Data analysis
2022BCEPR2env_set1

- 202240BCEPR_cere
- 202241BCEPR_stom

Luis Fernando Delgado Munoz

luis.delgado@cgiar.org

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@BiovIntCIAT_eng
@BiovIntCIAT_esp

#Alliance4Science

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
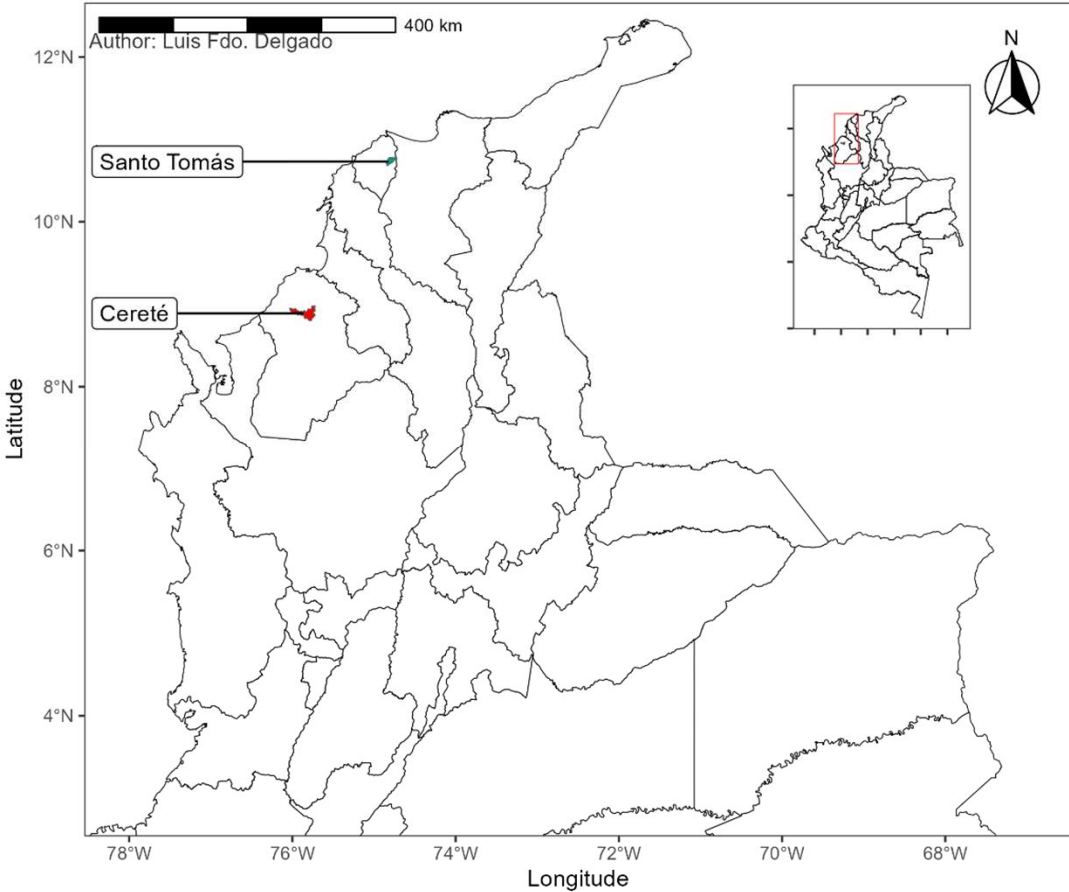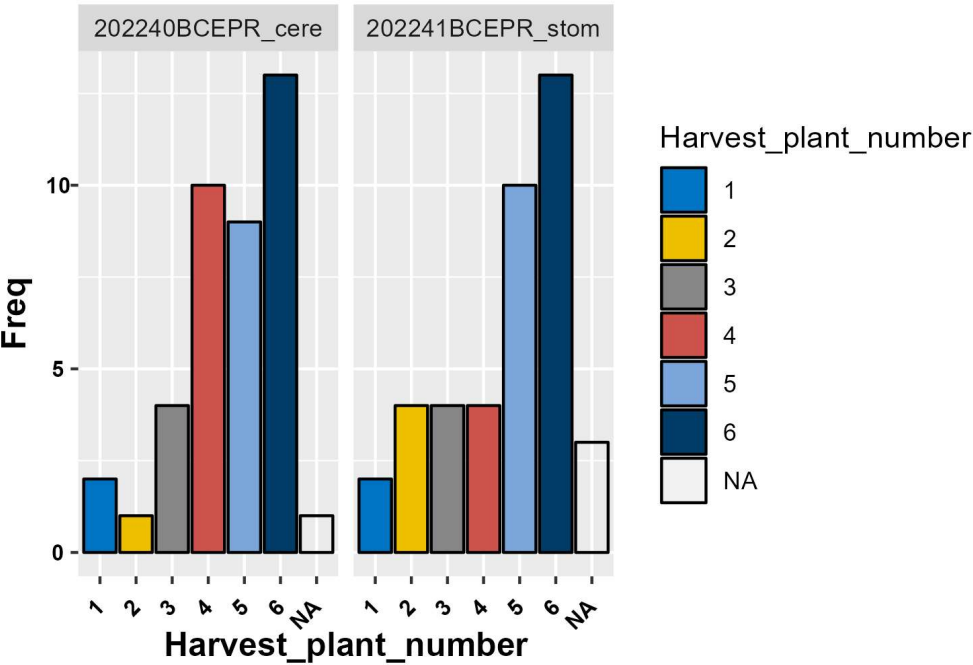
Trial Design – Row col

