Genetics/ Original Article

Combining ability of forage maize S₃ progenies in topcrosses for traits of the vegetative part and whole plant

Abstract – The objective of this work was to evaluate the combining ability of S₃ forage maize (*Zea mays*) progenies for traits related to forage yield and bromatological quality, with and without the ear, as well as to evaluate the ability of testers to discriminate progenies for these traits. The trials were carried out in the 2017/2018 and 2018/2019 crop seasons, in the municipality of Guarapuava, in the state of Paraná, Brazil. Topcross hybrids obtained from the crosses of 28 S₃ maize progenies with three testers were evaluated. The following forage qualitative traits of the whole plant and of the plant without the ear were evaluated: neutral and acid detergent fibers, lignin, and in situ dry mass digestibility, as well as digestible dry mass yield of the whole plant. The progenies that stood out for forage qualitative traits were 85.1 and 42.1 for the whole plant and for the plant without the ear, respectively. For the qualitative and productive traits of whole-plant forage, progenies 91.1, 106.2, 126.2, 138.1, 152.1, 235.1, and 251.1 are promising to continue in the breeding program aiming to generate hybrids with a high yield and fiber quality. Testers LEM3 and AG8025 are efficient in discriminating progenies for forage yield and bromatological traits.

Index terms: *Zea mays*, acid detergent fiber, digestibility, neutral detergent fiber, partial diallel.

Capacidade de combinação de progênies S₃ de milho forrageiro em topcrosses para características da parte vegetativa e da planta inteira

Resumo – O objetivo deste trabalho foi avaliar a capacidade de combinação de progênies S₃ de milho (*Zea mays*) forrageiro em relação a características relacionadas com o rendimento e a qualidade bromatológica da forragem, com e sem a espiga, bem como avaliar a capacidade de testadores para a discriminação das progênies para estas características. Os ensaios foram realizados nas safras de 2017/2018 e 2018/2019, no município de Guarapuava, no estado do Paraná, Brasil. Foram avaliados os híbridos topcross obtidos dos cruzamentos de 28 progênies de milho S3 com três testadores. As seguintes características qualitativas da forragem da planta inteira e da planta sem a espiga foram avaliadas: fibras em detergente neutro e ácido, lignina e digestibilidade in situ da massa seca, além do rendimento da massa seca digerível de toda a planta. As progênies que se destacaram quanto às características qualitativas da forragem foram 85.1 e 42.1 para a planta inteira e para a planta sem a espiga, respectivamente. Para as características qualitativas e produtivas da forragem da planta inteira, as progênies 91.1, 106.2, 126.2, 138.1, 152.1, 235.1 e 251.1 são promissoras para continuar no programa de melhoramento com vistas à geração de híbridos com altos rendimento e qualidade de fibra. Os testadores LEM3 e AG8025 são eficientes na discriminação de progênies para as características produtivas e bromatológicas das forragens.

Termos para indexação: *Zea mays*, fibra em detergente ácido, digestibilidade, fibra em detergente neutro, dialelo parcial.

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Introduction

Maize (*Zea mays* L.) is present in the main farming chains and is the main crop used for silage production due to its easy cultivation, high and stable dry mass yield, suitable fermentation in the silo, high nutritional value, and high acceptance by ruminants (Mandic et al., 2018). To obtain maize silage with a high yield and quality, several factors are determining, such as forage fiber content, feed digestibility, and the used hybrid (Silva & Queiroz, 2002; Carvalho et al., 2019; Schils et al., 2020).

Forage fiber quality can be determined by the chemical analysis of cell-wall components, including neutral detergent fiber (indicating hemicellulose, cellulose, and lignin contents), acid detergent fiber (indicating cellulose and lignin contents), and lignin (Silva & Queiroz, 2002). Since digestibility measures the usable energy of the feed in the rumen, the greater it is, the greater energy absorption is, allowing of a better feed conversion ratio (Carvalho et al., 2019).

Traditionally, maize hybrids are chosen on the basis of dry mass production of the whole plant, including the ear, whose grains have a high energy content originated from starch (Nogoy et al., 2019), leading to an increase in total dry mass digestibility (Zhao et al., 2016). However, considering the fiber quality of the vegetative part of the plant (Ferreira et al., 2013), in addition to the high energy content of the grains (Nogoy et al., 2019), can lead to the selection of genotypes with better forage quality.

To guarantee ruminal health without limiting consumption and an efficient feed use, breeding programs need to develop hybrids with forage potential, i.e., with a high dry mass yield, energetic value, and fiber quality (Li et al., 2017; Stefańska et al., 2017). Obtaining inbred lines and evaluating their combining ability are essential for the development of hybrids, aiming at identifying the most promising ones, which, when crossed, can complement each other and be used to obtain new superior hybrids (Paterniani & Campos, 2005). The topcross method allows of evaluating a group of progenies in initial generations of inbreeding in crosses with one or more testers in common, after which the best hybrids must be evaluated in trials (Borém et al., 2017).

Therefore, information on the combining ability in topcross evaluations help in the selection of progenies that are promising for obtaining hybrids. In this case, the

additive and non-additive gene effects are an indicative of the possibility of selecting superior progenies and of obtaining hybrid combinations with desirable traits by exploring heterosis effects, respectively (Chinthiya et al., 2019; Kolisnyk et al., 2020).

The objective of this work was to evaluate the combining ability of S_3 forage maize progenies for traits related to forage yield and bromatological quality, with and without the ear, as well as to evaluate the ability of testers to discriminate progenies for these traits.

Materials and Methods

The trials were carried out in the municipality of Guarapuava, in the state of Paraná, Brazil (25º23'02"S, 51º29'43"W, at an altitude of 1,100 m), in the 2017/2018 and 2018/2019 crop seasons, considered as environments 1 and 2, respectively. The soil of the region is classified as a Latossolo Bruno aluminíco, according to the Brazilian soil classification system (Santos et al., 2018), corresponding to an Aluminic Oxisol. Soil chemical analysis showed: 5.8 pH ($CaCl_2$), 50.3 g dm^{-3} organic matter (wet combustion), 3.97 mg dm^{-3} P (Mehlich-1), 0.37 $cmol_c$ dm^{-3} K, cation exchange capacity of 15.64 $cmol_c$ dm^{-3}, and base saturation of 58%. According to Köppen-Geiger's classification, the climate is of the Cfb type, temperate, with no defined dry season, with the average temperature of the coldest month below 18°C and of the hottest month below 22°C, and annual precipitation from 1,800 to 2,000 mm. The average daily temperature during the maize crop cycle was 20.5–21.2°C, and the accumulated precipitation was 1,185.6 and 716.7 mm in the first and second crop seasons, respectively (Figure 1).

