

## Combining ability for grain chemistry quality traits in a white oat diallelic cross

Maraisa Crestani · Solange Ferreira da Silveira Silveira · Elisane Weber Tessmann · Itamara Mezzalira · Henrique de Souza Luche · José Antonio Gonzalez da Silva · Luiz Carlos Gutkoski · Fernando Irajá Félix de Carvalho · Antonio Costa de Oliveira

Received: 20 May 2011 / Accepted: 13 February 2012 / Published online: 26 February 2012  
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**Abstract** There has been a strong demand for oat genotypes that contain caryopsis with high chemical quality which can suit the different market niches. Therefore, the objectives of this study were to assess the general (GCA) and specific combining ability (SCA) of white oat cultivars through diallelic crosses providing information about the genetic effects on expression of grain chemical quality components. Also, it was aimed to estimate the heterosis on F<sub>1</sub> and F<sub>2</sub> generations and the vigor loss due to inbreeding. During 2008, 21 hybrid populations F<sub>1</sub> and F<sub>2</sub> were obtained from artificial crossing among seven Brazilian white oat cultivars, following the complete diallel

design, without considering the reciprocals. These populations and their parents were evaluated in the 2009 season in the experimental field in Capão do Leão, RS, Brazil. The higher values of mean squares associated to GCA indicates a strong contribution of additive genetic effects to the expression of grain chemical components. The parents tested showed a tendency to develop progeny with negative heterosis regarding protein, lipid,  $\beta$ -glucan and soluble dietary fiber in the grain, and positive for the content of nitrogen-free extract, total and insoluble dietary fiber. IAC 7 features a potential parent for obtaining grains with high protein and dietary fiber content, and low caloric content, fit to human diet. Meanwhile, UPF 15 and FAPA Louise can represent donors of alleles to increase lipid contents, while FAPA Louise and URS Guapa can be used to raise the grain nitrogen-free extract contents of lines intended for animal feeding.

This article is the part of the Doctor of Science thesis of Crestani Maraisa.

M. Crestani · S. F. S. Silveira · E. W. Tessmann · I. Mezzalira · H. S. Luche · F. I. F. de Carvalho · A. Costa de Oliveira (✉)  
Plant Genomics and Breeding Center, Eliseu Maciel School of Agronomy, Federal University of Pelotas (UFPEL), Gomes Carneiro, 01, P.O. Box 354, 96010-900, RS, Pelotas, Brazil  
e-mail: acostol@terra.com.br

J. A. G. da Silva  
School of Agronomy, Department of Agrarian Studies, Regional University of Northwest of Rio Grande do Sul State (UNIJUÍ), RS, Ijuí, Brazil

L. C. Gutkoski  
Food Research Center, Cereal Laboratory, University of Passo Fundo (UPF), RS, Passo Fundo, Brazil

**Keywords** General and specific combining ability · Gene action · Heterosis · Inbreeding depression · Brazilian cultivars

### Abbreviations

Prot	Protein content
Lip	Lipid
$\beta$ -glu	$\beta$ -glucan
NFE	Nitrogen-free extract
TDF	Total dietary fiber
IDF	Insoluble dietary fiber
SDF	Soluble dietary fiber

SCA	Specific combining ability
GCA	General combining ability
H <sub>1</sub>	Heterosis
Id	Inbreeding depression
LV	Loss of vigor

## Introduction

Presently oat is mostly used as feed for animals in the world. However, the white oat grains stand out for their high levels of carbohydrates, proteins, essential lipids and dietary fiber, besides adequate physical structure to industrial processing, featuring this cereal as a quality product for human consumption and also recognized for its functional properties (FDA Food Labeling 1997; Floss et al. 1998; ANVISA 1999). Because of higher oat grain quality demands by the industry, changes are needed in the oat breeding programs in Brazil in order to achieve higher quality grains regarding caryopsis chemical composition.

Grain-producing genotypes suitable for human diet need to present high industrial yield of grains, which is closely dependent on high grain yield, grains of larger size (volume) and higher caryopsis/grain hull ratios. Besides, in general, it is desirable that these grains present lower calories and lower lipid and nitrogen-free extract contents. Also, they need to be rich in protein and dietary fiber contents, mainly the  $\beta$ -glucan fraction (Holland 1997). The  $\beta$ -glucan corresponds to the main component responsible for the reduction of serum cholesterol, and thus reducing the risk of cardiovascular disease, conferred by the regular oat grains consumption when is associated to proper diet and healthy lifestyle (McDonald et al. 1992; Anderson and Bridges 1993; Wood 1993; Bell et al. 1999; Andon and Anderson 2008; Butt et al. 2008). For the industrialization of food, oat grains with appropriate physical structure, low breakage index obtained by mechanical peeling, plus acceptable color and odor traits are desirable. In this sense, lower levels of lipids can reduce difficulties in oat grain industrial processing due to a smaller rancidity potential that is triggered by the action of enzymes (lipases) that are activated with the peeling and/or milling of grains (Baker and McKenzie 1972; Price and Parsons 1975). Meanwhile, low  $\beta$ -glucan genotypes are the goal for animal feeding in order to avoid body mass losses (Wood 1993; Holland 1997).

An increase in the selection of grain chemical components has become a major trend in worldwide white oat grain breeding programs (Gullord 1980; Thro and Frey 1985; Lim et al. 1992; Manthey et al. 1999; Frey and Holland 1999; Ahokas and Manninen 2000; Loskutov 2000; Peterson et al. 2005; Chernyshova et al. 2007). Likewise, a similar trend is occurring in Brazil (Doehlert et al. 2001; De Sá et al. 1998; Gutkoski and Trombetta 1999; Pedó et al. 1999; De Sá et al. 2000; Beber et al. 2002; Silva et al. 2006, 2008; Crestani et al. 2010). One of the great caveats of selecting genotypes based on chemical components of caryopses lies in having a structured breeding program, capable to use rapid, inexpensive and non-destructive methods of analyzing grain chemical components or that require small enough amounts of grain to allow the evaluation and selection of individual plants in early generations. Additionally, little information is available regarding the expression of the main chemical components of caryopsis in white oat cultivars recommended in Brazil.

The selection of parents based on the performance of phenotypic traits per se is insufficient to ensure a progeny with high genetic potential, since the segregating populations following a cross between two given genotypes are formed at random and are difficult to repeat (Carvalho et al. 2008). Therefore, it is necessary that the parents involved in the crosses have a high combining ability to allow the production of a high frequency of favorable recombinants that can be selected when efficient methods are applied (Lorenzeti et al. 2005; Carvalho et al. 2008). Diallel studies stand out for allowing information in this regard, providing estimates of useful parameters in parents selecting for artificial crosses and also for the understanding of the genetic effects involved in the phenotypic performance of target traits (Cruz et al. 2004). Among the main procedures employed in the analysis and interpretation of diallel crosses, the method proposed by Griffing (1956) provides estimates of the effects of general (GCA) and specific combining ability (SCA) of parents involved in crosses. These estimates allow the breeder to assess the performance of a genotype as a parent in crosses, as well as to identify the best hybrid combinations that express higher heterosis (hybrid vigor) and potential for the formation of superior segregating populations.

The hybrid vigor is the result of an increased frequency of dominant alleles, arranged in homozygous

and/or heterozygous loci, all contributing to the increase or reduction of character value. It is manifested when individual hybrids (e.g.,  $F_1$  or  $F_2$ ) show performance above or below the mean of their parents, or when they show performance outside the range presented by the parents (Allard 1999; Carvalho et al. 2008). In self-pollinating species, such as white oat, the measure of heterosis levels allows the assessment of recombination of different alleles, resulting in a wider range of genotypic classes that will be obtained in the  $F_2$  generation, characterizing the basic population for selection (Falconer and Mackay 1996; Bertan et al. 2009). Thereafter, with generation advancing, there is the formation of genetically distinct genotypic classes, increasing the possibility of selecting superior individuals with fixed characters and homozygous alleles in most of their loci (Allard 1999; Carvalho et al. 2008; Bertan et al. 2009).

Previous studies have reported the combining ability and genetic effects involved in the phenotypic expression of white oat grain quality characters (Brown et al. 1973; Thro and Frey 1985; Holthaus et al. 1996; Humphreys and Mather 1996; Zhu et al. 2004; Chernyshova et al. 2007). However, the present work features unique traits and genotypes (Brazilian cultivars) and can provide novel information that can be exploited by white oat breeding programs worldwide.