Check varieties are completely randomized
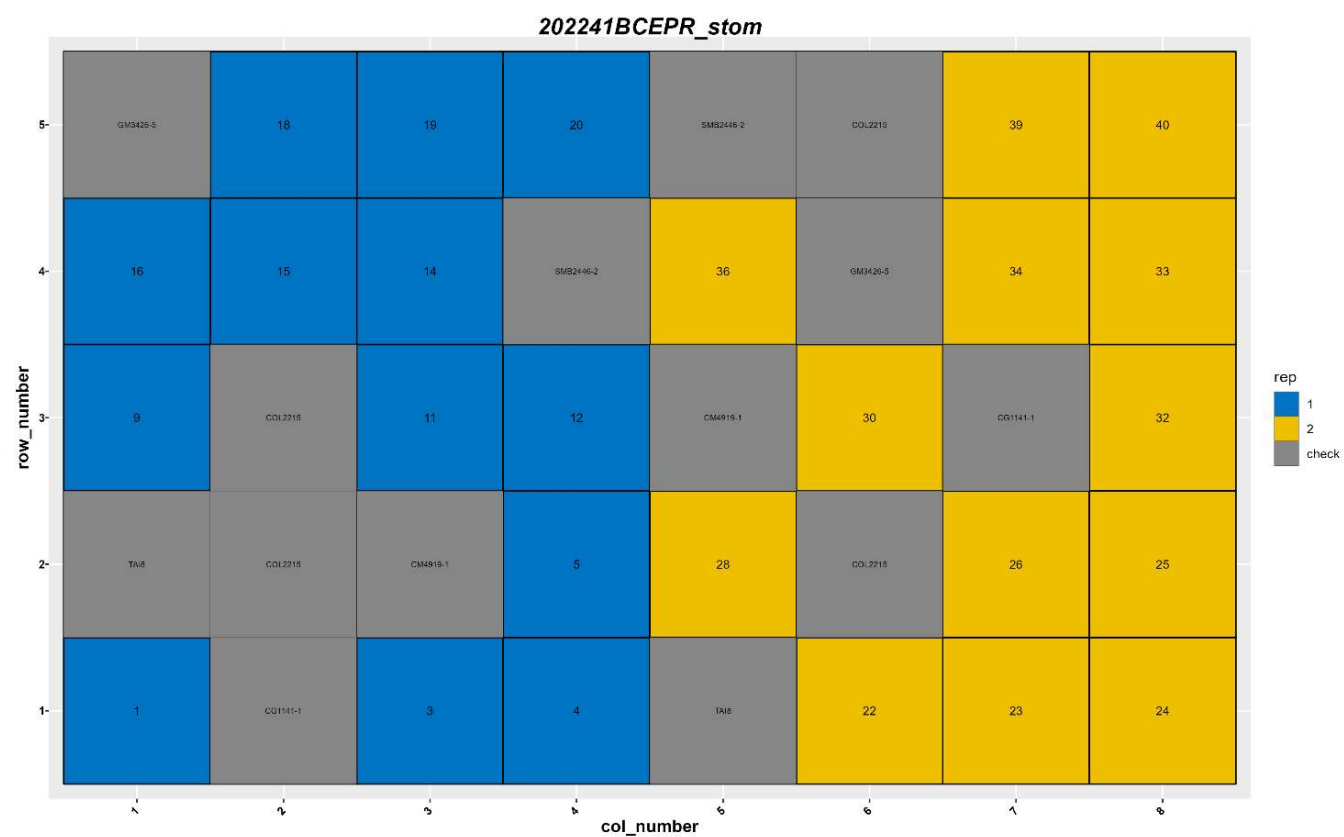