Topcross hybrids resulting from the crosses of 28 S_3 maize progenies with three testers were evaluated. The used testers were: LEM 2 and LEM 3, two elite inbred lines; and AG8025, a commercial hybrid. The obtained topcross hybrids were grouped according to each tester and evaluated together with two commercial hybrids (AG9025 and P30F53) used as checks, totaling 30 genotypes for each group. The genotypes were evaluated in a randomized complete block design, in independent and simultaneous trials, arranged in a contiguous area.

Sowing was carried out in a tillage system after the desiccation of the area with 4.0 L ha^{-1} glyphosate, with black oak (*Avena strigosa* Schreb.) as the previous crop. Each plot was formed by 5.0 m length rows,

spaced 0.5 m apart, with a stand equivalent to 72,000 plants per hectare. For base fertilization, 350 kg ha^{-1} N-P$_2$O$_5$-K$_2$O (08-30-20) were applied. Two cover fertilizations, each with 113 kg ha^{-1} N, were performed in stages V3–V4 and V6.

Forage was collected by cutting manually ten plants from each plot, at 20 cm from the soil, when the grains presented ¾ of the milk line, in the pasty to floury stage, considered the ensilage point. Two samples of five plants each were used to evaluate the traits of the whole plant and of the plant without the ear, respectively. For each sample, forage dry mass yield (DMY), expressed in kg ha^{-1}, was determined using forage green mass yield and dry mass percentage (Silva & Queiroz, 2002). Then, the forages of the whole plant and of the plant without the ear were subjected to bromatological analyses to obtain the contents of neutral detergent fiber (NDF), acid detergent fiber (ADF), and lignin (Van Soest et al., 1991).
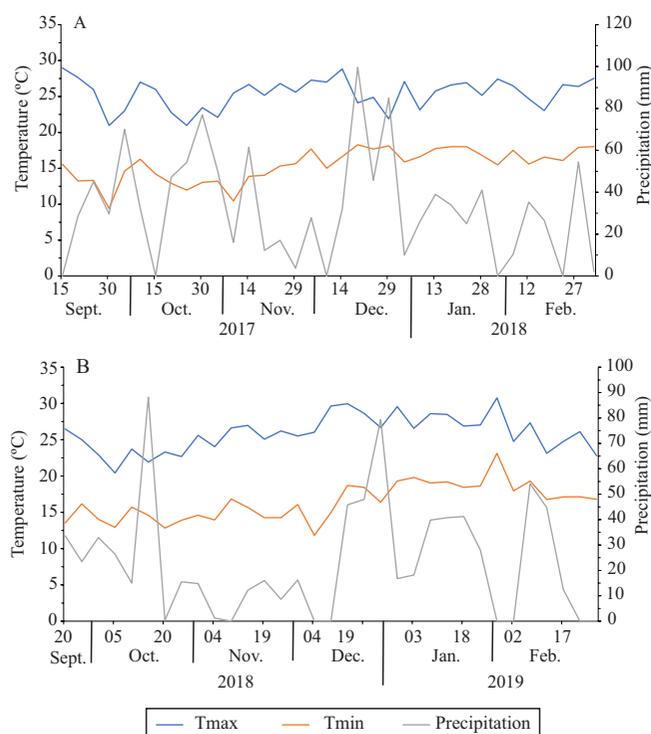
The ruminal digestibility of forage dry mass (DIG) was estimated using the in situ technique (Nocek, 1988), with an incubation time of 48 hours. For this, two 36-month-old calves of the Jersey breed, with an average live weight of 750 kg, were cannulated. The experimental procedures were approved by the Ethics Committee on Animal Use of Universidade Estadual do Centro Oeste, under number 021/2018. The digestible dry mass yield (DIGDMY) of the whole plant, expressed in kg ha^{-1}, was determined using whole-plant dry mass yield and digestibility.

Accepting the hypothesis that variances are homogeneous by Bartlett's test, analyses of variance were carried out for each topcross group individually in each environment, in which the topcross hybrids were evaluated with two additional checks, considering all the effects as random, except the mean, as suggested by Ramalho et al. (2005). When the ratio between the highest and lowest medium square of the residue among trials in the different environments was lower than seven, the joint analysis of each topcross was performed in each environment, considering the effects as random.

The components of genetic and phenotypic variance, broad-sense heritability, and coefficient of genetic variance were obtained on the basis of the joint analysis of variance, with randomized complete blocks, considering the effects as random. A joint diallel analysis was carried out according to method 4 of Griffing (1956), adapted for partial diallel, aiming to estimate the general combining ability (GCA) of parents and testers, as well as the specific combining ability (SCA) of the hybrid combinations obtained from crosses between progenies of group I and testers of group II, considering only F₁ (Cruz et al., 2012). All analyses were performed using the GENES software (Cruz, 2013). GCA and SCA estimates were represented graphically, and, to aid in selection, 1.5 time the standard deviation of the GCA and SCA of each trait was used as the cut-off line, as done by other authors (Figueiredo et al., 2018; Rosa et al., 2020; Silva et al., 2021).

Figure 1. Minimum (Tmin) and maximum (Tmax) temperatures, and precipitation in the 2017/2018 (A) and 2018/2019 (B) crop seasons, representing environments 1 and 2, respectively, in the municipality of Guarapuava, in the state of Paraná, Brazil. Source: Nitsche et al. (2019).

Results and Discussion

For whole-plant traits, genetic variance (σ²$_G$) estimates were close for NDF in the average of the environments, using testers LEM 3 and AG8025

Table 1. Estimates of the variance components and genetic parameters obtained by the joint analysis of variance of topcross (TC) hybrids from 28 S_3 maize (*Zea mays*) progenies crossed with three testers for traits of the whole plant and of the plant without the ear, evaluated in the municipality of Guarapuava, in the state of Paraná, Brazil, in the 2017/2018 (environment 1) and 2018/2019 (environment 2) crop seasons[1].

