



# Data analysis

## 2022BCEPR2env\_set1

- 202240BCEPR\_cere  
- 202241BCEPR\_stom

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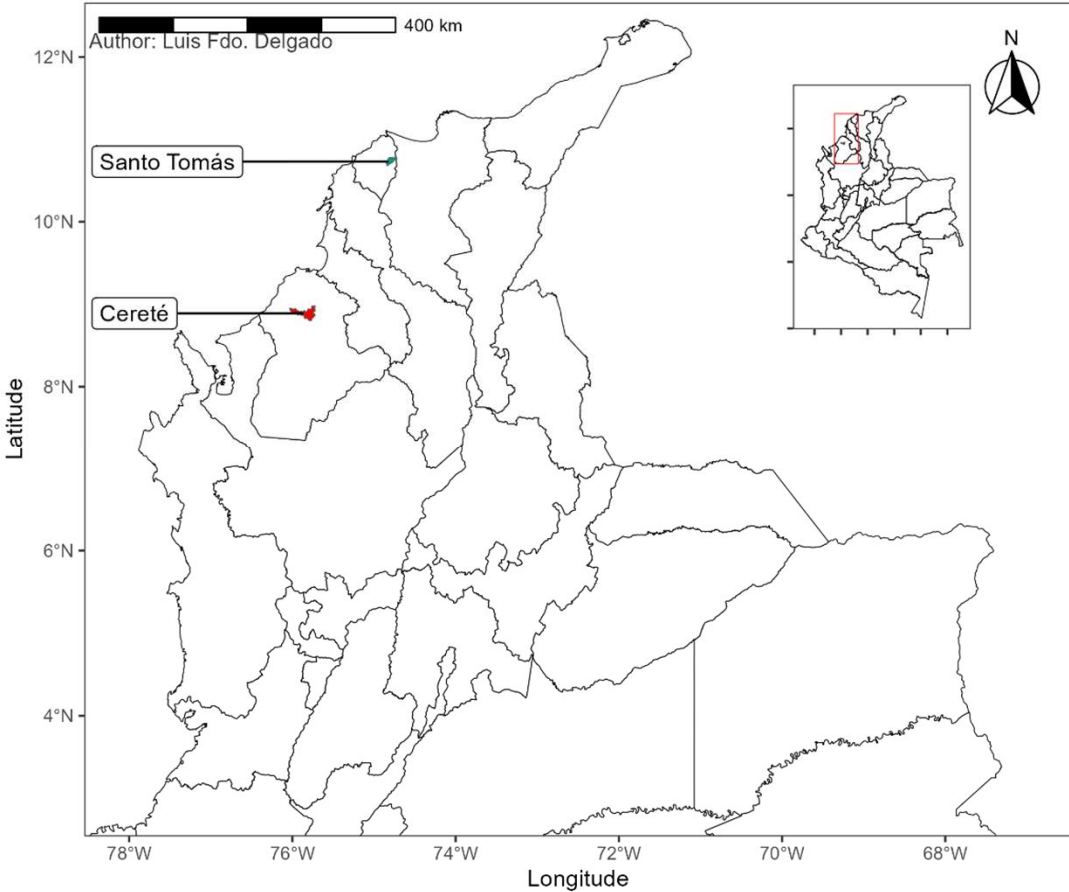
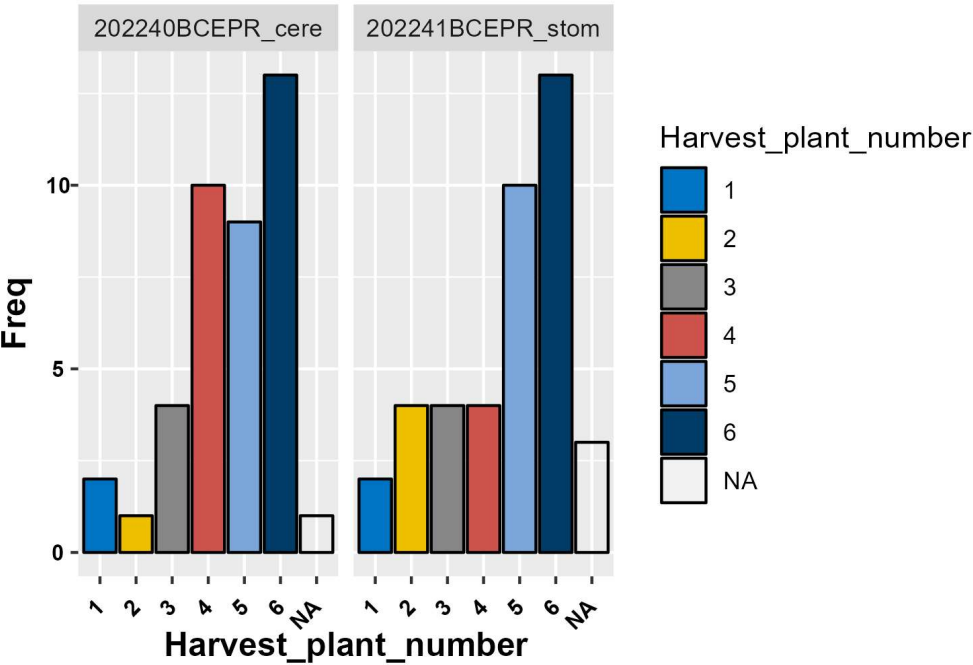
The Alliance of Bioversity International and the International Center for Tropical Agriculture (CIAT) is part of CGIAR, a global research partnership for a food-secure future

