



Data analysis BCEAR 2 environments

202224BCEAR_cere 202225BCEAR_saha

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@BiovIntCIAT_eng
@BiovIntCIAT_esp

#Alliance4Science

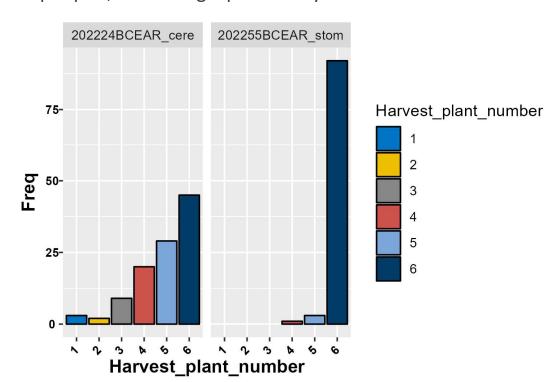
The Alliance of Bioversity International and the International Center for Tropical Agriculture (CIAT) is part of CGIAR, a global research partnership for a food-secure future

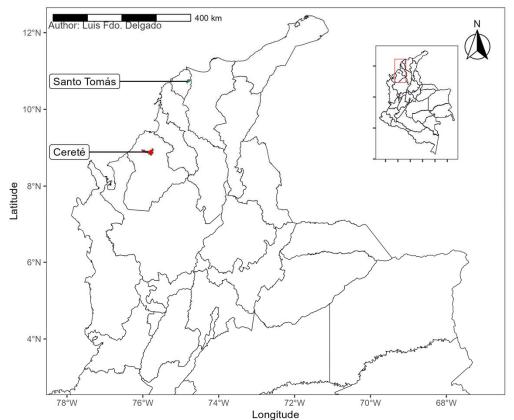
Resolvable row-col with randomized checks

use_trial_name	use_plant_date	use_harvest_date	harvesting_time	use_location	n_gen
202224BCEAR_cere	2022-June-03	2023-April-10	10month 7day	Cerete. Cordoba, Colombia	33
202255BCEAR_stom	2022-August-05	2023-April-10	8month 5day	Santo Tomas. Atlantico, Colombia	29

Plot size:

- 202224BCEAR_cere: 20 plants per plot, harvesting 6 plants for yield
- 202255BCEAR_stom: **20** plants per plot, harvesting **6** plants for yield