Genetic parameter	Average of the environments – NDF-WP					
	TC1	TC2	TC3			
σ^2_F	3.68	3.24	2.90			
σ^2_G	0.53	1.20	1.40			
h_a^2	0.14	0.37	0.48			
CVg	0.99	1.47	1.60			
	Environment 1			Environment 2		
	TC1	TC2	TC3	TC1	TC2	TC3
Genetic parameter	ADF-WP			ADF-WP		
σ^2_F	4.69	3.38	5.22	6.71	5.47	8.91
σ^2_G	2.51	0.67	2.60	1.84	1.68	5.93
h_a^2	0.53	0.20	0.50	0.27	0.31	0.67
CVg	5.56	2.73	5.42	4.62	4.33	8.87
Genetic parameter	LIG-WP			LIG-WP		
σ^2_F	1.36	5.42	2.80	1.01	2.06	1.15
σ^2_G	1.18	4.98	2.59	0.83	1.82	0.94
h_a^2	0.86	0.92	0.93	0.82	0.89	0.82
CVg	20.00	27.98	25.11	17.44	20.85	16.69
Genetic parameter	DIG-WP			DIG-WP		
σ^2_F	34.23	63.41	8.31	20.21	22.88	19.30
σ^2_G	26.65	56.77	1.49	9.77	14.93	2.99
h_a^2	0.78	0.90	0.18	0.48	0.65	0.15
CVg	10.25	15.36	2.33	5.86	6.36	2.93
Genetic parameter	NDF-WE			NDF-WE		
σ^2_F	8.28	3.47	2.89	5.37	7.07	5.93
σ^2_G	4.88	1.30	0.31	1.49	4.22	2.88
h_a^2	0.59	0.37	0.11	0.28	0.60	0.49
CVg	3.12	1.59	0.79	1.59	2.63	2.20
Genetic parameter	ADF-WE			ADF-WE		
σ^2_F	3.96	2.21	2.25	6.71	5.27	4.31
σ^2_G	2.41	0.97	0.62	2.44	2.84	2.12
h_a^2	0.61	0.44	0.28	0.36	0.54	0.49
CVg	3.64	2.28	1.84	3.48	3.69	3.19
Genetic parameter	LIG-WE			LIG-WE		
σ^2_F	0.93	0.79	0.84	0.97	0.84	0.50
σ^2_G	0.83	0.53	0.78	0.87	0.75	0.45
h_a^2	0.90	0.67	0.92	0.90	0.89	0.89
CVg	11.43	9.60	10.99	11.45	11.52	8.44
Genetic parameter	DIG-WE			DIG-WE		
σ^2_F	12.51	8.37	7.85	62.87	20.67	13.59
σ^2_G	7.92	2.64	1.30	53.41	14.86	4.45
h_a^2	0.63	0.32	0.17	0.85	0.72	0.33
CVg	6.19	3.73	2.62	16.13	8.67	4.30
Genetic parameter	DIGDMY-WP			DIGDMY-WP		
σ^2_F	4.31	3.09	2.71	5.89	5.44	5.02
σ^2_G	3.35	2.44	1.40	3.99	4.07	2.30
h_a^2	0.78	0.79	0.52	0.68	0.75	0.46
CVg	19.37	19.28	11.84	15.93	14.49	10.37

[1]σ^2_F, phenotypic variance; σ^2_G, genetic variance; h_a^2, broad-sense heritability; CVg, coefficient of genetic variance; NDF-WP and NDF-WE, neutral detergent fiber of the whole plant and of the plant without the ear, respectively; ADF-WP and ADF-WE, acid detergent fiber of the whole plant and of the plant without the ear, respectively; LIG-WP and LIG-WE, lignin of the whole plant and of the plant without the ear, respectively; DIG-WP and DIG-WE, in situ digestibility of the whole plant and of the plant without the ear, respectively; and DIGDMY-WP, digestible dry mass yield of the whole plant.

(Table 1). For ADF, testers LEM 2 and AG8025 stood out in environment 1, whereas, for lignin and DIG, AG8025 had a higher estimate in environment 2. Out of the testers, LEM 3 presented the highest coefficient of σ^2$_G$ (CVg) in both environments. As for DIGDMY, LEM 2 and LEM 3 showed σ^2$_G$ estimates close to those of the topcrosses evaluated in the first and second environments, which differed mainly from each other regarding precipitation volume (Figure 1).

For the traits of the plant without the ear, the estimates of σ^2$_G$ were higher for NDF in environments 1 and 2 using LEM 2 and LEM 3, respectively. For lignin, close values were found using LEM 2 and AG8025 in environment 1, as well as LEM 2 and LEM 3 in environment 2. For DIG, LEM 2 presented a superior estimate of σ^2$_G$ and CVg for the topcrosses evaluated in the two study environments. Therefore, LEM 2 showed a better ability to explore variability among progenies regarding qualitative traits.

The summary of the joint diallel analysis of variance showed the significant effect of the topcross hybrids x environments interaction for all traits, except for lignin of the plant without the ear. Moreover, unfolding confirmed the significant effect of the GCA of testers x environments interaction on all traits of the whole plant and on DIG of the plant without the ear. The GCA of parents x environments interaction was significant for lignin and DIG of the whole plant, as well as for ADF and DIG of the plant without the ear. There was also an isolated significant effect of the GCA of progenies for NDF, ADF, lignin, and DIGDMY of the whole plant and for NDF and lignin of the plant without the ear. However, the SCA x environments interaction was significant for ADF, lignin, DIG, and DIGDMY of the whole plant and for NDF, ADF, and DIG of the plant without the ear; there was also a significant isolated effect of SCA for lignin without the ear (Table 2).

For whole-plant forage, considering the sum of squares of the combining ability for qualitative traits, a balance between the additive and non-additive effects was observed. The low prevalence of non-addictive effects for ADF and the slight superiority of the addictive effects for lignin (Table 2) highlighted the importance of both types of effects. Silva et al. (2021) reported similar results, whereas Rosa et al. (2020) found a greater contribution of SCA to these traits.

For the traits of the vegetative part of the plant without the ear, greater addictive effects were observed

Table 2. Joint partial diallel analysis of the crosses between 28 S$_3$ maize (*Zea mays*) progenies and three testers for traits of the whole plant and of the plant without the ear, evaluated in the municipality of Guarapuava, in the state of Paraná, Brazil, in the 2017/2018 (environment 1) and 2018/2019 (environment 2) crop seasons[1].

