of Iturama, the genetic variance was not significant in the year of 2016, when infestation index by borer was low (6.37%), but it was significant in 2015 and 2017, where infestation index were higher (13.85 and 9.22%, respectively) (Table 2). To overcome this issue, the sugarcane breeding program the USDA's (United States Department of Agriculture) commonly enhances borer pressure by an adjacent planting of maize (Zea mays L.) which is artificially inoculated with borer larvae and apply insecticides to control borer natural enemies (White et al., 2001). However, in experiments located in field areas of mills, artificial infestation is not appropriated due 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 showed that the genotypic variance was significant in four of eight experiments indicating difference among genotypes for borer resistance (Table 2). The genetic gain of selection (selection intensity ~20%) varied from -28.82 to -14.52, which may be considered high.

In the analysis of infestation index by borer in the three selection sceneries studied, there were no significant genotype x year, genotype x location or genotype x year x location interactions (Table 2). In addition, the genotypic correlations between years, locations and years x locations combinations were high, indicating the high consistency in classification of genotypes among environments (years or locations). These results are in agreement with Viator & Henderson (1971), who found a moderately strong agreement in classifications of sugarcane genotypes to borer resistance in two years. White et al. (2003) studying the resistance of sugarcane families to D. saccharalis found no significant family x year interaction. Previous studies also indicated no significant genotype x location interaction in sugarcane resistance to D. sacharalis (Milligan et al., 2003) and spotted borer Chilo sacchariphagus (Nibouche & Tibere, 2008). However, our study seems to be the first to consider the genotype x

location x year triple interaction. In all selection sceneries studied the genotypic variance was significant, which enable to achieve genetic gains for borer resistance (table 2).

The broad-sense heritability for infestation index by borer in individual experiments or in the selection sceneries studied were moderate to high and relatively similar ($0.53 < h^2 < 0.78$). These heritabilities are similar to that found by Milligan et al. (2003) for infestation index by D. saccharalis ($h^2 = 0.62$) and to that found by Nibouche & Tibere (2008) for infestation index by spotted borer Chilo sacchariphagus ($h^2 = 0.80$). The high heritabilities enables to obtain satisfactory genetic gains by selecting for borer resistance (- 28.82% < GG < - 8.89%) (Table 2).

Table 2. genetic parameters for infestation index by D. saccharalis in individual trials and three selection sceneries.

Genetic parameters	First year (2015)			Second year (2016)			Third year (2016)	
	Itapagipe	**Iturama**	**Ituiutaba**	**Itapagipe**	**Iturama**	**Tupaciguara**	**Iturama**	**Tupaciguara**
σ^2_g	2.22^{NS}	4.93*	13.88**	0.02^{NS}	0.97^{NS}	1.15*	4.50**	0.06^{NS}
σ^2	8.95	17.62	15.72	1.94	9.91	5.1	9.53	5.19
σ^2_p	11.17	22.55	29.6	1.96	10.87	6.25	14.03	5.25
h^2_{gm}	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

	1 location[1], 3 years[2]	**3 locations[3], 1[4] year**	**4 locations[5], 3 years**
σ^2_g	2.18*	5.86**	1.80**
σ^2_{gy}	1.28^{NS}	-	0.47^{NS}
σ^2_{gl}	-	1.87^{NS}	0.63^{NS}
σ^2_{gyl}	-	-	0.77^{NS}
σ^2	12.2	14.6	9.18
σ^2_p	15.82	22.34	14.69
h^2_{gm}	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
GA (%)	-8.89	-16.82	-14.17

σ^2g = Genetic variance, σ^2 = Residual variance, σ^2p = phenotypic variance, h^2gm = heritability of genotype mean, Ac = Accuracy of selection by genotype mean, CV = Coefficient of residual variance, GG = genetic gain, considering an selection intensity ~ 20% of six genotypes, σ^2gy = variance of genotype x year interaction, σ^2gl = variance of genotype x location interaction, σ^2gyl = variance of genotype x year x location triple interaction, rgy = genotypic correlation between years, rgl = genotypic correlation between locations, rgly = genotypic correlation among locations and years, ND = non-determined. ^{NS} non-significant, * 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.