# Resolvable row-col with randomized checks

use_trial_name	use_plant_date	use_harvest_date	harvesting_time	use_location	n_gen
202240BCEPR_cere	2022-June-24	2023-May-10	10month 16day	Cerete. Cordoba, Colombia	19
202241BCEPR_stom	2022-August-05	2023-April-28	8month 23day	Santo Tomas. Atlantico, Colombia	19

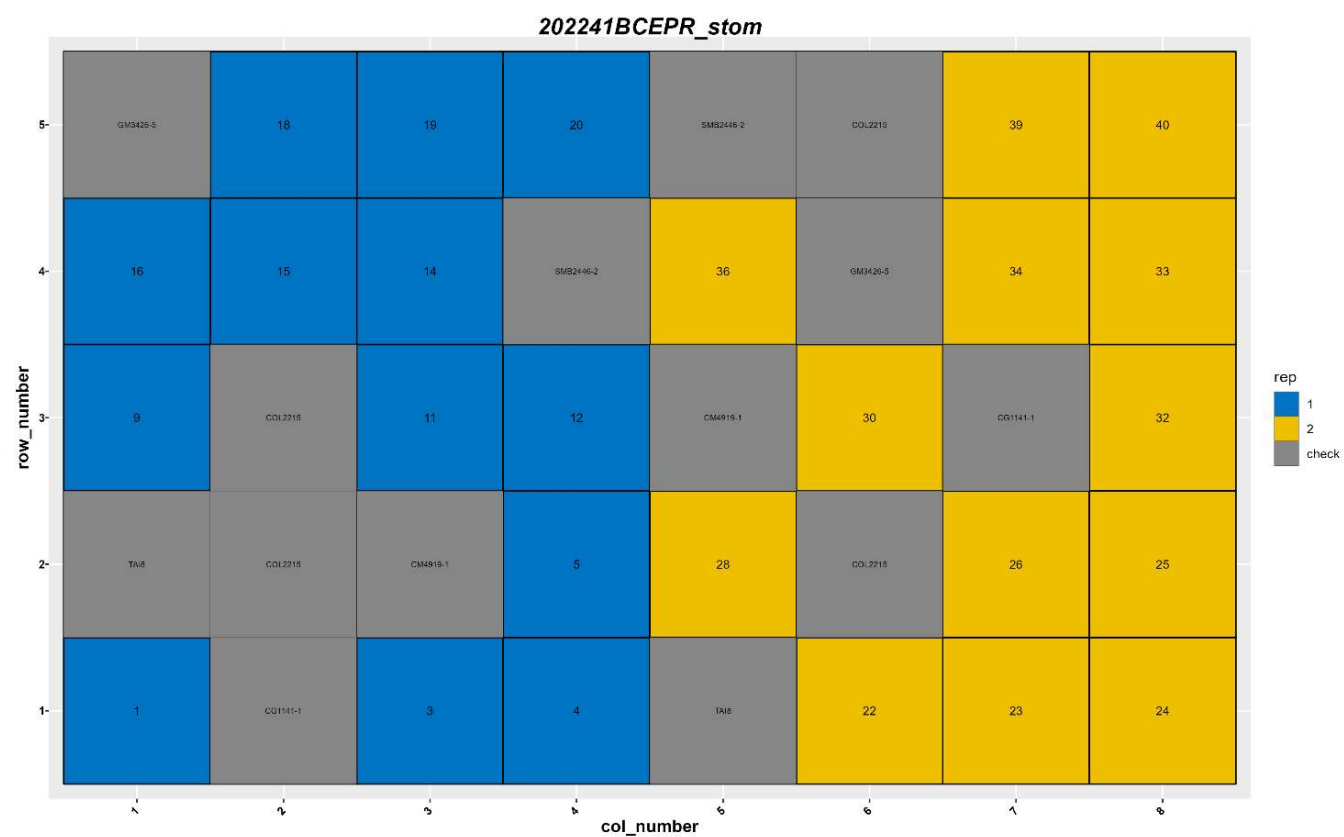
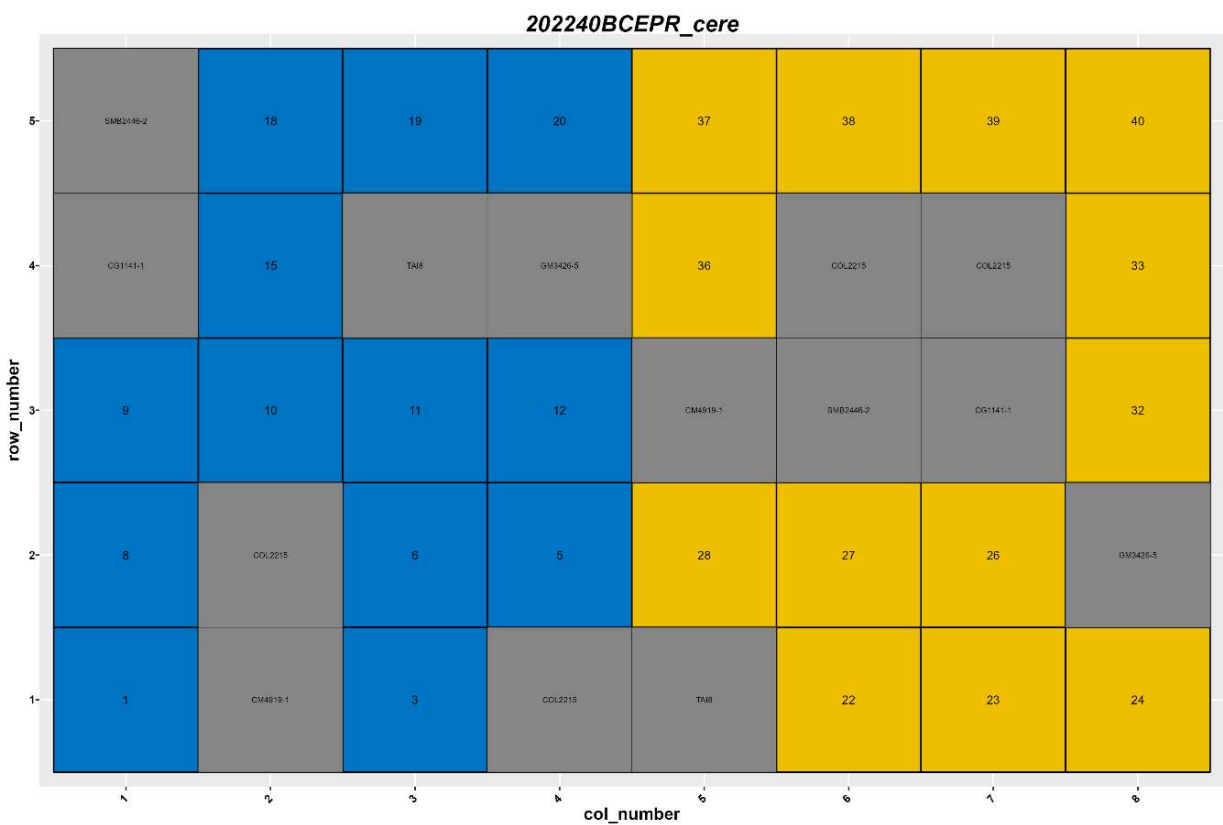
## Plot size:

- 202240BCEPR\_cere, **10** plants per plot, harvesting **6** plants for yield
- 202241BCEPR\_stom, **10** 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

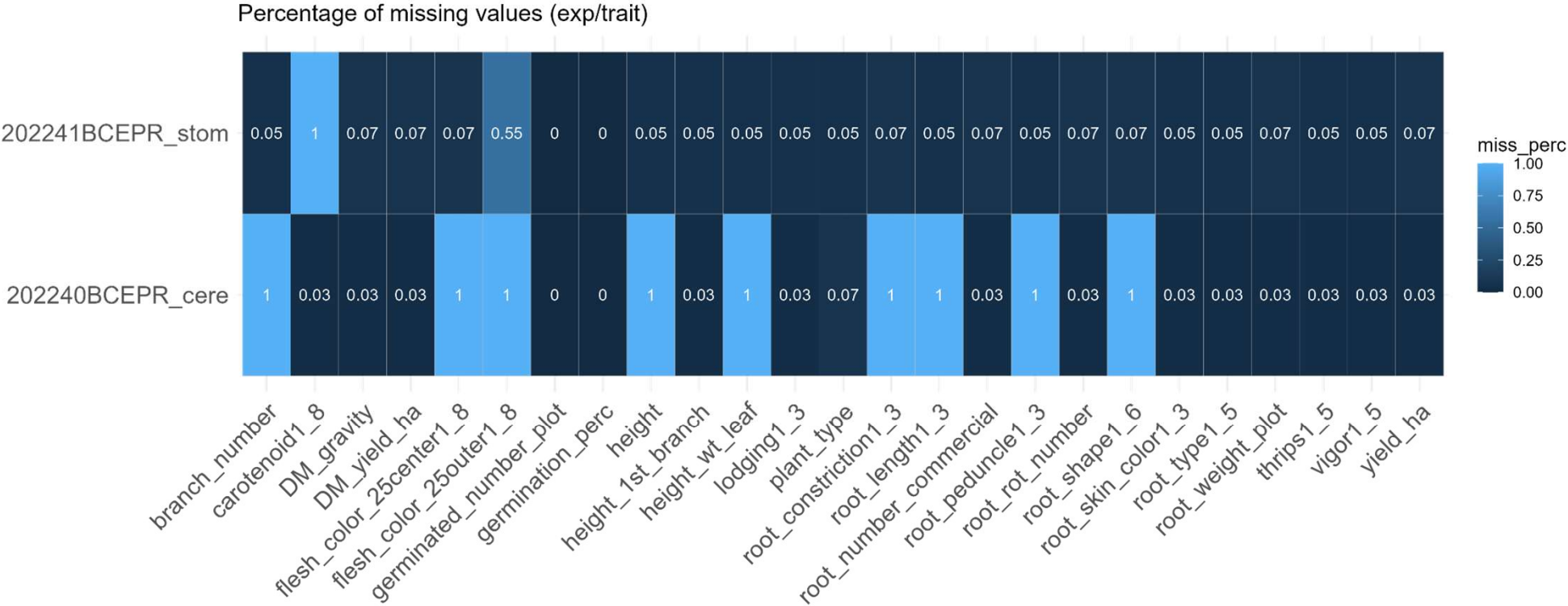


# Exploratory data analysis

# Traits evaluated

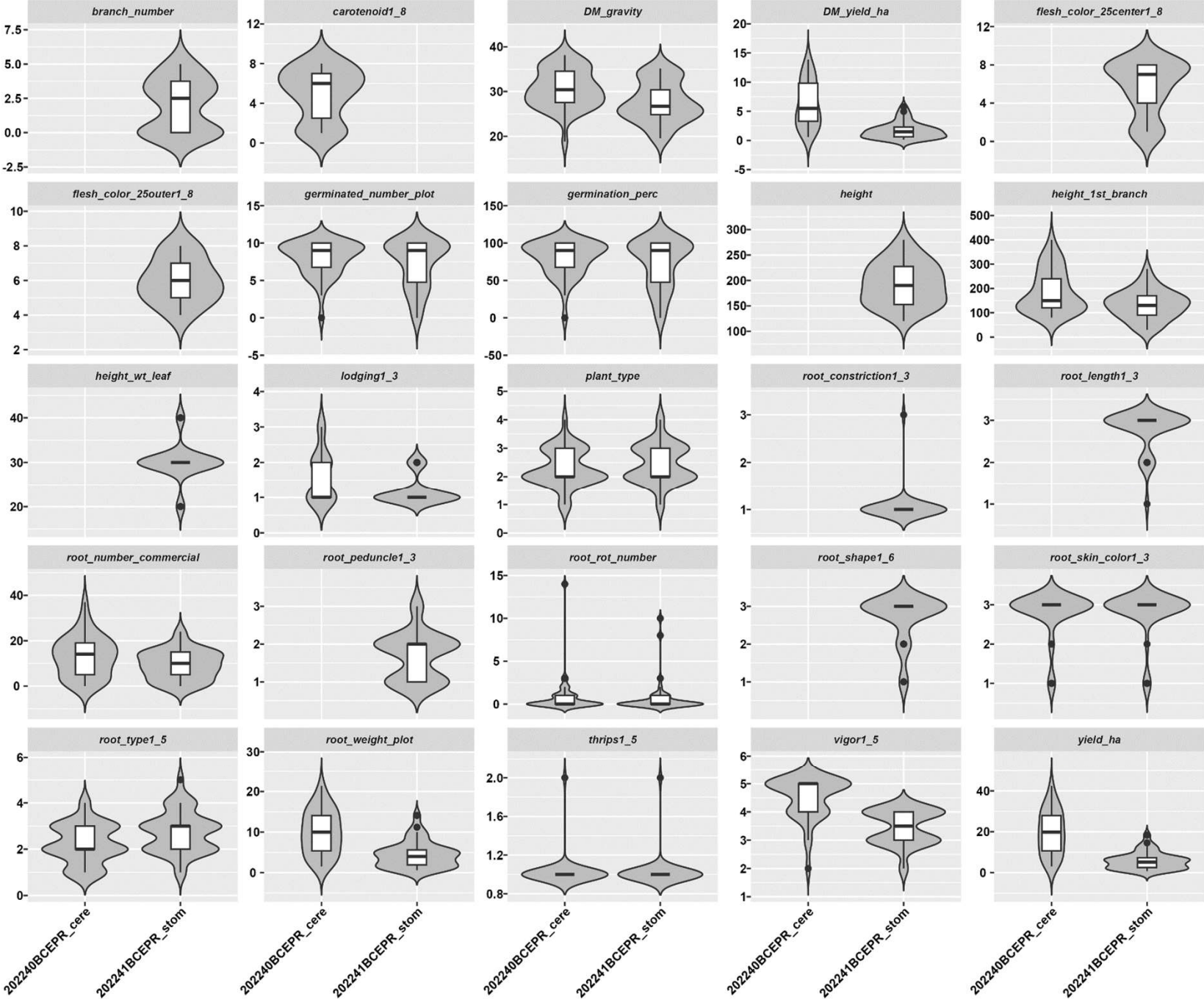
Agronomic traits
branch_number
carotenoid1_8
DM_gravity
DM_yield_ha
flesh_color_25center1_8
flesh_color_25outer1_8
germinated_number_plot
germination_perc
height
height_1st_branch
height_wt_leaf
lodging1_3
plant_type
root_constriction1_3
root_length1_3
root_number_commercial
root_peduncle1_3
root_rot_number
root_shape1_6
root_skin_color1_3
root_type1_5
root_weight_plot
thrips1_5
vigor1_5
yield_ha

## Missing values across trials





# Trait variation across trials (phenotypic value)



# Shared genotypes

19 shared genotypes found.