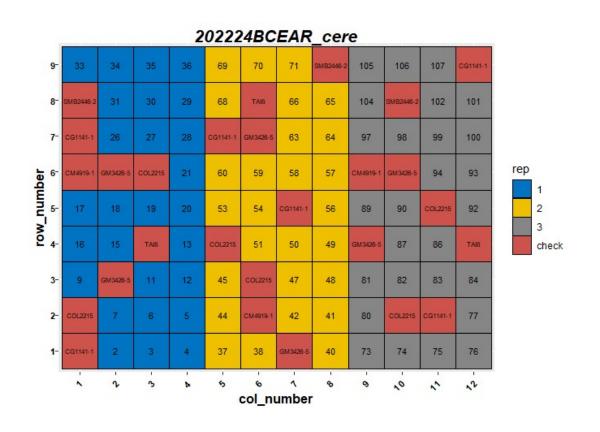


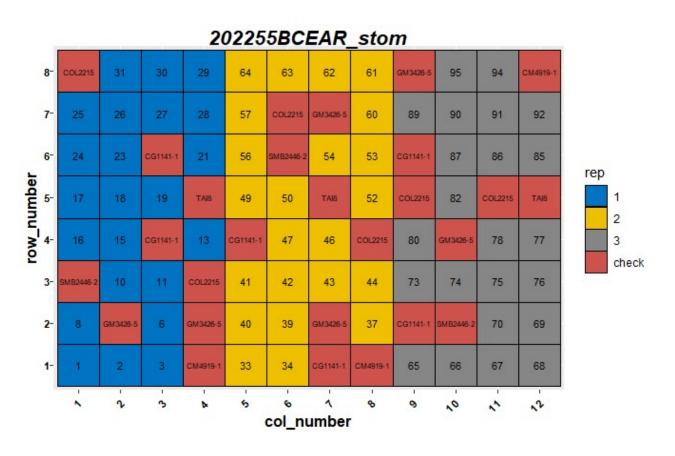




Trial Design – Row col

Check varieties are completely randomized



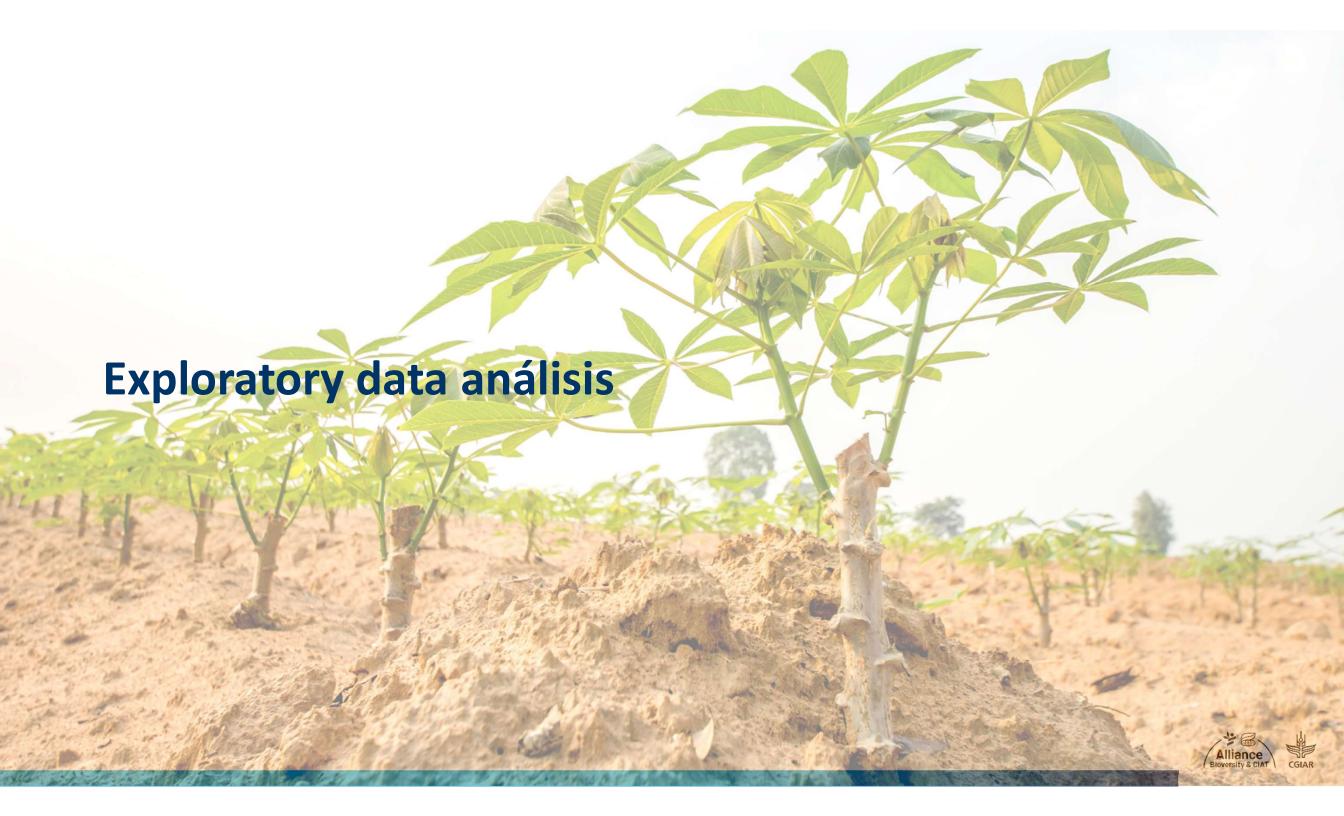




Check genotypes

- 1. CG1141-1_is_Costena
- 2. CM4919-1_is_Veronica
- 3. COL2215_is_Venezolana
- 4. SMB2446-2_is_Caiseli
- 5. TAI8_is_TAI