The Brazilian white oat germplasm has a strong genetic influence of genotypes introduced from USA, Uruguay, Argentina, Canada and Australia. However, in the course of approximately 40 years of breeding in Brazil, high yield and strongly adapted genotypes have been obtained, phenotypically very distinct from the original germplasm (Barbosa Neto et al. 2000; Federizzi et al. 2005). Thus, since the gene effects involved in the character expression are strongly dependent on the genotypes involved in the crosses (Mather and Jinks 1982; Falconer and Mackay 1996; Allard 1999; Carvalho et al. 2008), it is extremely important to perform these evaluations considering cultivars routinely adopted as source of genes in breeding programs. Thus, it is possible to verify their performance as parentals, along with the assessment of genetic effects within the evaluated populations. Therefore, the objectives of this study were to assess the general (GCA) and specific combining ability (SCA) of Brazilian white oat cultivars through diallel crosses, providing information about the genetic

effects on the expression of grain chemical quality. Also, to estimate the heterosis on  $F_1$  and  $F_2$  generations, the vigor loss due to inbreeding, and to select parental combinations to maximize genetic gain in characters related to grain chemical composition.

## Materials and methods

### Plant material

Crosses were performed between seven Brazilian white oat cultivars recommended for cultivation in Brazil, which were Albasul, UPFA 22, URS Guapa, UPF 15, UFRGS 19, FAPA Louise and IAC 7. These parents were selected based on the performance shown in preliminary tests, aiming to detect the combinations between parents with high and low performance in traits related to the chemical quality of grains, and thus to provide a broad phenotypic variability in the segregating populations to be formed. The crosses were performed from April to November 2008 in a greenhouse, obtaining the  $F_1$ , considering all combinations without reciprocals. In the same year, a sample of the  $F_1$  seeds of each combination was sown in a greenhouse and the  $F_2$  generations were obtained. The remaining seeds were stored in storage chamber, with temperatures around 10°C and relative humidity near to 45%.

The crosses and advancing of generations were conducted in order to allow the adoption of the diallel's Model 2 proposed by Griffing (1956), which includes in the mathematic analysis the performance of  $p(p-1)/2$  hybrids and their parents, without considering the reciprocal crosses. Thus, a total of 21 hybrids combinations [ $7(7-1)/2 = 21$ ], in the  $F_1$  and  $F_2$  generations plus seven parental genotypes (7 Brazilian white oat cultivars) were evaluated regarding their performances.

In the 2009 season, seeds of  $F_1$  and  $F_2$  populations and their parents were sown in the experimental field of Palma Agricultural Station which belongs to the Federal University of Pelotas, located in the County of Capão do Leão, Rio Grande do Sul State (latitude 31°45'S, longitude 52°29'W, altitude 13 m), Brazil. The experimental design consisted of randomized blocks with three replications. The seven parents and  $F_1$  populations formed the experimental plots of 10 plants, grown in a 3.0 m long row, spaced 0.3 m

between plants and between rows. The F<sub>2</sub> populations formed plots with 50 plants, grown in five 3.0 m long rows, spaced 0.3 m between plants and between rows.

### Experimental conditions

The experimental soil area is described as Dystrophic Yellow Red Argisol (Santos et al. 2006), presenting the following chemical characteristics at the time of the experiment set up: organic matter 2.1%, water pH 5.5; SMP index 6.5, P 19.7 mg dm<sup>-3</sup>, K 80.0 mg dm<sup>-3</sup>, Al 0.1 cmol<sub>c</sub> dm<sup>-3</sup>, Ca 2.5 cmol<sub>c</sub> dm<sup>-3</sup>, Mg 0.8 cmol<sub>c</sub> dm<sup>-3</sup>. The soil preparation and fertility corrections followed the recommendations of Brazilian Oat Research Committee (2006). The fertilization corrections with macronutrients (NPK) were performed according to the levels observed in the soil chemical quality analysis in order to supply the demands for a grain yield around 2.0 t ha<sup>-1</sup>. Tebucnazole fungicide applications at a dosage of 0.75 L ha<sup>-1</sup> (Folicur EC—Bayer CropScience Ltda, São Paulo, Brazil) were performed according to the need for shoot diseases control during the crop development cycle.

### Chemical analyzes

The following characters related to white oat grain chemical composition were evaluated: protein content, lipid,  $\beta$ -glucan, nitrogen-free extract, total dietary fiber, soluble dietary fiber and insoluble dietary fiber. These characters were chosen because of their high influence on the definition of white oat grain commercial standards. For these analyses, samples of manually dehulled 300 grains larger than 2 mm, originating from a bulk harvest on each plot, were used. The kernels were ground in Willey type mill (Marconi, Piracicaba, Brazil) with a 0.25 mm sieve. The milled material was analyzed in the Food Research Center, University of Passo Fundo adopting the near infrared reflectance spectrometer (NIRS), brand Perstorp Analytical, model 5000 (Maryland, USA). The calibration curves for chemical quality traits determination in white oat grain adopting the NIRS were built by the Laboratory of Physical Chemistry of the Food Research Center, University of Passo Fundo. The New Infracsoft International

software (ISI 1996) was used to obtain these curves, considering the analysis of 100 white oat following the methods recommended by the AACC (1999) and AOAC (1997). The value of protein content was obtained by multiplying the correction factor 6.25 for N content identified in the sample. NIRS readings were performed in triplicate and the results expressed in g 100 g<sup>-1</sup> in dry weight basis.

### Statistical analysis

Based on the variance analyses results, the sum of squares for treatments were partitioned into general (GCA) and specific combining ability (SCA), without reciprocal crosses. For this partitioning, the Model 2 of balanced diallel described by Griffing (1956) was used, adopting the following statistical model:  $Y_{ij} = m + g_i + g_j + s_{ij} + \bar{e}_{ij}$ , where  $Y_{ij}$  corresponds to the hybrid ( $i \neq j$ ) or to the parent ( $i = j$ ) combination mean value;  $m$ : general mean;  $g_i, g_j$ : general combining ability effects of the  $i$ th and  $j$ th parent, respectively;  $s_{ij}$ : specific combining ability effect for the crosses among the parents of the order  $i$  and  $j$ ;  $\bar{e}_{ij}$ : mean experimental error.

The heterosis was calculated over mean parental value, following the model  $H_1(\%) = [(\bar{F}_1 - \overline{PM}) / \overline{PM}] * 100$ , where  $H_1$  corresponds to the heterosis observed over mean parental value;  $\bar{F}_1$ : hybrid mean; and  $\overline{PM}$ : mean parental value  $[(P_1 + P_2)/2]$ . The statistical significance of the heterosis over mean parental value was checked using the  $t$  test for each evaluated character, associated to  $(j - 1)(i - 1)$  degrees of freedom, according to the formula  $t = (\bar{F}_1 - \overline{PM}) / \sqrt{(3EMS/3r)}$ , where  $t$  corresponds to the  $t$  statistic for assessing the significance of heterosis over mean parental value;  $EMS$ : error mean square,  $r$ : number of repetitions.

The calculation of loss of vigor (inbreeding depression) by the effects of inbreeding was done considering the mean performance of each population in generations F<sub>1</sub> and F<sub>2</sub>, following this mathematical formula:  $Id(\%) = LV = [(S_{oi} - S_{li})/S_{oi}] * 100$ , where  $Id$  represents the percentage of inbreeding depression;  $LV$ : loss of vigor;  $S_{oi}$ : character mean in the F<sub>1</sub> generation; and  $S_{li}$ : character mean in the F<sub>2</sub> generation. The analyses were performed using the Genes computer software (Cruz 2001).

## Results

Variance analyses, GCA and SCA of  $F_1$  and  $F_2$  generations for grain chemical quality characters

Aiming to measure the variability among the genotypes (parents and populations) and to verify its effects on the general (GCA) and specific (SCA) combining abilities, variance and diallel analyses using the Model 2 described by Griffing (1956) were performed. A summary of the variance analyses of fixed ( $F_1$  and parents) and segregating ( $F_2$ ) generations, effects of the general (GCA) and specific (SCA) combining ability, and the variation range observed in the seven

characters related to the chemical quality of grain is shown on Table 1. The mean squares related to  $F_1$  and  $F_2$  generations showed significance for all characters considered. In the variance analysis of the  $F_1$  generation, the treatments were significant for the characters protein content, lipid, nitrogen-free extract and  $\beta$ -glucan in the grain. In the  $F_1$  generation, significant effects of SCA for the nitrogen-free extract content were found, while for the other characters significant effects of GCA were detected. At the same time, in the  $F_2$  generation the characters protein, lipid and total dietary fiber grain content showed significant effects regarding GCA, and the content of nitrogen-free extract showed SCA significant effects.