Factor of variation	DF	Mean square								
		NDF-WP	ADF-WP	LIG-WP	DIG-WP	DIGDMY-WP	NDF-WE	ADF-WE	LIG-WE	DIG-WE
Topcross hybrid	83	38.3	20.1	13.9**	65.1	17.7**	20.6*	12.9	4.9**	56.8
GCA of testers	2	45.8	76.4	152.4	601.7	84.4	58.9	18.9	10.5	283.8
GCA of progenies	27	54.5**	23.0*	12.2**	57.6	22.4**	29.3**	17.9	6.0**	46.7
SCA	54	30.0	16.6	9.6**	49.0	12.8	14.8	10.2	4.0**	53.4
Environment (E)	1	134.1*	26.7	73.4**	5,433.3**	2,531.2**	4,731.9**	755.6**	0.7	483.0**
Topcross hybrids x E	83	35.8**	18.0**	3.7**	61.4**	10.5**	13.2*	11.7**	0.5	70.5**
GCA of testers x E	2	496.1**	110.8**	18.9**	599.4**	69.7**	7.0	1.8	1.9	392.9**
GCA of progenies x E	27	17.6	10.7	2.8**	35.6*	5.9	11.1	10.7*	0.5	59.2**
SCA x E	54	27.8	18.1**	3.6**	54.4**	10.7**	14.5*	12.5**	0.4	64.2**
Residue	332	21.6	9.5	0.8	23.1	4.0	9.7	7.0	0.8	17.2
SSGCA of testers (%)		2.9	9.2	26.4	22.3	11.5	6.9	3.5	5.2	12.0
SSGCA of progenies (%)		46.2	37.2	28.5	28.8	41.2	46.4	45.1	40.5	26.8
SSGCA (%)		49.1	46.4	55.0	51.0	52.7	53.3	48.6	45.7	38.8
SSSCA (%)		50.9	53.6	45.0	49.0	47.3	46.7	51.4	54.3	61.2

[1]DF, degrees of freedom; GCA, general combining ability; SCA, specific combining ability; SSGCA, sum of squares of GCA; SSSCA, sum of squares of SCA; NDF-WP and NDF-WE, neutral detergent fiber of the whole plant and of the plant without the ear, respectively; ADF-WP and ADF-WE, acid detergent fiber of the whole plant and of the plant without the ear, respectively; LIG-WP and LIG-WE, lignin of the whole plant and of the plant without the ear, respectively; DIG-WP and DIG-WE, in situ digestibility of the whole plant and of the plant without the ear, respectively; and DIGDMY-WP, digestible dry mass yield of the whole plant. ** and *Significant by the F-test, at 1 and 5% probability, respectively.

for NDF. For ADF, lignin, and DIG, however, there was no significant difference regarding the SCA for DM, pointing out the contribution of non-additive effect genes, which were more pronounced for DIG (Table 2). According to Chinthiya et al. (2019) and Kolisnyk et al. (2020), this result is an indicative of a possible success in obtaining hybrid combinations aiming to improve qualitative traits.

The sum of squares of the GCA of progenies, compared with that of testers, was responsible for most of the observed variation due to the addictive effect genes for all traits, being more marked for NDF and ADF of the whole plant and for NDF, ADF, lignin, and DIG of the plant without the ear (Table 2). This means that it is possible to select promising progenies with a good fiber quality using the vegetative part of the whole plant, i.e., that the qualitative value of the forage is not defined only by grain inclusion.

Negative estimates of GCA and SCA are desirable for traits related to fiber content and for NDF, ADF, and lignin of the whole plant and of the plant without the ear, aiming to reduce mean fiber contents, which are less digestible by ruminants. This improves forage quality since NDF content is related to the DM passage rate through the digestive tract (Zhao et al., 2016; Movahedi et al., 2017). Contrastingly, high ADF contents reduce animal DM consumption, leading to a low production performance (Li et al., 2017). Movahedi et al. (2017) concluded that, the lower the contents of ADF and lignin, the greater the energetic value of the forage, which is associated with the content of non-digestible fibers.

For the traits related to an efficient feed use and for DIG of the whole plant and of the plant without the ear, high positive values are desirable to identify progenies that can contribute to increase the content of digestible DM in the animal rumen. According to Carvalho et al. (2019), superior contents of DM digestibility indicate a better use of the consumed feed. Similarly, for digestible DM yield and whole-plant DIGDMY, positive GCA and SCA estimates are desirable for a higher forage yield and quality.

The GCA of testers showed their differentiated behavior in the evaluated environments. For whole-plant traits, the testers that stood out were: LEM 2 and AG8025, in environments 1 and 2, respectively, for NDF and ADF (Figure 2 A and B); LEM 2, in both environments, for lignin (Figure 2 C); LEM 3

and AG8025, in environment 2, for DIG (Figure 2 D); and AG8025, in both environments, for DIGDMY (Figure 2 E). For the plant without the ear, LEM 2 and AG8025 were highlighted in environments 1 and 2, with positive estimates for DIG (Figure 2 F). These results are an indicative of the possible favorable contribution of the additive effect genes present in the testers to the qualitative traits of the fiber, expressed in the topcross hybrids. According to Li et al. (2017) and Carvalho et al. (2019), NDF and DIG, which determine animal consumption and the most efficient use of the consumed feed, respectively, are important traits to obtain promising genotypes for forage quality.

However, the fact that a tester stands out for a trait due to its combining ability does not necessarily mean it can be used to explore σ^2_G among progenies. AG8025, for example, provided the highest σ^2_G estimates for NDF and ADF of the whole plant but not for DIG of the whole plant and the plant without the ear. In the literature, testers with the best combining-ability estimates for the evaluated traits were not always the ones that provided the highest σ^2_G in crossings with progenies; however, these same testers tended to contribute more to obtain topcross hybrids with a better SCA performance (Figueiredo et al., 2018; Rosa et al., 2020, 2021; Silva et al., 2021).

For progeny selection, the GCA of progenies should be taken into account and the SCA of the originated topcross hybrids should be evaluated. The topcross hybrids located in the lower left quadrant are desirable for: NDF of the whole plant in the average of the environments (Figure 3 A); ADF and lignin of the whole plant in both environments (Figure 3 B, C, D, and E); NDF and ADF of the plant without the ear in both environments (Figure 4 A, B, C, and D); and lignin of the plant without the ear in average of the environments (Figure 4 E). In addition, the topcross hybrids located in the upper right quadrant are desirable for DIG and DIGDMY of the whole plant and DIG of the plant without the ear in both environments (Figure 3 F and G, Figure 4 F and G, and Figure 5 A and B).

For NDF and ADF of the whole plant, topcrosses 42.1xT2 and 85.1xT3 were allocated in the left lower quadrant and stood out in environment 2, respectively (Figure 3 A and C). For whole-plant lignin, seven topcross hybrids (2.1xT1, 138.1xT2, 152.1xT2, 185.1xT2, 251.1xT2, 137x1xT3, and 185.1xT3) were

classified in the left lower quadrant in environment 1, indicating negative GCA and SCA estimates, which are desirable, whereas eight topcrosses (2.1xT1, 90.4xT1, 42.1xT2, 106.2xT2, 111.2xT2, 137.1xT2, 251.1xT2, and 137.1xT3) were highlighted in environment 2. When considering the two environments simultaneously, topcrosses 2.1xT1, 251.1xT2, and 137.1xT3 stood out (Figure 3 D and E).