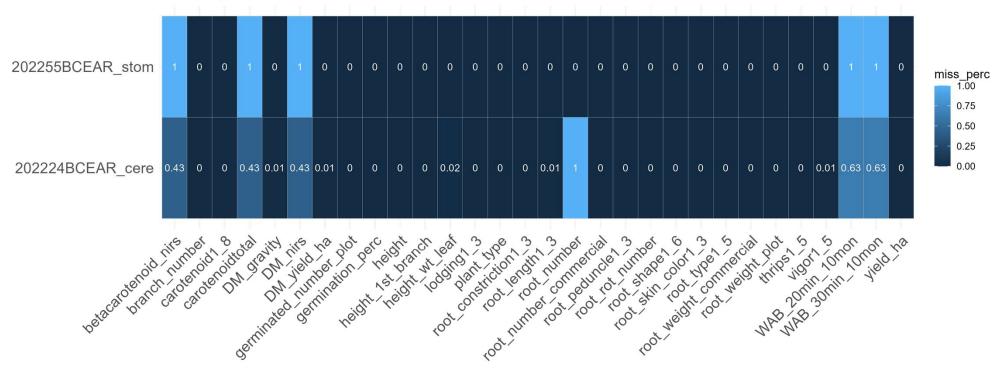


Traits evaluated

Assessed agronomic traits
betacarotenoid_nirs
branch_number
carotenoid1_8
carotenoidtotal
DM_gravity
DM_nirs
DM_yield_ha
germinated_number_plot
germination_perc
height
height_1st_branch
height_wt_leaf
lodging1_3
plant_type
root_constriction1_3
root_length1_3
root_number
root_number_commercial
root_peduncle1_3
root_rot_number
root_shape1_6
root_skin_color1_3
root_type1_5
root_weight_commercial
root_weight_plot
thrips1_5
vigor1_5
WAB_20min_10mon
WAB_30min_10mon
yield_ha

Missing values across trials

Percentage of missing values (exp/trait)

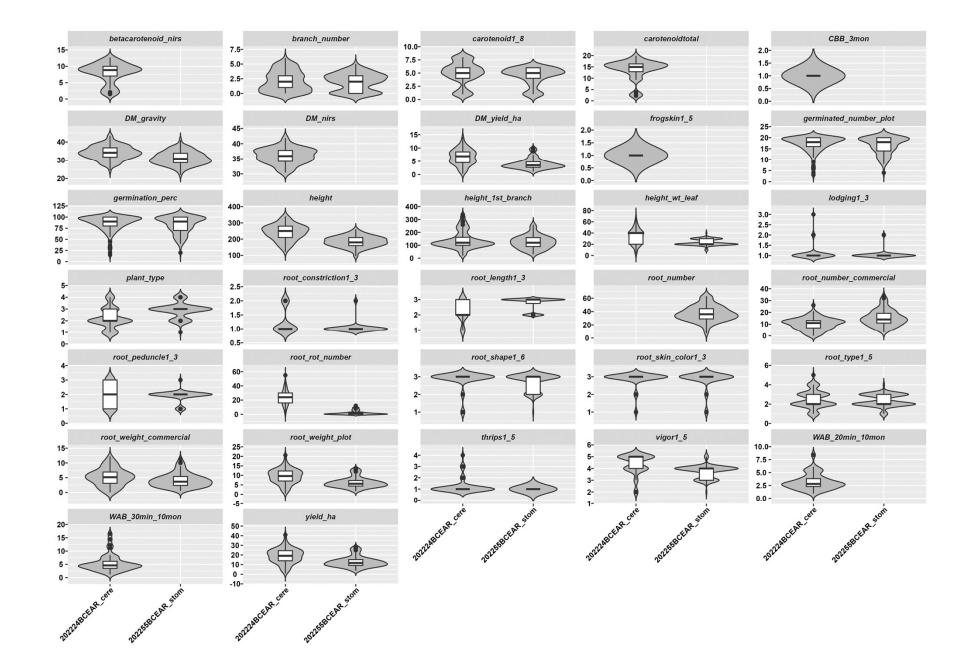






0.50

Trait variation across trials (phenotypic value)