Connectivity Matrix

202241BCEPR_stom	19	19
202240BCEPR_cere	19	19

202240BCEPR\_cere

202241BCEPR\_stom



## Multiple corr trait (phenotypic value)

# Multiple corr trait (phenotypic value)

Trait	branch_number	DM_gravity	height_1st_branch	yield_ha	germination_perc	DM_yield_ha	root_weight_plot	vigor1_5	lodging1_3	root_number_commercial	plant_type	height	height_wt_leaf	root_skin_color1_3	root_constriction1_3	root_type1_5	flesh_color_25center1_8	flesh_color_25outer1_8	root_length1_3	root_rot_number	germinated_number_plot	root_peduncle1_3	root_shape1_6	thrips1_5	carotenoid1_8
branch_number	1.0																								
DM_gravity	-0.42 ns	1.0																							
height_1st_branch	-0.74 ***	0.11 ns	1.0																						
yield_ha	-0.32 ns	0.62 ***	0.17 ns	1.0																					
germination_perc	-0.39 ns	0.51 ***	0.04 ns	0.42 *	1.0																				
DM_yield_ha	-0.35 ns	0.69 ***	0.17 ns	0.99 ***	0.41 ns	1.0																			
root_weight_plot	-0.32 ns	0.65 ***	0.12 ns	0.98 ***	0.49 **	0.97 ***	1.0																		
vigor1_5	-0.56 ns	0.36 ns	0.27 ns	0.63 ***	0.45 **	0.58 ***	0.6 ***	1.0																	
lodging1_3	0.21 ns	-0.29 ns	0.13 ns	0 ns	-0.04 ns	-0.06 ns	-0.08 ns	0.29 ns	1.0																
root_number_commercial	-0.3 ns	0.6 ***	0.1 ns	0.81 ***	0.53 ***	0.8 ***	0.87 ***	0.44 *	-0.21 ns	1.0															
plant_type	0.22 ns	-0.03 ns	-0.19 ns	-0.09 ns	-0.06 ns	-0.1 ns	-0.1 ns	-0.12 ns	0.37 ns	-0.09 ns	1.0														
height	0.23 ns	-0.77 ***	0.32 ns	-0.47 ns	-0.45 ns	-0.55 ns	-0.47 ns	-0.25 ns	0.16 ns	-0.42 ns	-0.33 ns	1.0													
height_wt_leaf	-0.28 ns	-0.31 ns	0.54 ns	-0.35 ns	-0.31 ns	-0.36 ns	-0.35 ns	-0.22 ns	0.17 ns	-0.35 ns	0.1 ns	0.4 ns	1.0												
root_skin_color1_3	0.21 ns	-0.16 ns	-0.01 ns	-0.27 ns	-0.23 ns	-0.28 ns	-0.33 ns	-0.17 ns	0.12 ns	-0.38 ns	0.06 ns	0.23 ns	0.24 ns	1.0											
root_constriction1_3	0 ns	-0.3 ns	0.01 ns	-0.2 ns	-0.16 ns	-0.19 ns	-0.2 ns	-0.13 ns	-0.08 ns	-0.24 ns	-0.11 ns	0.07 ns	-0.01 ns	0.06 ns	1.0										
root_type1_5	0.15 ns	-0.57 ***	-0.08 ns	-0.69 ***	-0.44 *	-0.66 ***	-0.75 ***	-0.47 **	0.15 ns	-0.77 ***	0.09 ns	0.43 ns	0.23 ns	0.32 ns	0.24 ns	1.0									
flesh_color_25center1_8	0.27 ns	-0.87 ***	0.24 ns	-0.58 *	-0.52 ns	-0.67 **	-0.58 *	-0.37 ns	0.35 ns	-0.56 ns	-0.24 ns	0.76 ***	0.36 ns	0.11 ns	0.15 ns	0.55 ns	1.0								