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

Table 3. Genotypic values of sugarcane genotypes for infestation index by D. saccharalis (IIB) in individuals 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	CTC-9	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	CTC-9	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	

Ac = Accuracy for genotypic value prediction. Bold letters represent the genotypes selected for borer resistance in 3 years – 4 locations selection scenary.

The accuracy of predicting genotypic values for the genotype in single experiments were high (Ac > 0.70) (Table 3). On the other hand, the accuracy of predicting genotypic values for infestation index by borer in several locations depends on the number of location that the clone is present (Table 4). The accuracy for the

genotype present at only one location are relatively low (Ac < 0.70) while the accuracy of the genotype present in at least two location are high (Ac > 0.70).

Table 4. Genotypic values of sugarcane genotypes for infestation index by D. saccharalis (IIB) in three selection sceneries.

Rank	4 locations[1], 3 years[2]				3 locations[3], 1 year[4]			1 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	CTC-9	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	CTC-9	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	CTC-9	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					

u + g = genotypic values (BLUP's) for infestation index by borer. 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 3 years – 4 locations selection scenary.

Overall, due the insignificant effect of genotype x environment (location or year) in the resistance of sugarcane to borer, the genotypes can be selected for borer resistance in a single experiment or by their means in experiments in several locations. The selection in a single location in one year as the advantage to be more cost effective

as assessment of borer damage is a labor task as highlighted by Milligan et al. (2003). However, in sugarcane breeding program sometimes the genotypes of experimental stage are not planted in all locations of experimental net due technical issues as lack of propagation material and land. The selection in a single location could exclude several genotypes from selection for borer resistance. In this case, the genotypes can be selected by their means of infestation index in all locations assessed. It would enable accurate prediction of the resistance of all the genotypes to sugarcane borer, especially the genotypes assessed in more than one location.

3.2 Effect of selection for borer resistance in yield traits selection index

The traits assessed to select sugarcane genotypes usually present significant genotype x location interaction (Silveira et al., 2013; Bastos et al. 2007). Therefore, the study of effect of selection for borer resistance in yield traits and use of selection index was performed at only one location. The analysis of the data TCH, TRS and TSH assessed in the experiment of Iturama in 2015, 2016 and 2017 showed that there was no genotype x year interaction for any trait. However, the genotypic variance was significant for all traits (Table 5). Therefore, genetic gains of selection can be obtained for all traits.

Despite the selection of the sugarcane genotypes for infestation index provides 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, even reaching negative values (Table 5). The selection only for borer resistance may result in genotypes with unfavorable traits and lower sugar yield (White et al., 2006, 2011). Therefore, the use of selection index is justified.

The use of selection index using II, TRS and TCH enabled to achieve high genetic gains for all traits, giving values close to the values that would be obtained by direct selection for each trait (Table 5). In addition, there was a high coincidence between the genotypes selected by selection index and the genotypes selected for TSH (coincidence coefficient = 83.33%), which is the main trait of sugarcane breeding, as it reflects the yield of the main product of sugarcane crop. It is noteworthy that in selection only for borer resistant, the check RB867515 would not be selected. However, this variety would be selected by both selection for TSH and selection index, which reinforces the need to combine selection for borer resistance to yield traits. This variety

is among the elite variety in Brazil and presents a high TBH (Bastos et al., 2007; Silveira et al., 2012).