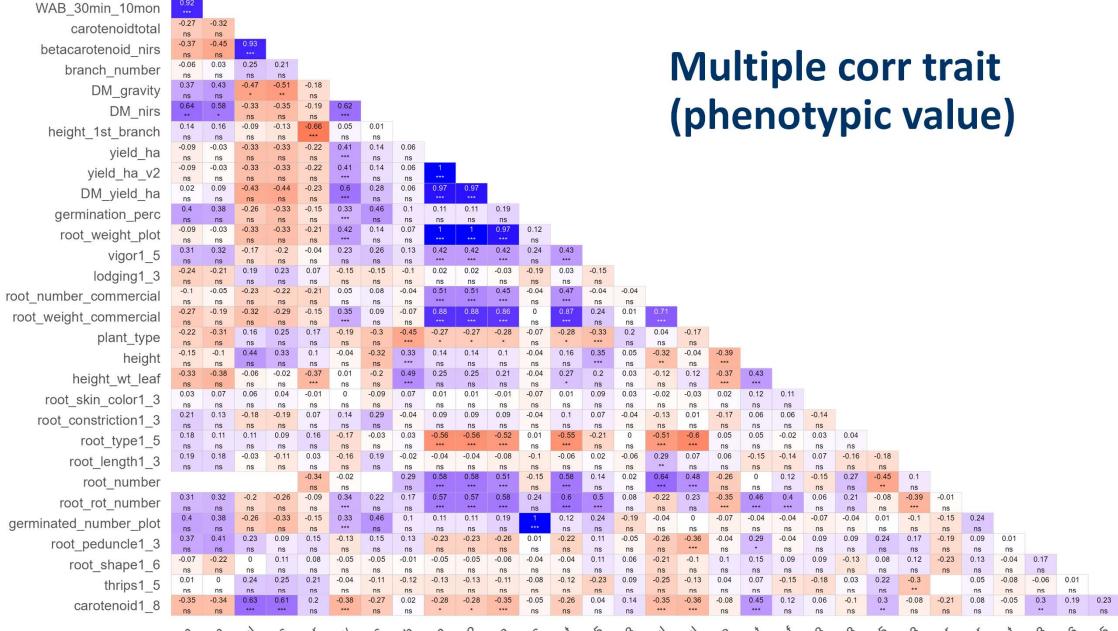


Shared genotypes

Connectivity Matrix







NARE WARE 30 min caroteroid branch humber height, 1st branch of permination weight, oot, weight, oot, weight, confine out, type height, leaf to the confine out, type height, leaf to th



Dropped traits

CBB_3mon frogskin1_5

These traits were dropped from the analysis because they had no variation within themselves.

Single heritability

Moderate to **high** heritability among two locations.

	WAB_20	WAB_30	caro	te betaca	aro			DΝ	√ height_			germin				root_numl	root_v	veig				root_ski	i		root_l	root_	root_ro g	erminated	root_pe	root_s	thri (arote
	min_10	min_10	noid	to tenoid	l_n b	ranch_nu	DM_gr	a_n	ir 1st_bra	a DM_yi	yield	ation_p	root_wei	vigor1	lodgi	er_comme	rht_cor	nme þ	olant_t		height_	n_color:	1root_const	root_ty	ength1	numb	t_numb_	_numberp	duncle1	hape1	ps1 r	ioid1
trial	mon	mon	tal	irs	n	nber	vity	s	nch	eld_ha	_ha	erc	ght_plot	_5	ng1_3	cial	rcial	<u> </u>	/pe	height	wt_leaf	_3	riction1_3	pe1_5	_3	er	er l	ot	_3	_6	_5	_8
202224E																																
CEAR_ce																																
re	0.5	0.	7	0.9	0.9	0.7	7 0.	8 0.	.7 0.	.8 0.8	0.8	0.9	0.8	0.6	0.4	0.	7	0.8	0.7	0.6	0.4		0.1	0.6	0.4		0.8	0.9	0.7	0	0.8	0.9
202255E	3																															
CEAR_st																																
om						0.9	0.	9	0.	.9 0.9	0.8	0.2	0.8	0.3	3 (0.	8	0.8	0.7	0.9	0.5		0.9	0.7	7 0.3	0.6	0.6	0.2	0.7	0.6		0.9

Traits with heritability lower than 0.1 were remove them from the GxE analysis.