For whole-plant DIG, topcrosses 85.1xT1, 193.1xT1, 251.1xT1, and 138.1xT2 showed better results in environment 1, with high positive SCA estimates (Figure 3 F), and 138.1xT1 and 111.2xT2, in environment 2. In this case, progeny 138.1 stood out, originating topcrosses with good SCA estimates when using two different testers, showing stability in the expression of combining-ability estimates (Figure 3 F and G).
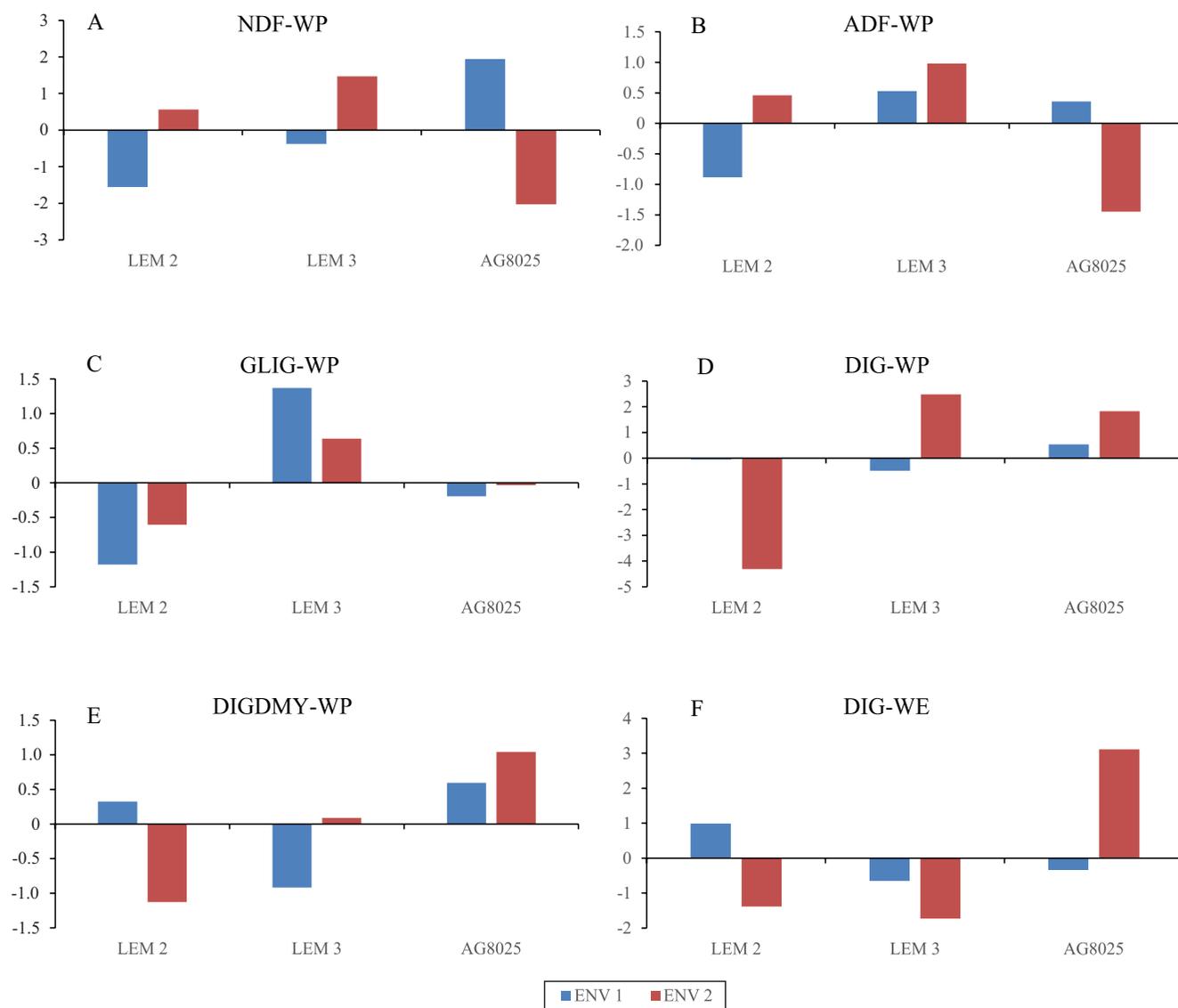
Figure 2. Estimates of the effects of the general combining ability of testers for the following traits of maize (*Zea mays*): neutral detergent fiber (NDF-WP) (A), acid detergent fiber (ADF-WP) (B), lignin (LIG-WP) (C), digestibility (DIG-WP) (D), and digestible dry mass yield (DIGDMY-WP) (E) of the whole plant; and digestibility of the plant without the ear (DIG-WE) (F). The evaluations were carried out in the municipality of Guarapuava, in the state of Paraná, Brazil, in the 2017/2018 and 2018/2019 crop seasons, representing environments 1 (ENV1) and 2 (ENV2), respectively.
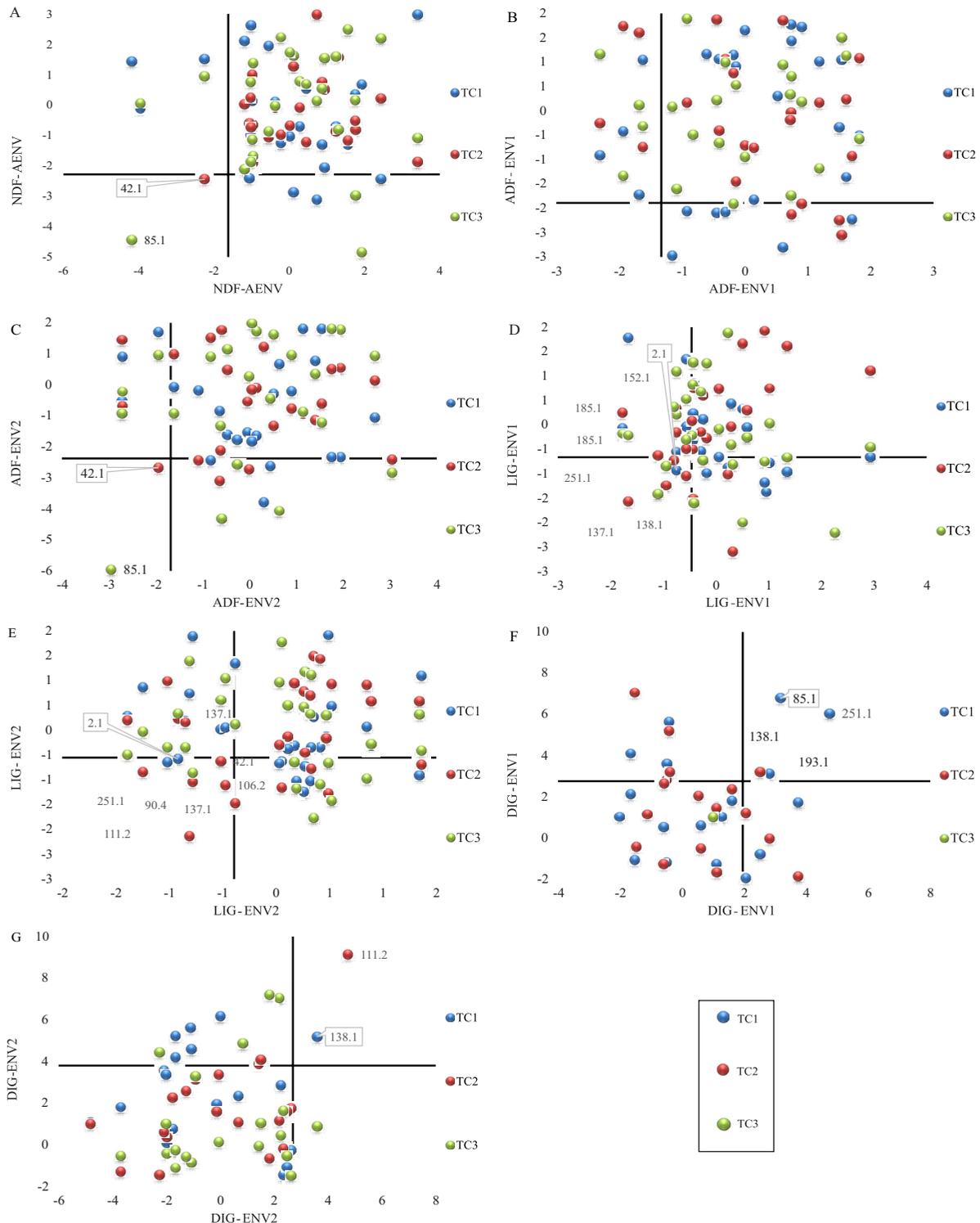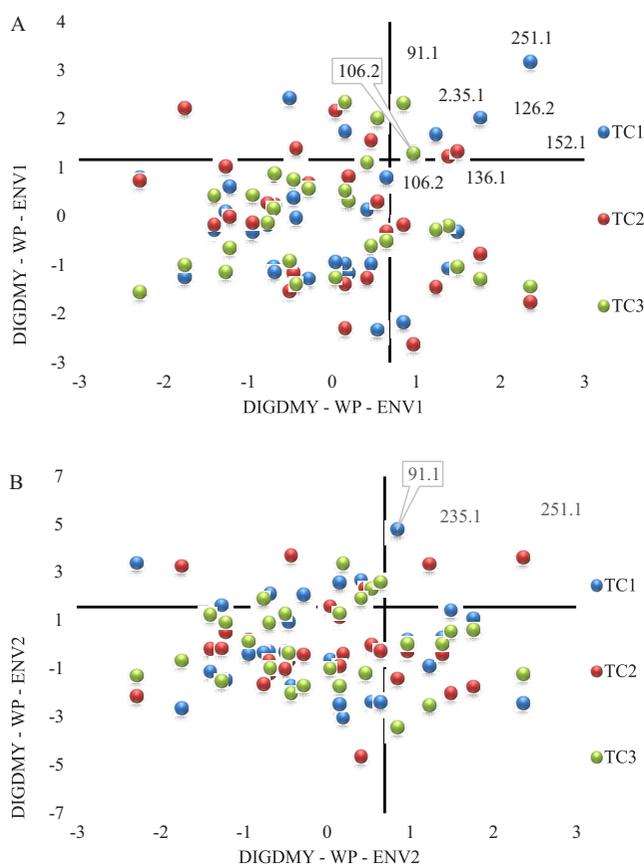
Figure 3. Dispersion of the estimates of the general combining ability (GCA) of progenies and of the specific combining ability (SCA) of topcross (TC) hybrids of crosses between 28 S₃ maize (*Zea mays*) progenies and three testers for the following whole-plant traits: neutral