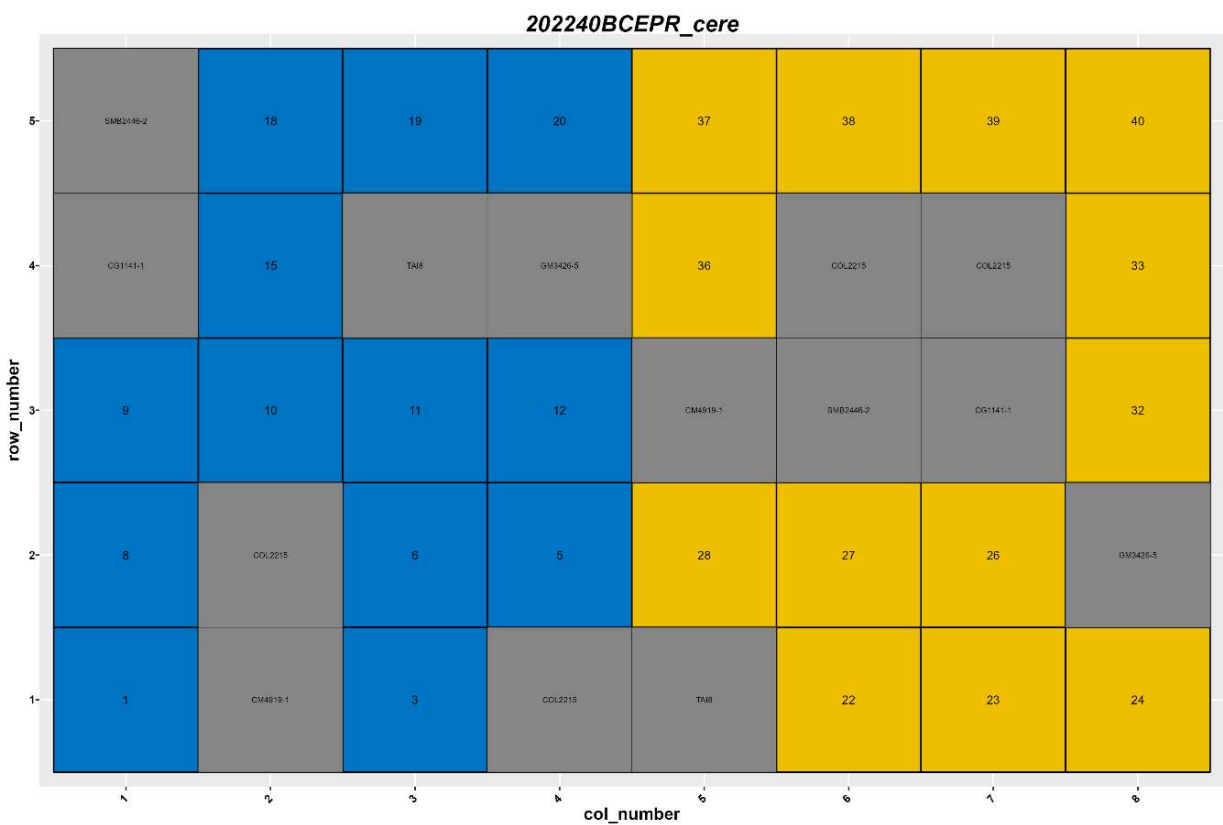
Check genotypes