**Table 1** Summary of variance analysis of individual and joint generations  $F_1$  and  $F_2$  <sup>(1)</sup>, and mean squares for treatments, general combining ability (GCA) and specific combining ability (SCA) for traits related to the chemical quality of white

oat grain according to the Model 2 described by Griffing (1956), considering the parents performance and their respective  $F_1$  and  $F_2$ , without reciprocal crosses

Source of variation	Df	Mean square						
		Protein	Lipid (g 100 g <sup>-1</sup> )	Nitrogen-free extract (g 100 g <sup>-1</sup> )	$\beta$ -glucan (g 100 g <sup>-1</sup> )	Total dietary fiber (g 100 g <sup>-1</sup> )	Insoluble dietary fiber (g 100 g <sup>-1</sup> )	Soluble dietary fiber (g 100 g <sup>-1</sup> )
Generation $F_1$	27	2.61**	1.67**	5.55**	2.01*	0.35**	0.33**	0.07*
Generation $F_2$	27	3.41**	1.33**	7.20**	2.32**	0.24**	0.29**	0.08**
$F_1 \times F_2$	1	4.27 <sup>ns</sup>	0.67 <sup>ns</sup>	17.56 <sup>ns</sup>	3.05 <sup>ns</sup>	0.19 <sup>ns</sup>	0.03 <sup>ns</sup>	0.39 <sup>ns</sup>
Error	110	0.78	0.19	1.78	1.03	0.06	0.03	0.04
Treatment ( $F_1$ )	27	2.57**	1.67*	5.53**	2.01**	0.35 <sup>ns</sup>	0.32 <sup>ns</sup>	0.06 <sup>ns</sup>
GCA	6	7.94**	6.74**	8.84 <sup>ns</sup>	6.51**	0.97**	0.62*	0.15**
SCA	21	1.04 <sup>ns</sup>	0.23 <sup>ns</sup>	4.59**	0.73 <sup>ns</sup>	0.17 <sup>ns</sup>	0.23 <sup>ns</sup>	0.04 <sup>ns</sup>
CV (%)		5.16	4.60	2.17	18.28	2.65	2.99	5.15
Range								
Max.		22.00	10.01	72.00	9.24	10.81	6.78	4.34
Min.		16.20	6.52	62.17	3.00	8.58	5.16	3.25
Treatment ( $F_2$ )	27	3.36**	1.33 <sup>ns</sup>	7.19**	2.32**	0.24 <sup>ns</sup>	0.27 <sup>ns</sup>	0.07 <sup>ns</sup>
GCA	6	9.88**	4.63**	7.32 <sup>ns</sup>	4.22 <sup>ns</sup>	0.45*	0.25 <sup>ns</sup>	0.10 <sup>ns</sup>
SCA	21	1.50 <sup>ns</sup>	0.38 <sup>ns</sup>	7.15**	1.77 <sup>ns</sup>	0.18 <sup>ns</sup>	0.28 <sup>ns</sup>	0.06 <sup>ns</sup>
CV (%)		4.34	5.74	1.77	17.84	2.32	3.07	4.89
Range								
Max.		22.00	9.80	70.67	9.24	10.40	6.76	4.34
Min.		15.94	6.52	62.17	3.11	8.58	5.16	3.11

Df degrees of freedom, CV coefficient of variation, in percentage; Max. maximum range, Min. minimum range

(1) <sup>ns</sup> Non significant

\*\* and \* Significant at 1 and 5% probability, respectively, by *F* test

## Mean performance of white oat parents and their hybrid generations

The mean performance shown by the parents and their hybrids ( $F_1$  and  $F_2$ ), considering the characters standard deviation in each assessment situation can provide an initial understanding of the genetic potential of parents and their progenies. The means from three replications for the seven parents ( $Y_{ii}$ ) and their progeny in the  $F_1$  and  $F_2$  generations ( $Y_{ij}$ ) are shown on Table 2. Regarding the parental performance, the cultivar IAC 7 showed higher values when compared to the parental mean plus one standard deviation for protein content,  $\beta$ -glucan, total dietary fiber, soluble dietary fiber and insoluble dietary fiber content in the grain. Also, IAC 7 showed a low performance for lipid content, lower than the parental mean minus one standard deviation unit. Meanwhile, the white oat cultivars Albasul and FAPA Louise expressed performance lower than the parental mean minus one standard deviation for the grain protein content and performance superior to parental mean plus one standard deviation regarding grain lipid content. The cultivar Albasul showed reduced performance for total dietary fiber and insoluble dietary fiber content in the grain, while FAPA Louise stood out with high content of insoluble dietary fiber in the grain. Among the evaluated cultivars, the URS Guapa showed the lowest mean grain lipid content.

The general means of  $F_1$  and  $F_2$  generations ( $\mu_{ii}$  and  $\mu_{ij}$ ) for the different chemical quality characters of white oat grains evaluated presented similar magnitude in this study (Table 2). For the protein content, lipids,  $\beta$ -glucan, total dietary fiber and soluble dietary fiber content, the  $F_1$  was slightly higher than the  $F_2$  mean performance, indicating a general loss of vigor with generation advancing (Tables 3, 4). Furthermore, considering the overall performance of the 21 combinations, medium to high significant positive correlations were identified between the  $F_1$  and respective  $F_2$  population performances, for six of the seven characters evaluated (Fig. 1). Higher coefficient values for correlations were observed for protein ( $r = 0.83^*$ ), lipid ( $r = 0.72^*$ ) and nitrogen-free extract ( $r = 0.62^*$ ) content. When dealing with different dietary fiber fractions, the associations between the  $F_1$  and  $F_2$  generations were not as high, i.e., for total dietary fiber ( $r = 0.52^*$ ), insoluble dietary fiber ( $r = 0.56^*$ ) and soluble dietary fiber

( $r = 0.58^*$ ). Also, no significant correlation was found for  $\beta$ -glucan content ( $r = 0.40^{ns}$ ), despite the positive association. The parental means for the characters protein and soluble dietary tended to be positioned in the region near to the trendline upper end. On the other hand, nitrogen-free extract and insoluble dietary fiber means were closer to the lower end of the trendline, while for the characters lipid,  $\beta$ -glucan and total dietary fiber content the parental means were more evenly distributed over the trendline (Fig. 1).

## GCA and SCA of white oat cultivars, and estimates of SCA, heterosis and inbreeding depression in their hybrids

Initially, the estimates of GCA, SCA, heterosis and inbreeding depression were performed in order to understand the dynamics of the phenotypic expression for grain chemical quality characters in this group of genotypes. Later, these analyses were conducted in order to identify the best parentals and respective crosses that may be more efficient regarding the improvement of white oat chemical quality of grains. The general combining ability of seven white oat cultivars evaluated for grain chemical quality characters considering the parentals and respective  $F_1$  and  $F_2$  generations is represented on Fig. 2. In general, the highest GCA for protein content,  $\beta$ -glucan, total dietary fiber and soluble dietary fiber in the grain was presented by the cultivar IAC 7. FAPA Louise showed the highest GCA in relation to grain lipid and insoluble dietary fiber concentration, while URS Guapa presented similar performance for nitrogen-free extract. The lowest GCA for protein content, lipid and soluble dietary fiber content, nitrogen-free extract content,  $\beta$ -glucan and insoluble dietary fiber was shown by FAPA Louise, URS Guapa, IAC 7, UPF 15 and Albasul, respectively. The estimates of specific combining ability (SCA) for the seven white oat cultivars ( $S_{ii}$ ) and their respective  $F_1$  and  $F_2$  populations ( $S_{ij}$ ), heterosis ( $H_1$ ) and inbreeding depression ( $Id$ ) values, in percentage, for seven characters associated to grain chemical quality are shown on Tables 3 and 4. All parentals showed positive SCA values for protein content. For nitrogen-free extract, total dietary fiber and insoluble dietary fiber, all parentals showed negative SCA values in any of the generations tested, in  $F_1$  and/or  $F_2$ . At the same time, negative values of