GxE analysis was performed without following traits - trials:

- WAB_20min_10mon, WAB_30min_10mon, carotenoidtotal, betacarotenoid_nirs, DM_nirs: **202224BCEAR_cere** (**only one trait to fit**).
- lodging1_3: 202255BCEAR_stom (h2 < 0.1, so only one trait to fit).
- root_rot_number: 202255BCEAR_stom (only one trait to fit).
- root_shape1_6: 202224BCEAR_cere (h2 < 0.1, so only one trait to fit).
- trips1_5: 202224BCEAR_cere (only one trait to fit).



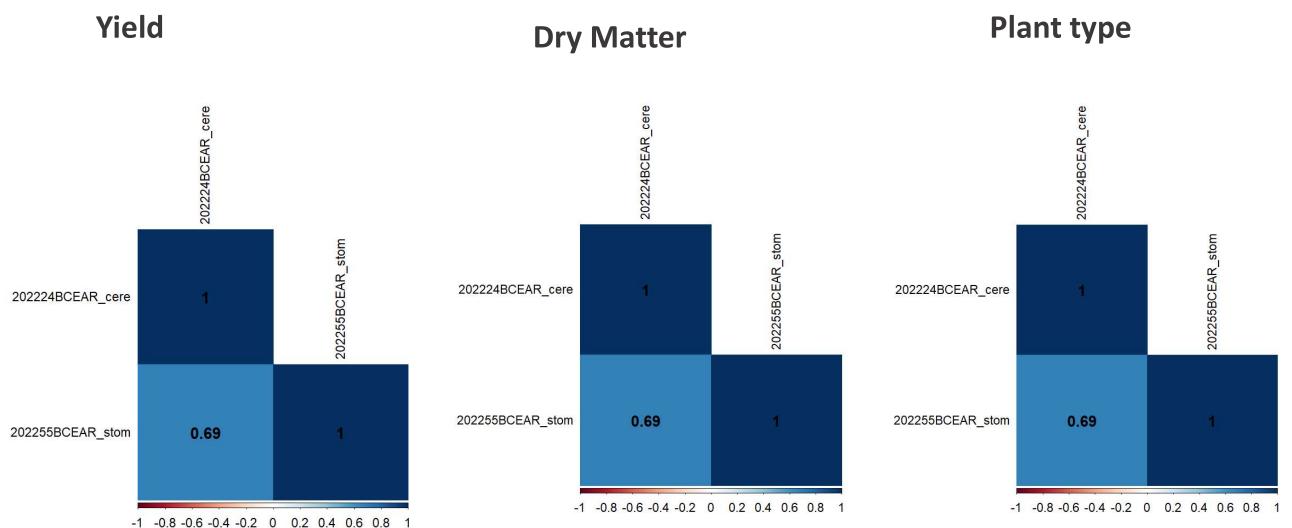
Heritability gxe all trials

trait	h2								
root_skin_color1_3	0.98								
carotenoid1_8	0.93								
height_1st_branch	0.9								
branch_number	0.88								
DM_gravity	0.86								
DM_yield_ha	0.84								
height	0.83								
yield_ha	0.82								
root_weight_plot	0.81								
root_weight_commercial	0.81								
plant_type	0.78								
root_number_commercial	0.74								
root_peduncle1_3	0.62								
height_wt_leaf	0.52								
root_length1_3	0.5								
germinated_number_plot	0.44								
germination_perc	0.44								
vigor1_5	0.38								
root_type1_5	0.38								
root_rot_number	0.08								
root_constriction1_3	0								