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

Percentage of missing values (exp/trait)
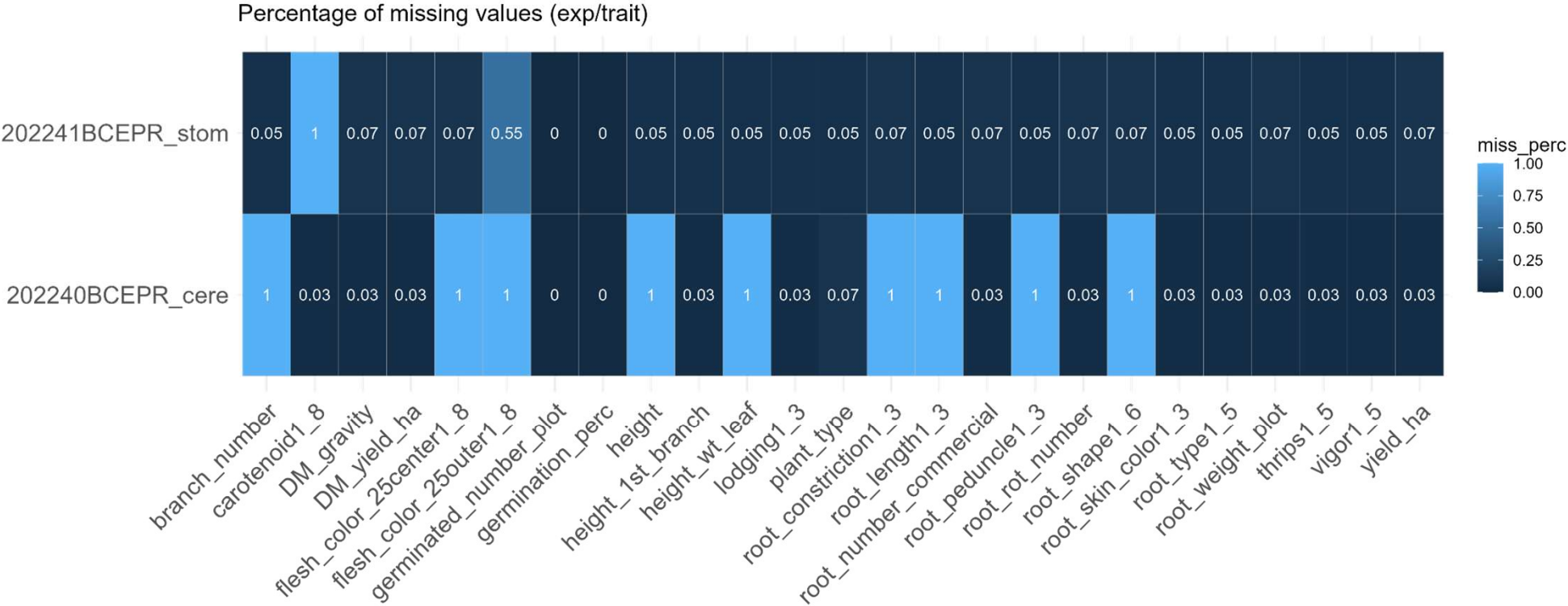