Parents	Protein	Lipid	Nitrogen-free extract	$\beta$ -Glucan	Total dietary fiber	Insoluble dietary fiber	Soluble dietary fiber
Albasul	17.91 <b>B</b>	9.03 <b>A</b>	66.38	6.30	8.91 <b>B</b>	5.20 <b>B</b>	3.71
UPFA 22	19.49	9.01 <b>A</b>	65.11	5.22	9.74	5.82	3.93
URS Guapa	19.88	6.89 <b>B</b>	66.32	6.40	9.30	5.60	3.71
UPF 15	19.54	8.98 <b>A</b>	65.47	4.97	9.88 <b>A</b>	5.94	3.95
UFRGS 19	19.87	8.17	65.64	5.28	9.90 <b>A</b>	6.02 <b>A</b>	3.89
FAPA Louise	17.31 <b>B</b>	9.51 <b>A</b>	66.51	5.75	9.82	6.03 <b>A</b>	3.79
IAC 7	20.37 <b>A</b>	7.64 <b>B</b>	64.28	8.09 <b>A</b>	10.03 <b>A</b>	5.96 <b>A</b>	4.09
General mean ( $\mu_{ij}$ )	19.21	8.48	65.67	6.00	9.63	5.75	3.88
Standard deviation	1.11	0.48	1.90	1.29	0.25	0.21	0.23

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Table 2 continued

Populations	F <sub>1</sub>	F <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>
General mean ( $\mu_{ii}$ and $\mu_{ij}$ )	18.66	18.34	8.39	8.26	67.18	67.83	5.80	5.53	9.90	9.83	6.13	6.16
Standard deviation	0.96	0.99	0.39	0.47	1.46	1.20	1.06	0.99	0.26	0.23	0.18	0.19

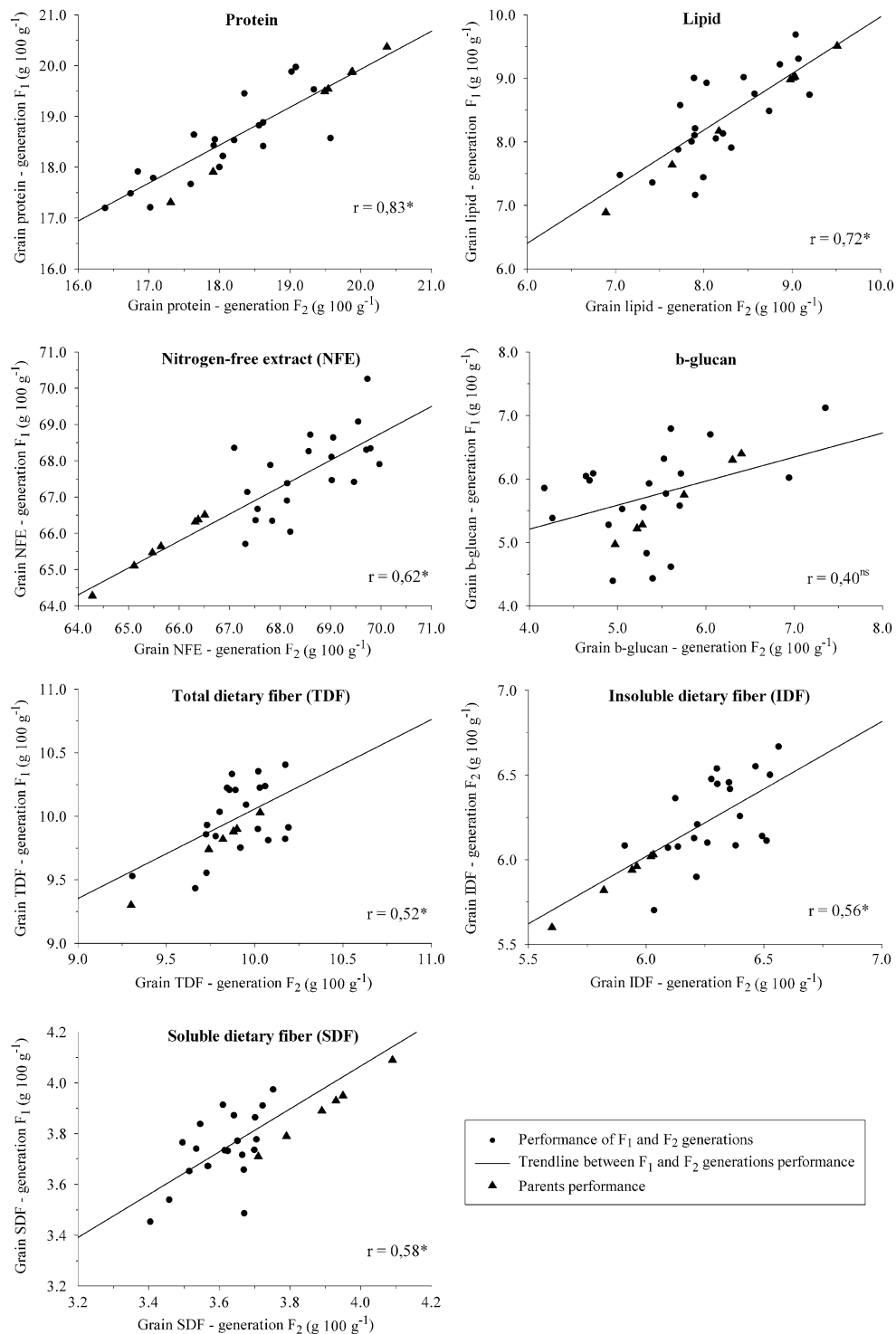
A: above the respective generation mean plus one standard deviation unit; B: below the respective generation mean minus one standard deviation unit;  $\mu_{ii}$ : parents,  $\mu_{ij}$ : populations

SCA were observed in some parents involved in the crosses for the characters  $\beta$ -glucan, lipid and soluble dietary fiber content.

All populations obtained revealed negative heterosis estimates for protein in the grain in at least one of the generations evaluated (Table 3). Comparing the average performances of F<sub>1</sub> and F<sub>2</sub> generations with the respective parental means for each cross by a t test, a significant negative heterosis for protein content was identified in the combinations URS Guapa  $\times$  FAPA Louise, in the F<sub>1</sub> generation, and UPFA 22  $\times$  URS Guapa, URS Guapa  $\times$  UFRGS 19, UPF 15  $\times$  UFRGS 19, UFRGS 19  $\times$  FAPA Louise, and UFRGS 19  $\times$  IAC 7, in the F<sub>2</sub> generation. Also, heterosis estimates equal to  $-3.71\%$  in the F<sub>1</sub> generation, and  $-5.95\%$  in F<sub>2</sub>, resulting in an inbreeding depression mean of 2.29% for protein content in the grain was observed with the advancing of generation for all populations. Regarding lipid content, significant heterosis was only found for the crosses UPF 15  $\times$  UFRGS 19 (5.17%) in the F<sub>1</sub>, and Albasul  $\times$  FAPA Louise ( $-14.00\%$ ) in the F<sub>2</sub> generation. The mean performance of populations resulted in heterosis means of  $-1.28\%$  and  $-3.12\%$  in the F<sub>1</sub> and F<sub>2</sub> generations, respectively, resulting in an overall inbreeding depression mean of 1.73% (Table 3). The most significant loss of vigor for this character was observed for the cross Albasul  $\times$  FAPA Louise, reaching 12.41%. For the character nitrogen-free extract content, all combinations showed positive heterosis, five of the 21 combinations tested (t test) showed average performance superior to the parental mean value in the F<sub>1</sub>, and eleven in the F<sub>2</sub> generation (Table 3). Despite the low value, a negative mean inbreeding depression for nitrogen-free extract content was observed, considering the combined performance of the 21 combinations tested, with an average performance of F<sub>1</sub> (67.18 g 100 g<sup>-1</sup>) slightly lower than the average presented by the F<sub>2</sub> (67.83 g 100 g<sup>-1</sup>) generation, as shown on Table 3.