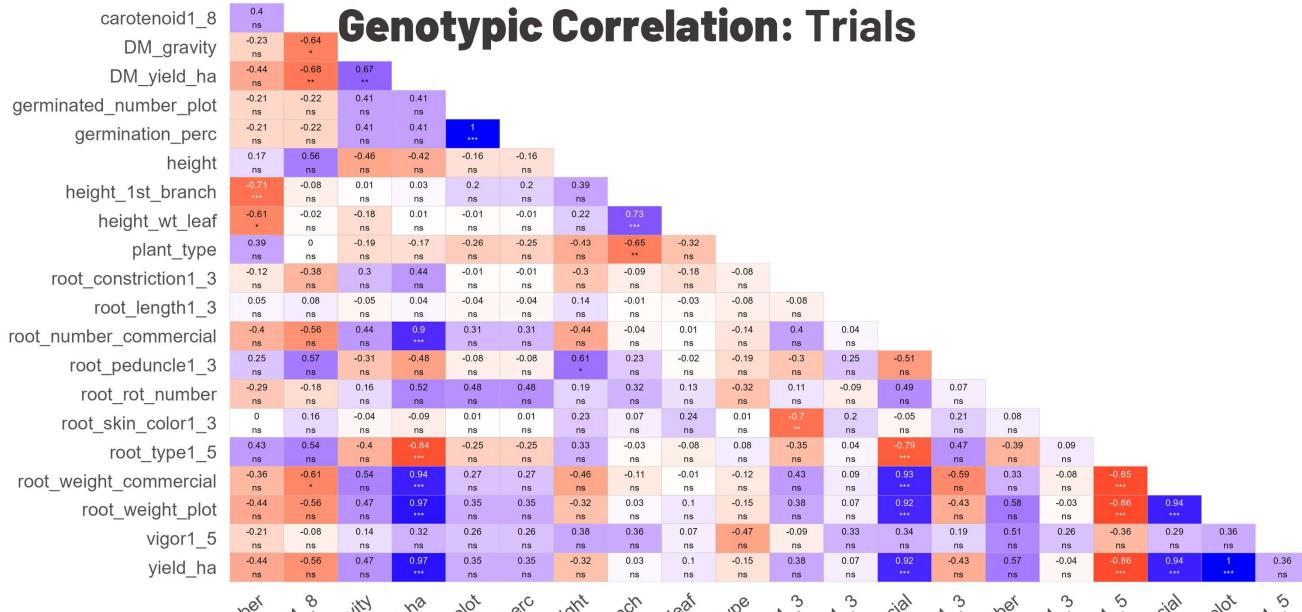
For traits with low heritability, please be careful. (blue square)



Genotypic Correlation: Locations





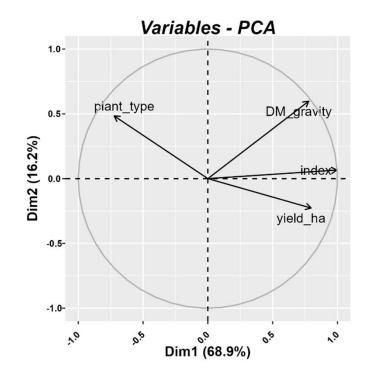


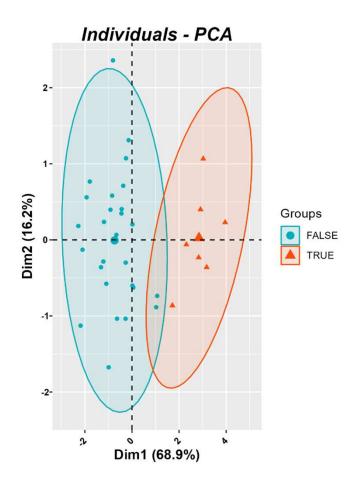
branch number old 3 gravity led ha promination perc height had number plot height half height in leaf root length 3 number commercial of height plot height height in leaf root length 3 number commercial control of height commercial number commercial control of height commercial number commercial number control of height control of height and height number control of height control of height and height number control of height number c



Selection comments

- 1) DM_gravity, plant_type & yield_ha were used to calculate index selection.
- 2) Scores given were:
 - DM_gravity = 10
 - plant_type = -5
 - yield_ha = 10
- 3) Percentage to be selected: **20**%









Thank you!