detergent fiber (NDF) in the average of environments (A), acid detergent fiber (ADF) in environments 1 (B) and 2 (C), lignin (LIG) in environments 1 (D) and 2 (E), and digestibility (DIG) in environments 1 (F) and 2 (G), evaluated in the municipality of Guarapuava, in the state of Paraná, Brazil, in the 2017/2018 and 2018/2019 crop seasons, representing environments 1 (ENV1) and 2 (ENV2), respectively. The vertical and horizontal axes pass through the values 1.5 time the standard deviation of the SCA of testers and GCA of progenies, respectively.
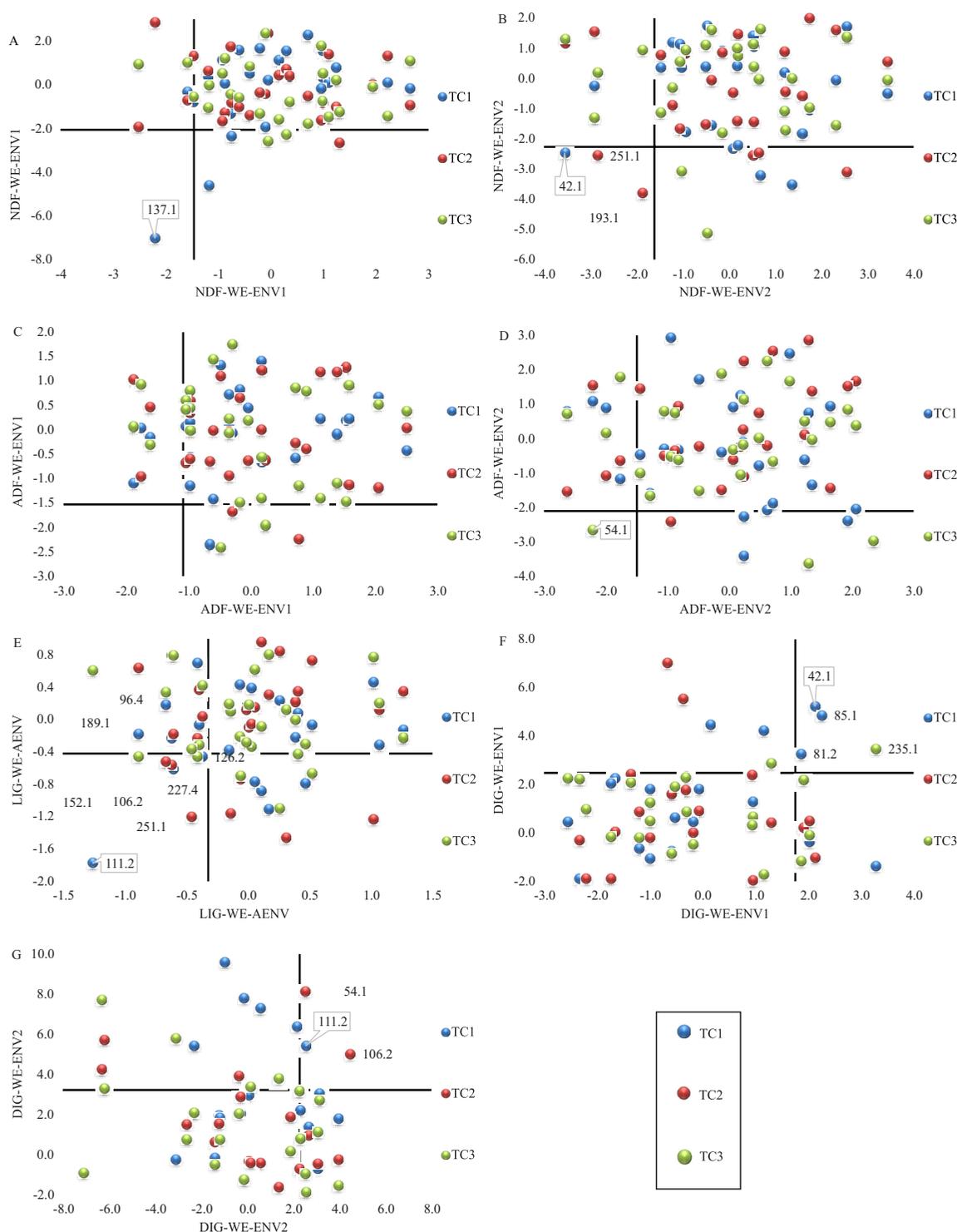
Figure 4. Dispersion of the estimates of the general combining ability (GCA) of progenies and of the specific combining ability (SCA) of topcrosses (TC) of maize (*Zea mays*) for the following traits of the plant without the ear: neutral detergent fiber (NDF) in environments 1 (A) and 2 (B), acid detergent fiber (ADF) in environments 1 (C) and 2 (D), lignin (LIG) in the average of the environments (E), and digestibility (DIG) in environments 1 (F) and 2 (G), evaluated in the municipality of Guarapuava, in the state of Paraná, Brazil, in the 2017/2018 and 2018/2019 crop seasons, representing environments 1 (ENV1) and 2 (ENV2), respectively. The vertical and horizontal axes pass through values 1.5 time the standard deviation of the SCA and GCA, respectively. AENV, average of the environments.