The cultivar Albasul stood out by showing the highest negative SCA estimates for total dietary fiber among the parents tested (Table 4). It is noteworthy that in three of the six combinations involving this cultivar, the populations showed superior performance than their mean parental values, evidenced by a significant positive heterosis. The mean heterosis values presented by the set of populations tested in the F<sub>1</sub> (3.42%) was slightly higher than the F<sub>2</sub>





**Fig. 1** Correlation ( $r$ ) among the performance of 21 white oat populations  $F_1$  and respective  $F_2$  (filled circle), and seven parents mean performance (filled triangle) for the characters grain protein content, lipids, nitrogen-free extract,  $\beta$ -glucan,

total dietary fiber, insoluble dietary fiber and soluble dietary fiber. <sup>ns</sup> Values of correlation non significant, and \* significant at 5% of probability by the  $t$  test

**Table 3** Specific combining ability (SCA), heterosis ( $H_1$ , in %) and inbreeding depression (Id, in %) in seven white oat cultivars and their respective  $F_1$  and  $F_2$  populations regarding protein content, lipid and nitrogen-free extract, according to Model 2 described by Griffing (1956), considering the parents performance and their respective  $F_1$  and  $F_2$ , without reciprocals crosses

Parents	Protein	Lipid				Nitrogen-free extract										
		SCA—F <sub>1</sub>		SCA—F <sub>2</sub>		SCA—F <sub>1</sub>		SCA—F <sub>2</sub>								
		SCA	H <sub>1</sub>	SCA	H <sub>1</sub>	SCA	H <sub>1</sub>	SCA	H <sub>1</sub>							
Albasul	0.15		0.38		0.22		0.40		-1.03		-1.72					
UPFA 22	0.43		0.86		0.33		0.23		-1.67		-2.25					
URS Guapa	1.15		1.10		0.24		-0.17		-2.76		-2.09					
UPF 15	0.59		1.09		-0.21		-0.05		-0.99		-2.03					
UFRGS 19	0.86		1.29		0.05		0.31		-1.80		-2.65					
FAPA Louise	0.47		1.07		-0.08		0.42		-1.19		-2.70					
IAC 7	0.12		0.20		0.00		0.30		-1.11		-1.64					
Populations	F <sub>1</sub>		F <sub>2</sub>		Id		F <sub>2</sub>		F <sub>1</sub>		F <sub>2</sub>		Id			
	SCA		SCA		SCA		SCA		SCA		SCA		SCA			
	SCA	H <sub>1</sub>	SCA	H <sub>1</sub>	SCA	H <sub>1</sub>	SCA	H <sub>1</sub>	SCA	H <sub>1</sub>	SCA	H <sub>1</sub>	SCA	H <sub>1</sub>		
Albasul × UPFA 22	-0.19	-2.55	-0.03	-3.48	0.96		-0.00	-3.06	0.49	1.99	-5.20	0.04	2.12	-0.39	2.44*	-0.31
Albasul × URS Guapa	0.19	-2.44	-0.23	-5.15	2.78		-0.56	-9.98	0.06	-0.72	-10.28	0.48	3.57	0.34	3.39	0.18
Albasul × UPF 15	0.29	-0.44	-0.35	-5.8	5.38		0.31	3.39	0.24	0.73	2.57	-0.89	0.18	0.40	3.45	-3.27
Albasul × UFRGS 19	-0.38	-4.68	-0.06	-4.72	0.04		0.12	-0.24	-0.52	-10.09	9.88	0.68	3.17	0.82	4.55	-1.34
Albasul × FAPA Louise	-0.09	-2.26	0.14	-3.34	1.10		-0.19	-2.81	-0.97	-14.87*	12.41	0.79	2.86	1.14	5.04*	-2.12
Albasul × IAC 7	-0.13	-1.36	-0.24	-2.74	1.40		-0.12	-2.80	-0.10	-5.30	2.58	0.98	3.13	1.13	4.30	-1.13
UPFA 22 × URS Guapa	-0.07	-4.34	-0.14	-5.7*	1.42		-0.22	-6.37	0.08	0.57	-7.43	0.34	3.88*	0.68	4.34*	-0.44
UPFA 22 × UPF 15	-0.59	-5.63	0.08	-4.59	-1.10		-0.18	-2.62	-0.33	-4.67	2.10	1.27	3.97*	0.38	3.85*	0.11
UPFA 22 × UFRGS 19	0.42	-1.15	-0.25	-6.75	5.66		-0.19	-4.37	-0.42	-8.01	3.80	0.36	3.20	1.19	5.58*	-2.30
UPFA 22 × FAPA Louise	-0.75	-6.52	-1.06	-10.97	4.76		0.09	-0.38	-0.07	-4.28	3.92	1.07	3.79	1.43	5.93*	-2.06
UPFA 22 × IAC 7	0.31	0.21	-0.32	-4.27	4.47		-0.16	-3.84	-0.20	-5.59	1.81	0.26	2.55*	1.21	4.87	-2.26
URS Guapa × UPF 15	-0.31	-5.97	-0.41	-7.62	1.76		-0.01	-0.35	0.27	4.73	-5.10	0.88	4.17	1.10	4.80	-0.60
URS Guapa × UFRGS 19	-1.20	-11.08	-1.08	-11.48*	0.44		-0.03	-2.26	-0.04	-1.49	-0.78	2.00	6.48	1.38	5.69*	0.75
URS Guapa × FAPA Louise	0.01	-4.32*	-0.44	-8.22	4.08		0.02	-0.79	0.14	0.23	-1.02	0.69	4.02*	0.74	4.72*	-0.68
URS Guapa × IAC7	-0.92	-7.70	0.10	-2.76	-5.35		0.33	2.91	-0.16	-2.99	5.74	1.13	4.69	-0.07	2.75	1.85
UPF 15 × UFRGS 19	-0.44	-5.88	-0.58	-8.99*	3.31		0.36	5.17*	0.00	-1.45	6.30	-0.05	2.05	0.24	3.94*	-1.85
UPF 15 × FAPA Louise	-0.41	-5.10	-0.61	-9.14	4.26		0.30	4.83	-0.02	-2.21	6.71	0.34	2.17	1.12	5.27*	-3.04
UPF 15 × IAC 7	0.28	-0.39	-0.30	-4.70	4.33		-0.37	-3.13	-0.06	-2.14	-1.02	0.44	2.29	0.81	4.07	-1.74
UFRGS 19 × FAPA Louise	-0.00	-3.61	-0.57	-9.39*	5.99		-0.37	-3.98	0.26	-1.13	-2.97	0.34	2.77	1.22	5.89	-3.04

**Table 3** continued

Populations	F <sub>1</sub>			F <sub>2</sub>			Id			F <sub>1</sub>			F <sub>2</sub>			Id		
	SCA	H <sub>1</sub>		SCA	H <sub>1</sub>		SCA	H <sub>1</sub>		SCA	H <sub>1</sub>		SCA	H <sub>1</sub>		SCA	H <sub>1</sub>	
UFRGS 19 × IAC 7	-0.10	-2.93		-0.04	-3.92		1.02	1.02		-0.01	-0.35		0.10	-2.51		2.18	2.18	
FAPA Louise × IAC 7	0.33	0.22		0.41	-1.18*		1.40	1.40		0.31	4.13		-0.19	-6.36		10.07	10.07	
Mean (heterosis and Id)	-	-3.71		-	-5.95		2.29	2.29		-	-1.28		-	-3.12		1.73	1.73	

\* Significantly higher (positive values) or lower (negative values) regarding the parental mean by a t test, at 5% of probability

generation (2.54%), resulting in an inbreeding depression mean of 0.84%. The cross UPFA 22 × IAC 7 featured the combination that provided the highest loss of vigor due to inbreeding (4.47%).

A large number of populations were statistically superior to the mean parental value for insoluble dietary fiber content in the grain, both in F<sub>1</sub> and in F<sub>2</sub>, resulting in a negative loss of vigor of -0.72% (Table 4). Meanwhile, the parentals tested originated populations that in mostly showed negative heterosis estimates for soluble dietary fiber, with mean heterosis equal to -3.33 and -6.63% in the F<sub>1</sub> and F<sub>2</sub> generation, respectively, and a loss of vigor equal to 3.34%.