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

Genetic parameters	TCH	TRS	II	TSH
σ^2_g	160.43**	35.61**	2.01**	5.00**
σ^2_{gy}	35.58^{NS}	7.20^{NS}	0.68^{NS}	0.82^{NS}
σ^2	233.06	54.05	13.36	7.16
σ^2_p	444.37	97.74	16.66	13.06
h^2_{gm}	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**	**II**	**TSH**
CTC-9*	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^2g = Genetic variance, σ^2gy = variance of genotype x year interaction, σ^2 = Residual variance, σ^2p = phenotypic variance, h^2gm = heritability of genotype mean, , rgy = genotypic correlation between years, GG = genetic gain, considering an selection intensity ~ 20% of six genotypes, , σ^2gl = variance of genotype x location interaction, σ^2gyl = variance of genotype x year x location triple interactionrgl = genotypic correlation between locations, rgly = genotypic correlation among locations and years, ND = non-determined. ^{NS} non-significant, * significant at $P < 0.05$ and ** significant at $P < 0.01$, according to deviance analysis. [1]* Genotypes selected by direct selection for the respective trait

As the genotypes used in this study compose the last stage of RIDESA's breeding program, they underwent several processes of selection and have favorable agronomic traits, which makes them potential varieties to be recommended to the

growers. The most resistant of these genotypes could be readily recommended to locations with higher borer pressure as long as they combine borer resistance with other favorable agronomic traits such as high sugar yield. The resistant clones can also be explored as genitors in sugarcane breeding prgrams for borer resistance. Kimbeng et al. (2006) demostrated that borer resistance can be increased in segregating sugarcane population by selecting and crossing among the most resistant parents and then focusing selection on progeny within those crossess.

4. CONCLUSIONS

- There are no genotype x year and genotype x location interactions neither genotype x year x location interactions for borer resistance so the genotypes could be selected either in a single location and single year or through genotypes means in several locations, years or location and year combinations;

- Selection for borer resistance reduces the genetic gains of TCH, TRS and TSH, justifying the use selection index;

- The use of selection index combining infestation index by borer with TCH and TRS may enable selection of genotypes with considerable borer resistance and sugar yield;

- The most resistant clones to borer were RB047050, RB047226, RB047055, RB047212, RB047201 and RB047258;

- The genotypes CTC9, RB047055, RB047409, RB047002, RB867515 and RB047201were selected for both borer resistance and stalk and sugar productivity.

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GENERAL CONCLUSIONS

- In T1 experiment, the heritability at family means level was higher than individual heritability so family selection is more effective than individual selection at T1 stage;

- The families RB027060 x RB957506, RB876030 x RB928064, RB988137 x RB951541, RB966928 x RB855156 and RB987649 x RB867515 were the most resistant families to borer;

- The additive genetic effect was more important for borer resistance than non-additive effects. Therefore, the parents may be selected through their additive effects for borer resistance;

- The genotypes RB987649, RB988137, RB928064, RB966928 were the most promising parents for borer resistance (considering the accuracy higher than 0.70);

- In T2 experiment, the heritability at clone means level was moderate (h^2 = 0.61), indicating the possibility of selecting clone for borer resistance.

- The genotypic variance among clones within families was significant so selection of families at T1 stage must be followed by a clone selection at T2 stage, to identify the superior clones within the selected families.

- The most resistant clones 56, 61, 47, and 54 were derived from a resistant family RB876030 x RB928064. We can conclude that family experiments enable selection of more promising families and parents for borer resistance.

- There are no genotype x year and genotype x location interactions neither genotype x year x location interactions for borer resistance so the genotypes could be selected either in a single location and single year or through genotypes means in several locations, years or location and year combinations;

- Selection for borer resistance reduces the genetic gains of TCH, TRS and TSH, justifying the use selection index;

- The use of selection index combining infestation index by borer with TCH and TRS may enable selection of genotypes with considerable borer resistance and sugar yield;

- The most resistant clones to borer were RB047050, RB047226, RB047055, RB047212, RB047201 and RB047258;

- The genotypes CTC9, RB047055, RB047409, RB047002, RB867515 and RB047201were selected for both borer resistance and stalk and sugar productivity.