Trait variation across trials (phenotypic value)
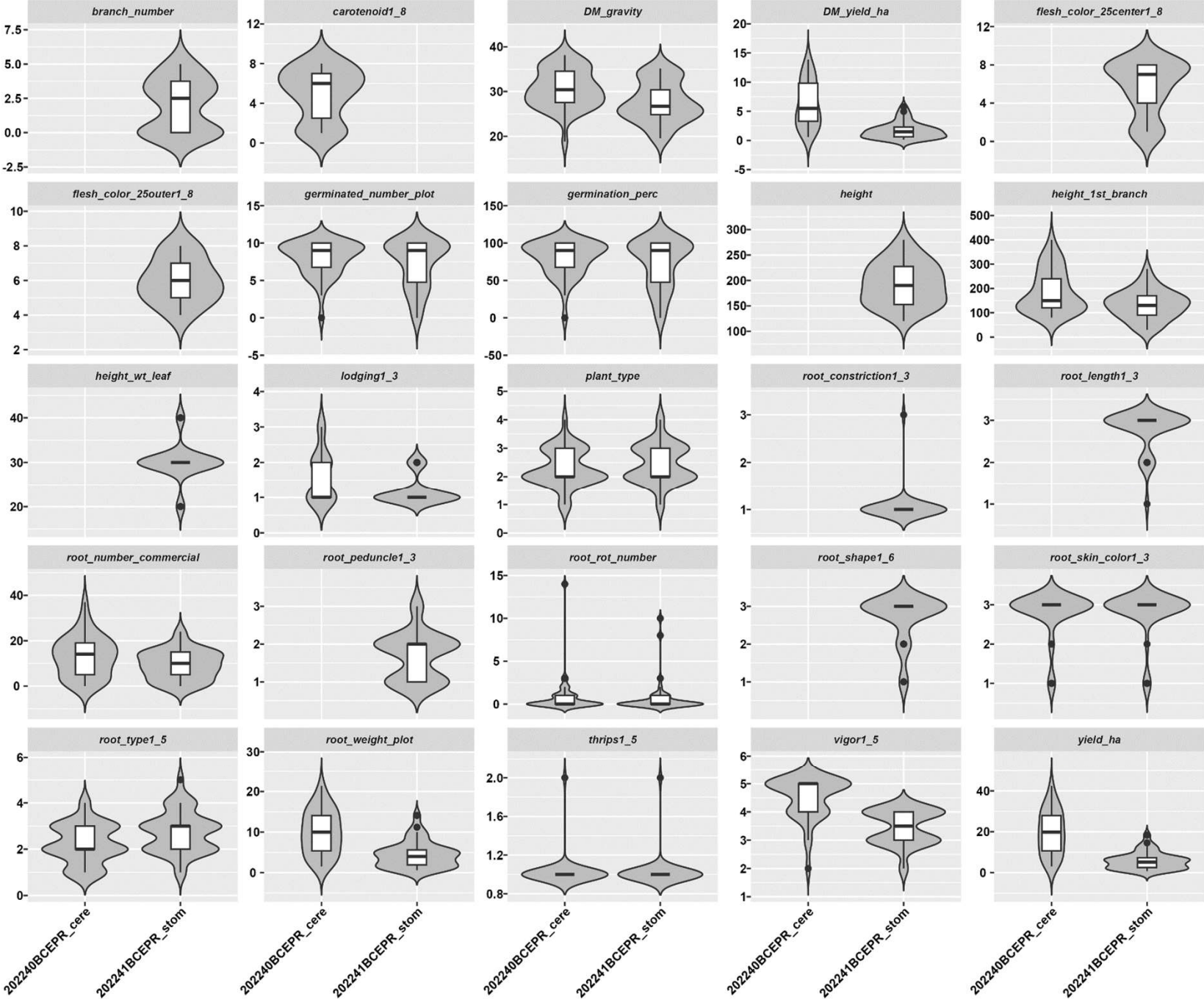
Shared genotypes

