# Report on evaluating *Brachiaria humidicola* population Bh16B hybrid performance

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#### Summary

The population Bh16b was formed from the remnant seed of the best crosses identified from Bh16 population. As the intra-family variance in that trial was higher than the inter-family variance, and considering the constrains to develop a new Bh hybrid population, the breeder decided to take advantage of intra-family variance and explore those hybrids stored in the seed storage room. Conformed by 1046 hybrids, Bh16b was phenotyped on the field in order to measure the hybrid performance for the following traits: Visual assessment of biomass production, vigor, high, visual assessment of leaf steam ratio and drone based measurements like biomass and greenness. The trials were stablished at two locations: CIAT Palmira and Llanos-Cabuyaro. Each trial followed an augmented design with 25 incomplete blocks. Data was obtained for various cuttings in each location, each cutting after 6 weeks from previous one, to pursue two cuttings from the dry and two from the wet season.

#### **General Objective**

Identify apomictic hybrids of *B. humidicola* that outperform the commercial benchmark in at least one of the traits of environmental and economic importance, without reducing the performance in any other important trait. Being nutritional quality one of the most important, but considering also biomass production, biotic and abiotic stress resistances.

### Specific Objective in 2019

After molecular marker identification for apomixis in the population and field trials establishment in 2018, the main goal for 2019 was to complete data capture, analyze, and select the most promising hybrids for the next phenotyping phase (Observation 2).

### Metodology and results

Currently, data for three cuttings has been obtained in each of both locations (Cabuyaro in Easterns plains and Palmira - CIAT Headquarters, both in Colombia). Table 1 describes dates from each

cutting and precipitation in millimeters for the period of time corresponding to each cutting. Table 2 express the dates and measurements taken in each evaluation per location. Table 3 shows the entry mean heritability values per cutting and per location, which reflects the quality of the data obtained. Variance components for the whole dataset combined were calculated (Table 4) and reflected that the factor which explains the highest proportion of the variance is the genotypic variance, followed by effect of the cutting and the experimental error.

**Table1**: Dates for each cutting and corresponding date for evaluation and precipitation in the periodbetween cutting and evaluation.

	1		2		3		4	
Localidad	FechaSiembra	Evaluacion1	Fecha Corte	Evaluacion2	Fecha Corte	Evaluacion3	Fecha Corte	Evaluacion4
Palmira	1-Aug-18	1-Nov-18	27-Feb-19	5-Apr-19	8-Apr-19	1-Jun-19	26-Aug-19	21-Oct-19
Precipitacion palmira	205 mm		67.9 mm		214 mm		?	
Llanos (Cabuyaro)	8-Aug-18	13-Nov-18	23-Nov-18	15-Feb-19	20-Feb-19	15-Apr-19	26-Apr-19	16-Jun-19
Precipitacion Cabuyar	n 364 mm		0 mm		34 mm		700 mm	

# Table2: Traits evaluated for each cutting

Dates and meassurements taken by cutting								
		Palm	ira	Cabuyaro				
	Evaluacion1	Evaluacion2	Evaluacion3	Evaluacion4	Evaluacion1	Evaluacion2	Evaluacion3	
	1-Nov-18	5-Apr-19	1-Jun-19	21-Oct-19	13-Nov-18	15-Feb-19	15-Apr-19	
Visual Biomass	x	x	Full flowering	x	x	x	x	
Visual Leaf/stem ratio	x				x	x	x	
High	x	x		x	x	x	x	
Drone Biomass	х	х		x	х	x	x	
Vigor		х			x	x	x	
Inflorescence	х				х	х	х	

**Table 3**: Entry-mean heritability, also called, repeatability for biomass trait in each location and each cutting.

Heritability for each cutting								
		Palm	ira	Cabuyaro				
	Evaluacion1	Evaluacion2	Evaluacion3	Evaluacion4	Evaluacion1	Evaluacion2	Evaluacion3	
	1-Nov-18	5-Apr-19	1-Jun-19	21-Oct-19	13-Nov-18	15-Feb-19	15-Apr-19	
Visual Biomass	0.54	0.42	х	0.49	0.7	0.44	0.4	
High	0.66	0.59	х	0	0.7	0.58	0.45	
Drone Biomass	0.47	0.17	х	X?X	0.7	0.62	0.6	

 Table 4: Variance components.

<pre>&gt; summary(m2)\$varcomp</pre>					
	gamma	component	std.error	z.ratio	constraint
Localidad!Localidad.var	0.24119829	0.14663291	0.509872292	0.2875875	Positive
Localidad:Corte_Eval!Localidad.var	0.98438967	0.59844504	0.423761406	1.4122217	Positive
Bloque!Bloque.var	0.03304961	0.02009202	0.007104788	2.8279543	Positive
Madre!Madre.var	0.16568472	0.10072556	0.035717031	2.8200988	Positive
Genotipo:Madre!Genotipo.var	1.15829420	0.70416771	0.037651798	18.7021004	Positive
Localidad:Corte_Eval:Genotipo:Madre!Localidad.var	0.31130298	0.18925201	0.024947191	7.5861048	Positive
R!variance	1.00000000	0.60793510	0.024216847	25.1038088	Positive

BLUPs for each cutting and each trait were calculated. Selection of the best genotypes was done based on an index selection.

## Next steps:

For a number of 132 selected genotypes additional measurements will be taken. On the current field plots, samples for quality assessments will be collected and analyzed during 2020. This selected population already started phenotyping for spittlebug resistance identification. Ideally, also multi-environment trials and drought tolerance data will be collected, in order to refine and cull down the selection of the best candidates for commercial release.