flesh_color_25outer1_8	-0.1 ns	0.34 ns	0.06 ns	-0.16 ns	0.16 ns	-0.14 ns	-0.16 ns	0 ns	0.37 ns	-0.21 ns	0.18 ns	-0.32 ns	0 ns	-0.19 ns	0.18 ns	-0.62 ns	-0.19 ns	1.0							
root_length1_3	-0.2 ns	0.17 ns	0.06 ns	0.37 ns	0.38 ns	0.35 ns	0.37 ns	0.34 ns	-0.08 ns	0.38 ns	-0.04 ns	-0.24 ns	0 ns	-0.15 ns	-0.3 ns	-0.33 ns	-0.15 ns	-0.32 ns	1.0						
root_rot_number	-0.32 ns	0.09 ns	0.06 ns	0.02 ns	0.25 ns	0.01 ns	0.03 ns	0.17 ns	0.18 ns	-0.01 ns	0.25 ns	-0.3 ns	-0.06 ns	0.06 ns	-0.06 ns	-0.11 ns	-0.38 ns	0.28 ns	0.13 ns	1.0					
germinated_number_plot	-0.39 ns	0.51 ***	0.04 ns	0.42 *	1 ***	0.41 ns	0.49 **	0.45 **	-0.04 ns	0.53 ***	-0.06 ns	-0.45 ns	-0.31 ns	-0.23 ns	-0.16 ns	-0.44 *	-0.52 ns	0.16 ns	0.38 ns	0.25 ns	1.0				
root_peduncle1_3	0.35 ns	-0.66 **	0.09 ns	-0.52 ns	-0.39 ns	-0.57 ns	-0.52 ns	-0.41 ns	0.25 ns	-0.51 ns	-0.23 ns	0.64 **	0.22 ns	0.22 ns	0.09 ns	0.48 ns	0.53 ns	0.47 ns	-0.32 ns	-0.16 ns	-0.39 ns	1.0			
root_shape1_6	-0.14 ns	0.02 ns	-0.08 ns	-0.24 ns	-0.13 ns	-0.22 ns	-0.24 ns	-0.07 ns	-0.22 ns	-0.21 ns	0.18 ns	-0.07 ns	0.04 ns	0.23 ns	0.08 ns	0.25 ns	0.06 ns	-0.24 ns	0.09 ns	0.14 ns	-0.13 ns	-0.26 ns	1.0		
thrips1_5	0.09 ns	0.12 ns	-0.22 ns	-0.12 ns	0.04 ns	-0.11 ns	-0.13 ns	-0.09 ns	0.16 ns	-0.15 ns	0.28 ns	-0.29 ns	0 ns	0.06 ns	-0.03 ns	0 ns	-0.28 ns	0.07 ns	0.05 ns	0.04 ns	-0.18 ns	0.08 ns	1.0		
carotenoid1_8	-0.74 ***	0.05 ns	-0.59 *	-0.34 ns	-0.69 ***	-0.59 *	-0.08 ns	0.36 ns	-0.55 ns	0.02 ns	0.39 ns	0.44 ns	0.07 ns	-0.34 ns	-0.25 ns	1.0									



# Statistical data analysis

# Single heritability

Moderate to low heritability among two locations.

trial	branch_number	carotenoid1_8	DM_gravity	DM_yield_ha	flesh_color_25center1_8	germinate_plot	germination_perc	height	height_1st_branch	height_wt_leaf	lodging1_3	plant_type	root_constriction1_3	root_length1_3	root_numbercommercial	root_peduncle1_3	root_rot_number	root_shape1_6	root_skin_color1_3	root_tuber1_5	root_weight_pot	thrips1_5	vigor1_5	yield_ha
202240BCEPR_cere		0.98	0.89	0.86		0.74	0.74		0.77		0.07	0			0.63		0.01		0.84	0.27	0.82	0.19	0.36	0.82
202241BCEPR_stom	0.97		0.95	0.87	0.91	0.87	0.87	0.93	0.76	0.62	0.73	0.45	0.01	0	0.66	0.44	0.45	0.04	0.69	0.71	0.84	0	0.75	0.84