In the SCA estimation for  $\beta$ -glucan content in the grain, only the cultivars Albasul and FAPA Louise showed negative values in the F<sub>1</sub>. However, this was not maintained in the next generation (Table 4). Thus, just few combinations showed positive heterosis estimates, and no significant heterosis in F<sub>1</sub> and F<sub>2</sub> generations was detected for this character. The highest average inbreeding depression was detected for  $\beta$ -glucan content (5.25%) among all the characters evaluated. However, it is possible to highlight the cross Albasul × FAPA Louise, whose F<sub>1</sub> and F<sub>2</sub> populations revealed high average performance for this character (7.12 and 7.35 g 100 g<sup>-1</sup>, respectively), being the only combination that showed positive heterosis estimates in both F<sub>1</sub> (18.17%) and F<sub>2</sub> (22.04%) generations (Tables 2, 4). Meanwhile, the cross between Albasul × IAC 7 originated progeny whose negative heterosis estimates were more pronounced for  $\beta$ -glucan content in the grain, with values equal to -15.47% and -20.58% in the F<sub>1</sub> and F<sub>2</sub> generations, respectively (Table 4). However, these populations showed superior performance (F<sub>1</sub>: 6.08 g 100 g<sup>-1</sup>; F<sub>2</sub>: 5.72 g 100 g<sup>-1</sup>) regarding the F<sub>1</sub> and F<sub>2</sub> general means (Table 2).

Correlations among heterosis estimates in F<sub>1</sub> and F<sub>2</sub> generations

Correlation analyses among heterosis values estimated in the F<sub>1</sub> and F<sub>2</sub> generations for different characters can aid to identify the effects that characters have on each other and their influence on population variability (Bertan et al. 2009). In this sense, the correlation estimates between heterosis values observed for the characters related to the chemical quality of white oat grains were obtained (Table 5). The heterosis estimates for nitrogen-free extract content showed

**Table 4** Specific combining ability (SCA), heterosis ( $H_1$ , in %) and inbreeding depression (Id, in %) of seven white oat cultivars and their respective  $F_1$  and  $F_2$  populations for  $\beta$ -glucan, total dietary fiber, soluble and insoluble dietaryfiber content, according to Model 2 described by Griffing (1956), considering the parents performance and their respective  $F_1$  and  $F_2$ , without reciprocal crosses

Parents	$\beta$ -glucan		Total dietary fiber		Insoluble dietary fiber		Soluble dietary fiber			
	SCA—F <sub>1</sub>	SCA—F <sub>2</sub>	SCA—F <sub>1</sub>	SCA—F <sub>2</sub>	SCA—F <sub>1</sub>	SCA—F <sub>2</sub>	SCA—F <sub>1</sub>	SCA—F <sub>2</sub>		
Albasul	−0.09	0.17	−0.43	−0.54	−0.38	−0.64	−0.05	0.10		
UPFA 22	0.39	0.08	−0.25	−0.27	−0.36	−0.43	0.12	0.15		
URS Guapa	0.67	0.61	−0.08	−0.23	−0.29	−0.39	0.21	0.16		
UPF 15	0.10	0.33	−0.24	−0.15	−0.31	−0.38	0.08	0.23		
UFRGS 19	0.24	0.52	−0.12	0.12	−0.27	−0.14	0.15	0.26		
FAPA Louise	−0.49	0.36	−0.40	−0.14	−0.47	−0.36	0.07	0.23		
IAC 7	0.61	1.24	−0.21	−0.06	−0.31	−0.27	0.10	0.22		
Populations	F <sub>1</sub>		F <sub>2</sub>		Id	F <sub>1</sub>		F <sub>2</sub>		Id
	SCA	H <sub>1</sub>	SCA	H <sub>1</sub>		SCA	H <sub>1</sub>	SCA	H <sub>1</sub>	
Albasul × UPFA 22	−0.03	−3.17	0.07	−1.05	−2.19	0.25	6.28	0.46	9.26*	−2.81
Albasul × URS Guapa	−0.14	−6.69	−0.61	−15.69	9.65	0.07	3.57	0.17	6.09	−2.44
Albasul × UPF 15	0.35	6.05	−0.71	−16.94	21.68	0.30	6.77*	0.06	4.29*	2.33
Albasul × UFRGS 19	0.05	−0.39	0.10	−4.21	3.84	0.16	4.66	0.17	3.98	0.65
Albasul × FAPA Louise	0.80	18.17	1.59	22.04	−3.27	0.31	7.77*	0.25	6.27*	1.39
Albasul × IAC 7	−0.85	−15.47	−0.78	−20.58	6.06	−0.24	0.97	−0.04	2.69	−1.81
UPFA 22 × URS Guapa	−0.85	−23.69	−0.07	−7.13	−21.69	0.21	3.95	0.24	5.19*	−1.19
UPFA 22 × UPF 15	−0.45	−13.69	0.05	−2.95	−12.46	−0.23	0.09	0.15	3.66	−3.56
UPFA 22 × UFRGS 19	−0.10	−7.96	0.38	1.51	−10.28	−0.07	1.13	−0.17	−0.92	2.02
UPFA 22 × FAPA Louise	−0.01	0.84	−0.21	−7.86	8.62	0.12	4.56	0.05	2.56	1.92
UPFA 22 × IAC 7	0.64	2.06	−0.39	−15.82	17.51	0.22	4.51*	−0.18	−0.17	4.47
URS Guapa × UPF 15	0.25	−2.39	0.08	−6.93	4.66	0.00	1.66	0.14	3.39	−1.70
URS Guapa × UFRGS 19	−0.11	−9.63	−0.38	−16.16	7.23	−0.17	−0.74	−0.35	−3.06	2.34
URS Guapa × FAPA Louise	0.10	0.22	−0.86	−22.25	22.42	0.06	3.12	−0.02	1.72	1.35
URS Guapa × IAC7	−0.59	−16.93	0.62	−4.23	−15.28	0.00	1.49	0.27	4.23*	−2.70
UPF 15 × UFRGS 19	−0.33	−9.89	0.90	9.36	−21.36	0.17	3.52	0.15	1.71	1.75
UPF 15 × FAPA Louise	−0.18	0.51	−0.75	−20.47	20.88	0.05	3.80	−0.15	−0.06	3.72
UPF 15 × IAC 7	0.15	−3.24	−0.22	−15.41	12.57	0.18	3.98	−0.04	0.63	3.22
UFRGS 19 × FAPA Louise	0.41	9.67	−0.43	−15.79	23.22	0.09	3.58	−0.01	0.01	3.46
UFRGS 19 × IAC 7	−0.40	−12.39	−1.63	−37.63	28.80	0.08	2.43	−0.04	−0.74	3.09
FAPA Louise × IAC 7	−0.16	−3.14	−0.07	−12.56	9.73	0.18	4.86*	0.15	2.51	2.23
Mean (heterosis and Id)	−	−4.34	−	−10.04	5.25	−	3.42	−	2.54	0.84
Populations	F <sub>1</sub>		F <sub>2</sub>		Id	F <sub>1</sub>		F <sub>2</sub>		Id
	SCA	H <sub>1</sub>	SCA	H <sub>1</sub>		SCA	H <sub>1</sub>	SCA	H <sub>1</sub>	
Albasul × UPFA 22	0.26	11.43*	0.45	17.82*	−5.74	−0.01	−1.16	0.01	−3.10	1.94
Albasul × URS Guapa	0.16	9.22	0.30	15.06*	−5.34	−0.09	−4.63	−0.12	−6.84	2.32
Albasul × UPF 15	0.21	9.96*	0.12	11.32*	−1.24	0.10	2.18	−0.05	−5.76	7.76
Albasul × UFRGS 19	0.14	8.35	0.14	9.35*	−0.93	0.02	−0.7	0.03	−3.88	3.21
Albasul × FAPA Louise	0.21	11.43*	0.28	13.94*	−2.25	0.10	2.36	−0.04	−5.43*	7.63