Another progeny that stood out was 85.1, since, when combined with at least one of the testers, it presented desirable estimates for the SCA of testers and the GCA of progenies for whole-plant NDF, ADF, and lignin (Figure 3 A, C, and E). This result is an indicative of the possible contribution of this hybrid to obtaining genotypes with desirable fiber contents, without limiting animal consumption and with an efficient nutrient use (Zhao et al., 2016; Movahedi et al., 2017; Daniel et al., 2019).

For whole-plant traits, phenotypic means were favorable for the topcrosses between progeny 85.1

Figure 5. Dispersion of the estimates of the general combining ability (GCA) of progenies and of the specific combining ability (SCA) of topcross (TC) hybrids of maize (*Zea mays*) for digestible dry mass yield of the whole plant (DIGDMY), evaluated in the municipality of Guarapuava, in the state of Paraná, Brazil, in the 2017/2018 and 2018/2019 crop seasons, representing environments 1 (ENV1) (A) and 2 (ENV2) (B), respectively. The vertical and horizontal axes pass through the values 1.5 time the standard deviation of the SCA and GCA, respectively.

and testers AG8025 (45.83% for NDF and 18.5% for ADF) and LEM 2 (61.96% for DIG). Compared with the means of the checks, those of NDF and ADF were inferior and of DIG were superior (Table 3). Neumann et al. (2020) found lower NDF and ADF means when evaluating commercial hybrids in the municipality of Guarapuava, whereas Paziani et al. (2019) reported higher DIG means studying maize hybrids.

Progenies 111.2, 138.1, and 251.1 generated topcross hybrids with favorable SCA estimates (Figure 3 D, E, and F) and good phenotypic values for lignin (3.53, 6.37, and 4.74%) and DIG (74.98, 63.10, and 62.80%) of the whole plant (Table 3). This allows of obtaining genotypes with an efficient nutrient use, but does not guarantee NDF content, which could limit animal consumption (Movahedi et al., 2017; Carvalho et al., 2019).

Considering the dispersions of the estimates of the SCA of hybrids and the GCA of progenies, the topcross hybrids that stood out for whole-plant NDF were: 137.1xT1 in environment 1; and 42.1xT1, 193.1xT2, and 251.1xT2 in environment 2 (Figure 5 A and B). However, for ADF of the plant without the ear, it was not possible to select topcross hybrids with desirable estimates using the established cutoff line in environment 1, whereas the 54.1xT3 topcross hybrid stood out in environment 2 (Figure 4 C and D).

For lignin of the plant without the ear, in the average of the environments, eight topcross hybrids (111.2xT1, 126.2xT1, 227.4xT1, 106.2xT2, 152.1xT2, 251.1xT2, 96.4xT3, and 189.1xT3) were placed in the left lower quadrant, which indicates that the parent progenies presented negative estimates of the GCA of progenies and SCA of testers (Figure 4 E). For DIG of the plant without the ear, the topcross hybrids that stood out were 42.1xT1, 81.2xT1, 85.1xT1, and 235.1xT3 in environment 1, as well as 111.2xT1, 54.1xT2, and 106.2xT2 in environment 2 (Figure 4 F and G).

When analyzing simultaneously the traits of the plant without the ear, it was not possible to identify topcross hybrids that stood out for all of them. However, progeny 42.1 showed desirable estimates for the GCA of progenies and originated topcross hybrids that stood out for NDF and DIG, which are important traits that allow of evaluating animal consumption and feed use, respectively (Li et al., 2017; Carvalho et al., 2019). Carvalho et al. (2019) added that genotypes with

desirable fiber contents in the vegetative part of the plant can contribute to improve the quality of the whole plant.