GxE analysis was performed without following traits - trials:

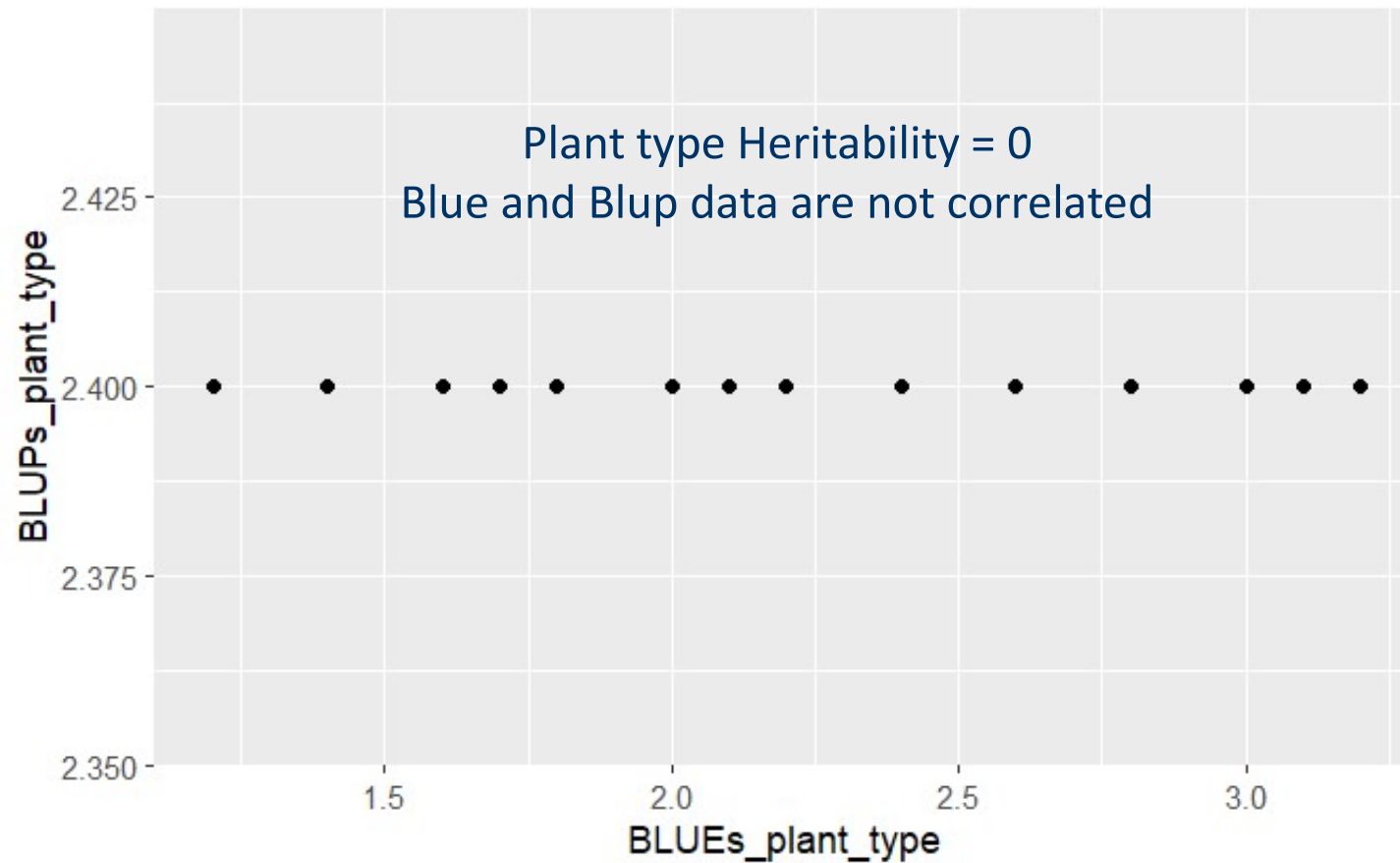
trial	traits	heritability
202240BCEPR_cere	branch_number	NA
202240BCEPR_cere	flesh_color_25center1_8	NA
202240BCEPR_cere	height	NA
202240BCEPR_cere	height_wt_leaf	NA
202240BCEPR_cere	lodging1_3	0.07
202240BCEPR_cere	plant_type	0
202240BCEPR_cere	root_constriction1_3	NA
202240BCEPR_cere	root_length1_3	NA
202240BCEPR_cere	root_peduncle1_3	NA
202240BCEPR_cere	root_rot_number	0.01
202240BCEPR_cere	root_shape1_6	NA
202241BCEPR_stom	carotenoid1_8	NA
202241BCEPR_stom	root_constriction1_3	0.01
202241BCEPR_stom	root_length1_3	0
202241BCEPR_stom	root_shape1_6	0.04
202241BCEPR_stom	thrips1_5	0

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

Due to low heritability and presence in only one trial, 16 traits were removed.



# 202240BCEPR\_cere – plant\_type



Plant\_type single heritability of trial 202240BCEPR\_cere does not make sense because height\_1st\_branch heritability is high. (These two traits are strongly correlated).

The plant\_type data may have a systematic error.