**Table 4** continued

Populations	F <sub>1</sub>		F <sub>2</sub>		Id	F <sub>1</sub>		F <sub>2</sub>		Id
	SCA	H <sub>1</sub>	SCA	H <sub>1</sub>		SCA	H <sub>1</sub>	SCA	H <sub>1</sub>	
Albasul × IAC 7	−0.22	2.29	0.01	8.22*	−5.82	−0.01	−0.94	−0.04	−5.11	4.22
UPFA 22 × URS Guapa	0.38	12.44	0.24	11.35*	0.97	−0.17	−8.78	0.01	−3.99	−5.26
UPFA 22 × UPF 15	−0.11	3.96	0.23	10.73	−6.52	−0.13	−5.68	−0.09	−7.03	1.41
UPFA 22 × UFRGS 19	−0.16	2.59	−0.11	2.95	−0.36	0.10	−0.95	−0.06	−6.86	5.97
UPFA 22 × FAPA Louise	0.21	10.60*	0.15	9.13	1.32	−0.09	−4.84	−0.10	−7.59	2.88
UPFA 22 × IAC 7	0.14	8.17*	−0.11	4.09	3.77	0.07	−0.92	−0.07	−6.46	5.59
URS Guapa × UPF 15	0.03	5.74	0.10	8.49*	−2.61	−0.03	−4.5	0.03	−4.22	−0.29
URS Guapa × UFRGS 19	−0.01	4.74	−0.16	1.75	2.87	−0.17	−9.07	−0.19	−10.39	1.43
URS Guapa × FAPA Louise	0.01	6.81	0.03	6.95	−0.13	0.05	−2.57*	−0.04	−6.28*	3.79
URS Guapa × IAC7	0.01	5.41	0.28	10.52*	−4.85	−0.01	−4.22	−0.01	−5.17	1.00
UPF 15 × UFRGS 19	0.23	8.72*	0.29	9.14	−0.37	−0.06	−4.49	−0.14	−9.78*	5.52
UPF 15 × FAPA Louise	0.08	7.89*	−0.01	6.12*	1.63	−0.03	−2.64	−0.14	−9.62*	7.17
UPF 15 × IAC 7	0.19	8.45	0.03	6.01	2.25	−0.02	−2.69	−0.07	−7.39	4.83
UFRGS 19 × FAPA Louise	0.14	8.58	0.03	4.61	3.65	−0.05	−4.25	−0.03	−6.99*	2.86
UFRGS 19 × IAC 7	0.20	8.26*	0.09	4.93*	3.08	−0.13	−6.37	−0.13	−9.13*	2.93
FAPA Louise × IAC 7	0.29	11.37*	0.26	9.59*	1.58	−0.12	−5.15*	−0.10	−8.23	3.23
Mean (heterosis and Id)	−	7.92	−	8.67	−0.72	−	−3.33	−	−6.63	3.34

\* Significantly higher (positive values) or lower (negative values) regarding the parental mean by a *t* test, at 5% of probability

negative correlations with the heterosis estimates of all other characters. Meanwhile, positive associations were found between the heterosis estimates for grain protein content and total dietary, insoluble and soluble dietary fiber content; and between total dietary fiber and  $\beta$ -glucan, insoluble and soluble dietary fiber content.

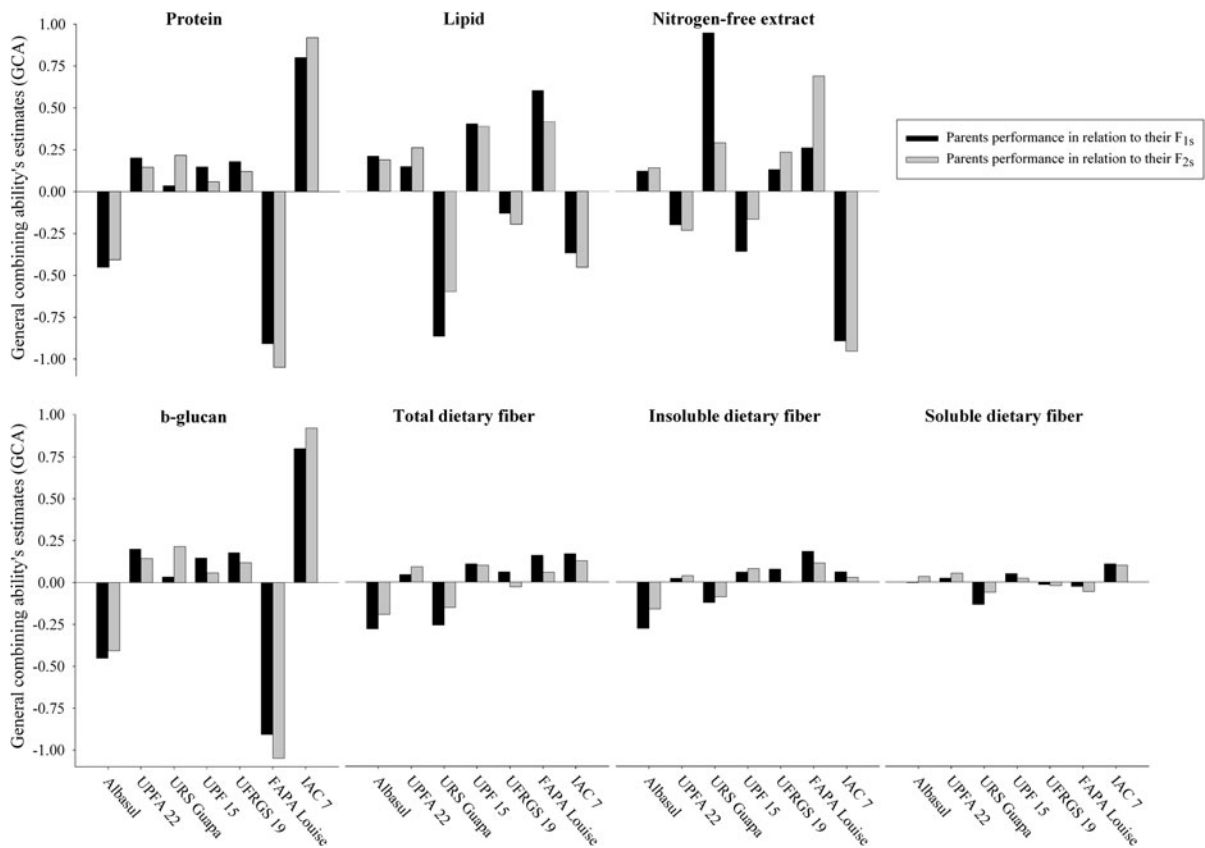
## Discussion

Selection of parents for chemical quality improvement of white oat grains based on F<sub>1</sub> and F<sub>2</sub> generations behavior

The variance analysis for F<sub>1</sub> and F<sub>2</sub> generations shows a higher phenotypic variability among the populations for the characters protein, nitrogen-free extract and  $\beta$ -glucan content in the grain when compared to the characters lipid, total dietary fiber, insoluble dietary fiber and soluble dietary fiber contents (Table 1). The absence of interactions between F<sub>1</sub> and F<sub>2</sub> generations for any character denote that the F<sub>1</sub> performance was similar to the F<sub>2</sub>, as has been reported for average seed lipid contents (Brown et al. 1973; Thro and Frey 1985).

The mean parental and respective F<sub>1</sub> and F<sub>2</sub> generations values suggest that the parents used in this evaluation tended to form populations with lower mean performance regarding protein and soluble dietary fiber content in the grain (Table 2; Fig. 1). However, the populations tended to have higher mean performance than the parents particularly for nitrogen-free extract and insoluble dietary fiber contents. Also, non-additive effects showed to be important in the grain nitrogen-free extract control, and may be contributing to its higher mean performances. Therefore, the effect presented by early generations (F<sub>1</sub> and F<sub>2</sub>), that are highly segregating, may decrease over the generations, culminating in the loss of vigor in homozygous lines.

The  $\beta$ -glucan content values obtained were comparable to those described by other reports, i.e., between 3.00 and 6.17 g 100 g<sup>−1</sup> (Aman and Graham 1987; Holthaus et al. 1996; Chernyshova et al. 2007). Characters such as  $\beta$ -glucan, lipid and protein content seem to be controlled by many genes, predominantly with additive effects (Brown et al. 1973; Karow and Forsberg 1984; Thro and Frey 1985; Holthaus et al. 1996; Cervantes-Martinez et al. 2001; Zhu et al. 2004; Chernyshova et al. 2007) and of partial dominance (Karow and Forsberg 1984; Zhou et al. 1999).