Still regarding the traits of plants without the ear, the favorable results of the combining ability of progeny 42.1 reflected in the phenotype of topcross hybrid 42.1xT1, which presented the lowest mean of 70.41% for NDF and the highest of 52.13% for DIG, surpassing the means of the checks (Table 3). These values are considered good if compared with those of 65–71% for NDF and 41–58% for DIG found by Ferreira et al. (2013) when evaluating maize hybrids without the ear.

For whole-plant DIGDMY, the following topcrosses stood out: 106.2xT1, 126.2xT1, 235.1xT1, 251.1xT1, 138.1xT2, 152.1xT2, 91.1xT3, and 106.2xT3 in environment 1; and 91.1xT1, 235.1xT2, and 251.1xT2 in environment 2. All of them were allocated in the right upper quadrant, and only 106.2xT1, 138.1xT2, and 91.1xT3 did not present favorable estimates for the traits of the plant without the ear, showing the importance of the vegetative part of the plant for obtaining genotypes with a high yield and fiber quality.

Considering all evaluated traits, progenies 91.1, 106.2, 126.2, 138.1, 152.1, 235.1, and 251.1 were

Table 3. Phenotypic means of maize (*Zea mays*) topcross hybrids for traits of the whole plant and of the plant without the ear, evaluated in the municipality of Guarapuava, in the state of Paraná, Brazil, in the 2017/2018 and 2018/2019 crop seasons, representing environments 1 (ENV1) and 2 (ENV2), respectively[1].

Topcross hybrid	NDF-WP (%)	ADF-WP (%)		LIG-WP (%)		DIG-WP (%)		DIGDMY-WP (Mg ha^{-1})	
	Joint analysis	ENV1	ENV2	ENV1	ENV2	ENV1	ENV2	ENV1	ENV2
42.1xT1	53.25	29.25	29.12	5.00	4.74	57.21	56.87	8,690	13,490
85.1xT1	51.26	26.12	30.08	5.10	5.10	61.96	50.78	11,650	10,620
85.1xT3	45.83	26.45	31.17	5.74	7.25	53.63	55.65	10,610	11,640
91.1xT3	56.47	31.16	18.55	6.80	5.34	53.56	60.55	13,030	17,780
106.2xT1	53.55	29.30	28.09	4.82	4.82	54.44	56.13	11,920	14,090
106.2xT3	55.52	27.20	28.98	6.38	6.38	52.69	56.78	12,180	16,090
111.2xT2	51.15	27.32	26.49	6.82	6.53	56.36	54.98	9,700	17,100
126.2xT1	50.52	25.08	27.90	5.82	5.82	51.83	55.20	12,980	16,220
138.1xT2	72.75	25.60	33.90	6.37	4.62	57.29	58.65	10,830	15,330
152.1xT2	75.93	29.26	29.25	6.45	6.45	53.89	62.87	10,680	14,150
235.1xT1	51.24	24.34	27.59	4.60	4.60	57.48	55.72	12,950	12,890
251.1xT1	52.98	26.09	31.81	5.54	4.86	62.80	51.05	15,570	12,440
AG9025	47.34	24.57	25.18	4.66	3.93	55.72	61.17	9,530	14,950
P30F53	51.04	27.49	27.49	5.00	5.00	61.57	61.57	10,360	17,470
Topcross hybrid	NDF-WE (%)		ADF-WE (%)		LIG-WE (%)	DIG-WE (%)			
	ENV1	ENV2	ENV1	ENV2	Joint analysis	ENV1	ENV2		
42.1xT1	69.16	70.54	40.53	41.95	8.50	52.13	29.14		
85.1xT1	71.99	77.34	43.31	46.12	7.59	51.88	47.39		
85.1xT3	69.65	75.09	41.30	43.61	7.27	42.94	46.28		
91.1xT3	72.59	81.02	44.64	49.18	8.41	43.15	50.92		
106.2xT1	71.91	76.47	42.18	43.77	7.20	49.37	46.75		
106.2xT3	70.69	77.64	42.58	43.76	8.15	41.53	50.39		
111.2xT2	73.81	79.80	45.95	47.61	7.49	39.87	42.99		
126.2xT1	67.61	74.01	39.66	39.66	7.21	47.02	52.89		
138.1xT2	71.75	81.05	43.60	49.80	8.34	44.20	43.22		
152.1xT2	70.16	81.86	41.69	46.88	6.39	44.16	43.30		
235.1xT1	68.80	80.84	40.93	48.32	9.53	46.70	48.42		
251.1xT1	71.70	76.10	43.03	43.06	9.16	43.00	46.74		
AG9025	70.63	75.13	41.16	43.73	6.72	48.61	47.91		
P30F53	71.53	75.03	43.78	45.00	7.72	46.31	48.57		

[1]NDF-WP and NDF-WE, neutral detergent fiber of the whole plant and of the plant without the ear, respectively; ADF-WP and ADF-WE, acid detergent fiber of the whole plant and of the plant without the ear, respectively; LIG-WP and LIG-WE, lignin of the whole plant and of the plant without the ear, respectively; DIG-WP and DIG-WE, in situ digestibility of the whole plant and of the plant without the ear, respectively; and DIGDMY-WP, digestible dry mass yield of the whole plant.

selected because they allowed of obtaining topcross hybrids with favorable SCA estimates for whole-plant DIGDMY (Figure 5 A and B) and presented desirable estimates and phenotypic values for forage qualitative traits of the whole plant and the vegetative part of the plant (Table 3). Therefore, these progenies can originate hybrids with a high DM yield and an efficient feed use. In addition, progeny 251.1 stood out for NDF of the plant without the ear (Figure 4 B), which can increase fiber contents without limiting consumption.

Conclusions

1. The maize (*Zea mays*) progenies that stand out for forage quality are 85.1 for the whole plant and 42.1 for the vegetative part of the plant (without the ear), being promising to obtain genotypes with an efficient feed use and that do not limit feed consumption.

2. For the whole plant, progenies 91.1, 106.2, 126.2, 138.1, 152.1, 235.1, and 251.1 are promising to continue in the breeding program aiming at the generation of hybrids with a high yield and fiber quality.

3. Although testers LEM3 and AG8025 are efficient in discriminating progenies for forage yield and bromatological traits, it is not possible to identify only one tester that is adequate for all traits.

Acknowledgments

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