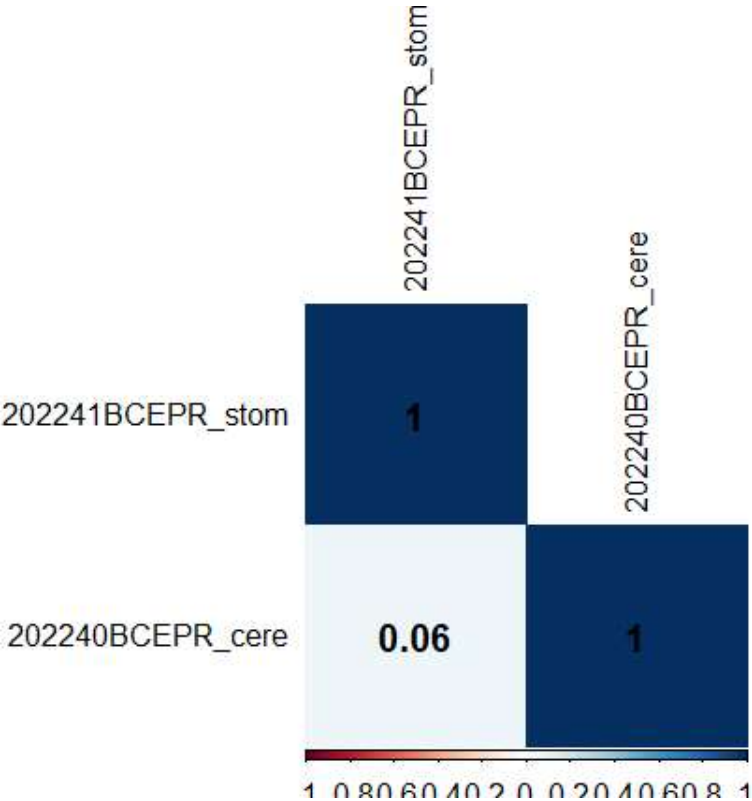
# Heritability gxe all trials

trait	h2
DM_gravity	0.91
root_skin_color1_3	0.81
height_1st_branch	0.72
germinated_number_plot	0.69
germination_perc	0.69
DM_yield_ha	0.6
root_number_commercial	0.44
root_type1_5	0.16
root_weight_plot	0
yield_ha	0
vigor1_5	0

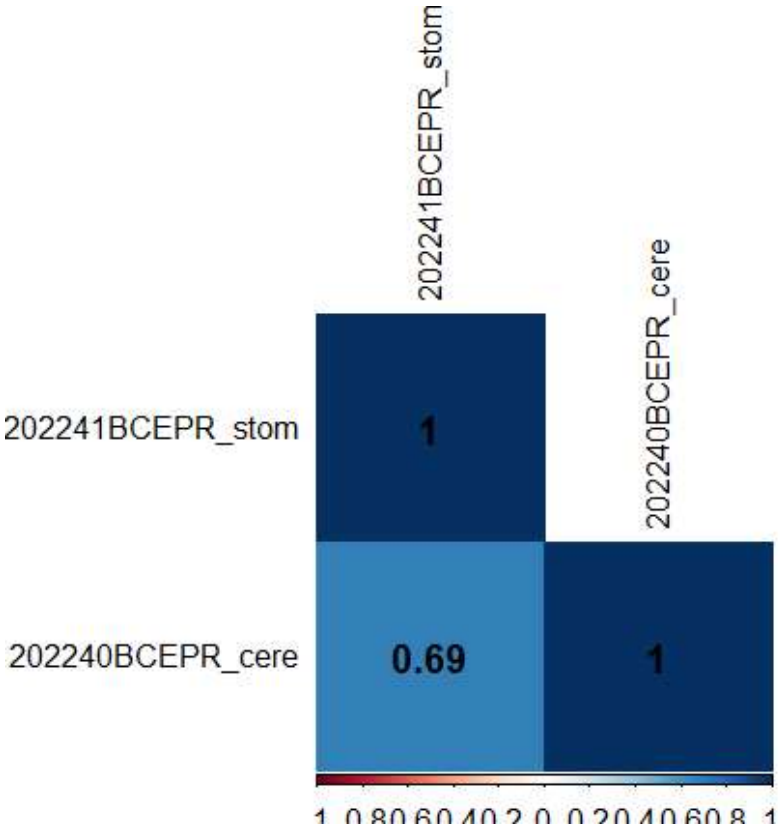
 For traits with low heritability, please be **careful**. (blue square)