**Fig. 2** Representation of general combining ability (GCA) of seven white oat cultivars for traits related to grain chemical quality, according to Model 2 described by Griffing (1956),

considering the parents performance and their respective  $F_1$  and  $F_2$ , without reciprocal crosses

The  $S_{ii}$  parameter refers to SCA effects of a parent  $i$  based on its self-pollination, and it is fundamentally important to indicate the presence and the direction of dominance deviations for the character (Cruz and Vencovsky 1989). Thus, as a consequence of all parents showing positive SCA values for grain protein content only the crosses between UPFA 22  $\times$  IAC 7 and FAPA Louise  $\times$  IAC 7 revealed positive heterosis estimates in the  $F_1$  generation (Table 3). On the other hand, as most parents tested showed negative SCA for nitrogen-free extract, total and insoluble dietary fiber contents, many of the combinations showed positive heterosis for these characters, with superior performance regarding the parental mean values (Tables 3, 4).

The cultivar Albasul showed a negative SCA value in the  $F_1$  generation, associated to a positive GCA value and a superior performance for  $\beta$ -glucan

content, suggesting it is a source of favorable genes for increasing  $\beta$ -glucan (Tables 2, 4; Fig. 2). The IAC 7 promoted negative heterosis in their progenies for  $\beta$ -glucan, but the progenies presented performance close to or higher than the  $F_1$  and  $F_2$  general mean (Tables 2, 4). Thus, associated to its high mean performance and high positive GCA, IAC 7 represents an important donor of alleles with positive effects to increase of  $\beta$ -glucan in white oat grains (Table 2; Fig. 2). Meanwhile, the adoption of UPF 15 and FAPA Louise in artificial crosses can represent a strategy to increase the lipid content in the grains, since these cultivars presented high mean performance and high positive GCA, associated to the negative SCA in this trait (Tables 2, 3, 4). Also, the URS Guapa and FAPA Louise expressed high negative SCA and high positive GCA for nitrogen-free extract, which reflected on the formation of many progenies showing higher mean

**Table 5** Correlation (*r*) among heterosis estimatives (%) for the characters grain protein content (Prot), lipids (Lip), nitrogen-free extract (NFE),  $\beta$ -glucan ( $\beta$ -glu), total dietary fiber (TDF),insoluble dietary fiber (IDF) and soluble dietary fiber (SDF), assessed in 21 hybrids of white oats, in the F<sub>1</sub> generation (above diagonal) and F<sub>2</sub> generation (below diagonal)

Trait	Prot	Lip	NFE	$\beta$ -glu	TDF	IDF	SDF
Prot	–	0.17 <sup>ns</sup>	–0.77**	0.29 <sup>ns</sup>	0.51*	0.25 <sup>ns</sup>	0.58**
Lip	–0.34 <sup>ns</sup>	–	–0.37 <sup>ns</sup>	0.10 <sup>ns</sup>	0.11 <sup>ns</sup>	0.03 <sup>ns</sup>	0.11 <sup>ns</sup>
NFE	–0.71**	–0.22 <sup>ns</sup>	–	–0.37 <sup>ns</sup>	–0.67**	–0.47*	–0.52*
$\beta$ -glu	0.07 <sup>ns</sup>	–0.42 <sup>ns</sup>	–0.01 <sup>ns</sup>	–	0.64**	0.35 <sup>ns</sup>	0.63**
TDF	0.48*	0.04 <sup>ns</sup>	–0.60**	0.46*	–	0.84**	0.58**
IDF	0.44*	0.05 <sup>ns</sup>	–0.64**	0.44*	0.98**	–	0.04 <sup>ns</sup>
SDF	0.45*	0.03 <sup>ns</sup>	–0.30 <sup>ns</sup>	0.29 <sup>ns</sup>	0.73**	0.56**	–

<sup>ns</sup> Non significant, \*\* and \* Significant at 1 and 5% of probability, respectively, by the *F* test

performance, and may represent potential parents to be adopted in crosses in order to increase the content of this component in the grain (Tables 2, 3; Fig. 2).

#### Improvement of chemical quality components in white oat grains

In self-pollinating species, the largest hybrid heterosis is associated to the higher probability to recover transgressive individuals in their segregating populations, leading to superior lines after the process of generation advancing, coupled to artificial selection (Falconer and Mackay 1996). Thus, one may aim at combinations that provide high or low hybrid vigor, but have a higher number of superior performance phenotypic classes in F<sub>2</sub> to apply the artificial selection. The achievement of more expressive genetic gains in characters related to white oat grain chemical quality components by artificial selection will probably be most effective when carried out based on the individual plants that comprise the selection target population by adopting genetic improvement methods such as pedigree, recurrent selection and single seed descent (SSD) (Ramalho et al. 1993; Carvalho et al. 2008).

The occurrence of loss of vigor due to inbreeding is directly related to the increased frequency of recessive alleles in the genetic constitutions that make up the population after generation advancing (Falconer and Mackay 1996). However, at the same time, inbreeding allows one to obtain a higher frequency of phenotypic classes, increasing the expectations of efficiency in the selection process (Bertan et al. 2009). Differently than expected, in this evaluation the character nitrogen-free

extract showed a negative loss of vigor, despite the low magnitude, as a result of the F<sub>2</sub>'s mean performance has been slightly higher than the F<sub>1</sub>'s, considering the general performance of all 21 combinations assessed (Table 3). It is possible to suggest that the inbreeding depression between F<sub>1</sub> and F<sub>2</sub> general performance observed for protein content, lipids,  $\beta$ -glucan, total dietary fiber and soluble dietary fiber in the grain was a function of the highest content of nitrogen-free extract, expressing a kind of performance compensation among the different chemical components of the grain. The higher concentration of carbohydrate components in the white oat grain, represented by the content of nitrogen-free extract, tends to be negatively correlated with the contents of protein, lipid and fibers in the grain, suggesting that the higher energetic capacity due to nitrogen-free extract content is related to lower quality relative to other grain chemical components (Crestani et al. 2009).

Since no single crosses could provide the adequate performance of its progeny for the set of traits of interest, the implementation of triple or composite crosses may represent another strategy for the formation of superior white oat populations for chemical quality of grains.

#### Implications of F<sub>1</sub> and F<sub>2</sub> heterosis correlations to the improvement of oat grain chemical quality

The positive correlations between heterosis of protein and dietary fibers fractions suggest its concurrent increase possibility (Table 5). Whereas the negative correlations for nitrogen-free extract's heterosis with all other characters suggest a general tendency that the



higher the mass of caryopsis forming the white oat grain, represented mainly by the non-structural carbohydrates, the lower will be the protein, lipid, and the dietary fiber content, agreeing with results of Peterson et al. (2005).

#### New developments in characters related to white oat grain chemical quality

Despite the fact that studies of oat molecular genetics have lagged behind those of other cereal crops, such as wheat and barley, important information has been generated on the genetics of characters related to chemical composition of white oat grains. Genomic regions associated with genes effecting quantitative traits—QTLs have been described (Kianian et al. 1999, 2000; Zhu et al. 2004; Orr and Molnar 2007). Comparative mapping strategies in the triticeae can allow the transfer of markers used in the evaluation of chemical quality characters of cereal grains more studied, such as corn, wheat and barley, to evaluate and select *A. sativa* genotypes (Bennetzen and Freeling 1997). Also, innovative techniques such as TILLING (*Targeting Induced Local Lesion in Genomes*) have been tested in experimental white oat populations in order to harness the power of induced mutations to target and recover lesions in specific genes, such as lignin and  $\beta$ -glucan biosynthesis key genes, and seems to be effective in the creation of potential variability for selection of superior genotypes (Chawade et al. 2010).

#### Conclusions

Considering de SCA, the parents involved in the study show a general tendency to develop progenies with negative heterosis for protein, lipid,  $\beta$ -glucan and soluble dietary fiber content in the grain, and positive heterosis for nitrogen-free extract, total and insoluble dietary fiber.

Based on the GCA, the cultivar IAC 7 features a potential parent to be adopted in artificial crosses aiming to obtain genotypes with high protein and dietary fiber content in the grain, associated with low calory content, fit to the human diet. Meanwhile, aiming to increase the lipid content in the grain, improving grains to feeding animals, the cultivars UPF 15 and FAPA Louise can represent potential parents.

Moreover, together with FAPA Louise, the URS Guapa can represent promising donors of alleles with positive effects to increase the nitrogen-free extract in the grain.

**Acknowledgments** The authors are thankful to the Brazilian Council for Research and Development (CNPq), Higher Education Improvement Bureau (CAPES) and Rio Grande do Sul State Research Assistance Foundation (FAPERGS) for grants and fellowship support.

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