# Genotypic Correlation: Locations

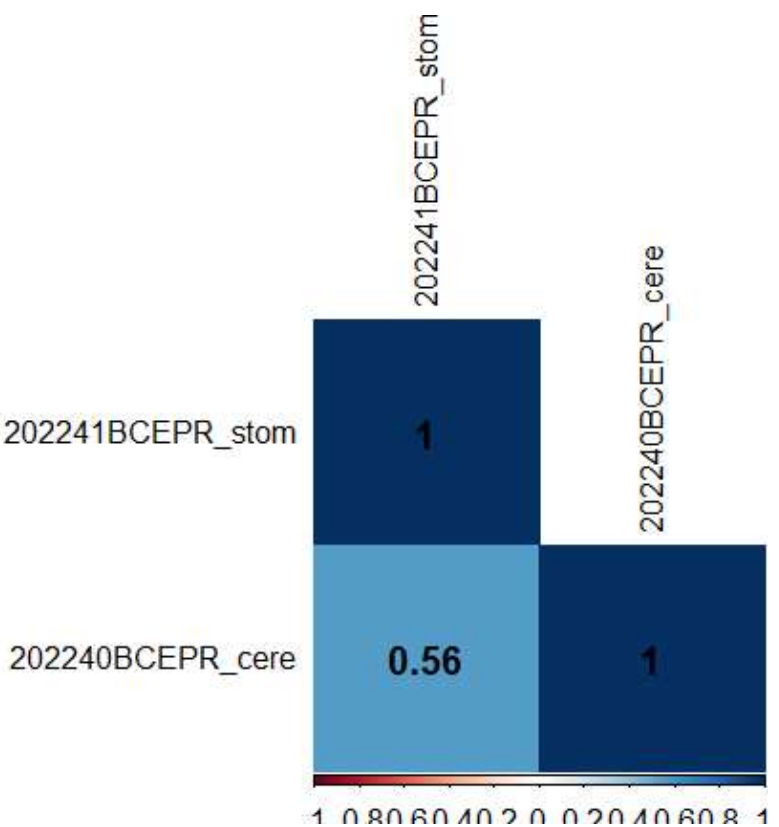
Yield



Dry matter



height\_1st\_branch





# Genotypic Correlation: Trials

DM_yield_ha	0.77 **									
germinated_number_plot	0.57 ns	0.52 ns								
germination_perc	0.57 ns	0.52 ns	1 ***							
height_1st_branch	0.07 ns	-0.07 ns	0.2 ns	0.2 ns						
root_number_commercial	0.72 *	0.83 ***	0.4 ns	0.4 ns	-0.09 ns					
root_skin_color1_3	-0.32 ns	-0.33 ns	-0.35 ns	-0.35 ns	-0.13 ns	-0.46 ns				
root_type1_5	-0.71 *	-0.71 *	-0.31 ns	-0.31 ns	0.06 ns	-0.91 ***	0.45 ns			
root_weight_plot	0.71 *	0.98 ***	0.5 ns	0.5 ns	-0.09 ns	0.87 ***	-0.39 ns	-0.74 *		
vigor1_5	0.33 ns	0.24 ns	0.38 ns	0.38 ns	0.28 ns	0.33 ns	-0.29 ns	-0.24 ns	0.28 ns	
yield_ha	0.66 ns	0.98 ***	0.49 ns	0.49 ns	-0.1 ns	0.81 **	-0.33 ns	-0.69 *	0.99 ***	0.25 ns
<div>DM_gravity</div> <div>DM_yield_ha</div> <div>germinated_number_plot</div> <div>germination_perc</div> <div>height_1st_branch</div> <div>root_number_commercial</div> <div>root_skin_color1_3</div> <div>root_type1_5</div> <div>root_weight_plot</div> <div>vigor1_5</div>										

A

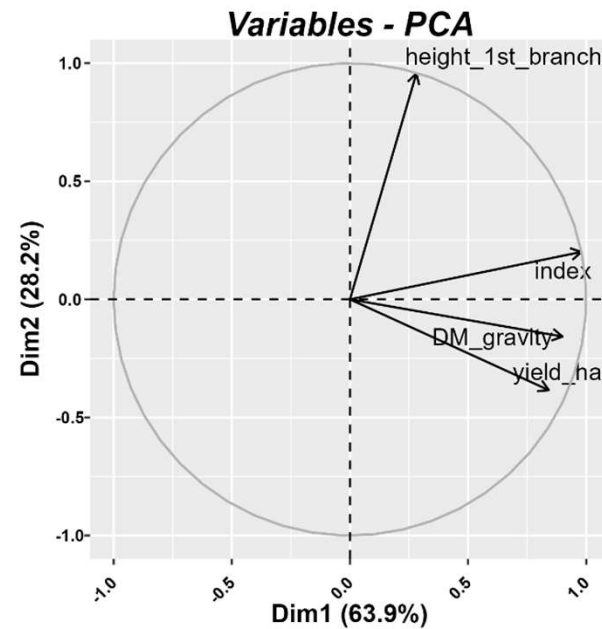
# Selection comments

1) **DM\_gravity**, **plant\_type** & **yield\_ha** were used to calculate index selection.

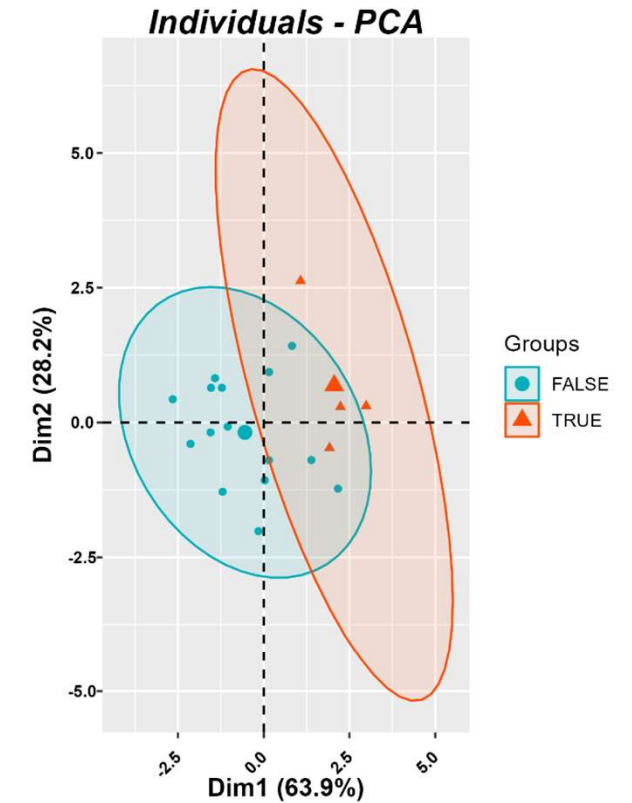
2) Scores given were:

- **DM\_gravity** = 10
- **height\_1st\_branch** = 10
- **yield\_ha** = 10

3) Percentage to be selected: **20%**



B





**Thank you!**