19 shared genotypes found.

Connectivity Matrix

	202240BCEPR_cere	202241BCEPR_stom
202241BCEPR_stom	19	19
202240BCEPR_cere	19	19

Multiple corr trait (phenotypic value)

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	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
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

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

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

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

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202240BCEPR_cere – plant_type
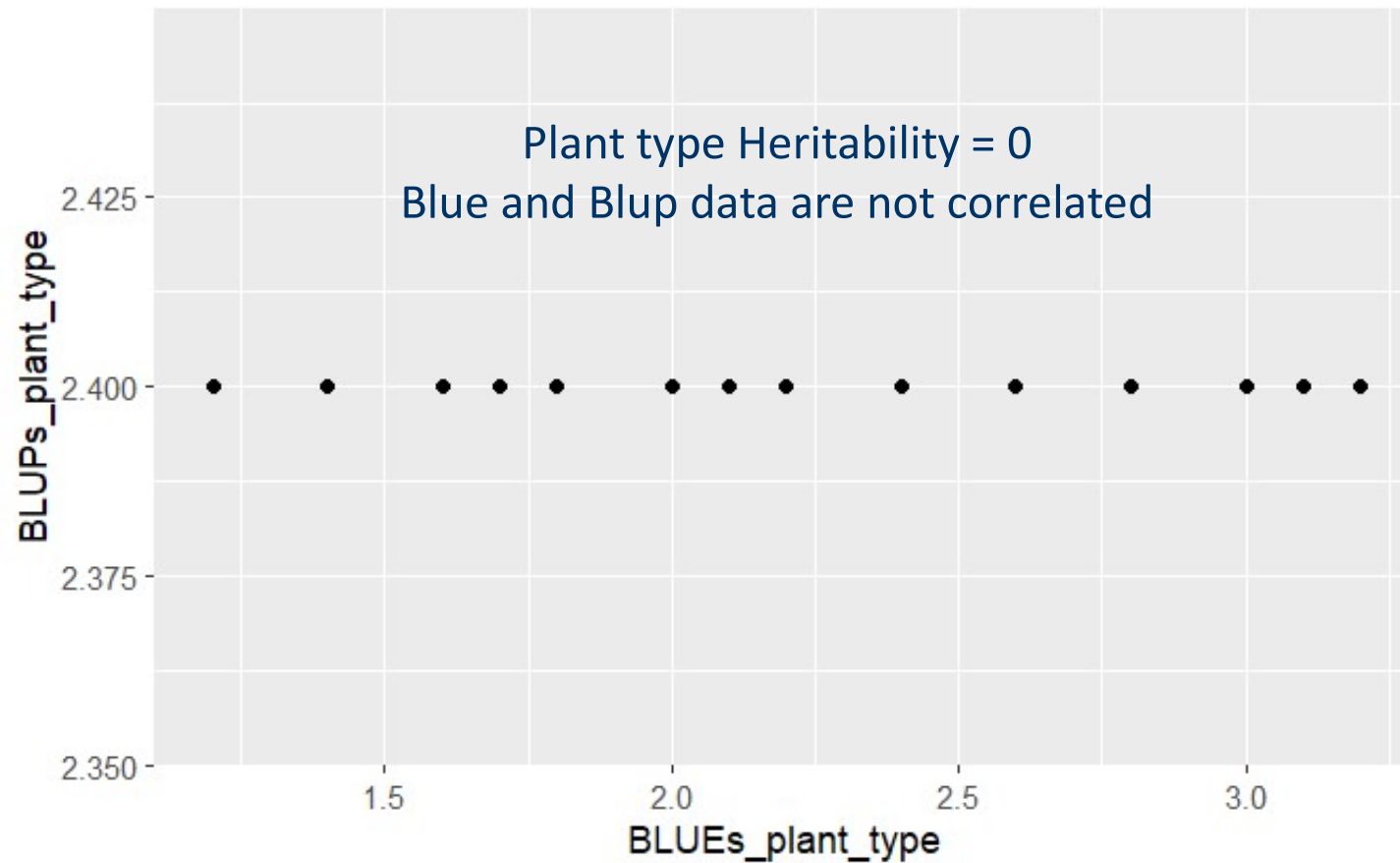
Plant_type single heritability of trial 202240BCEPR_cere does not make sense because height_1st_branch heritability is high. (These two traits are strongly correlated).
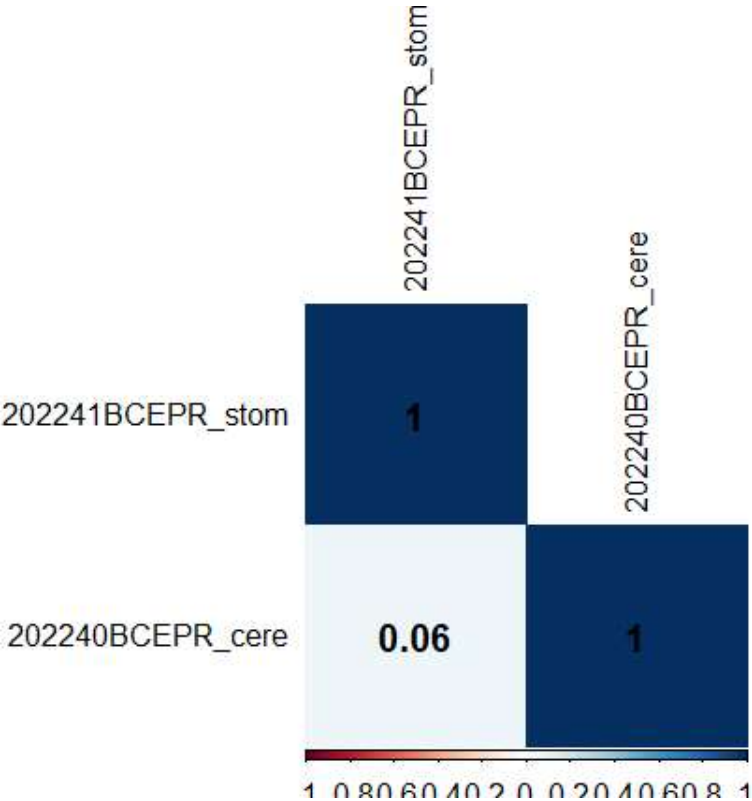
The plant_type data may have a systematic error.

Heritability gxe all trials

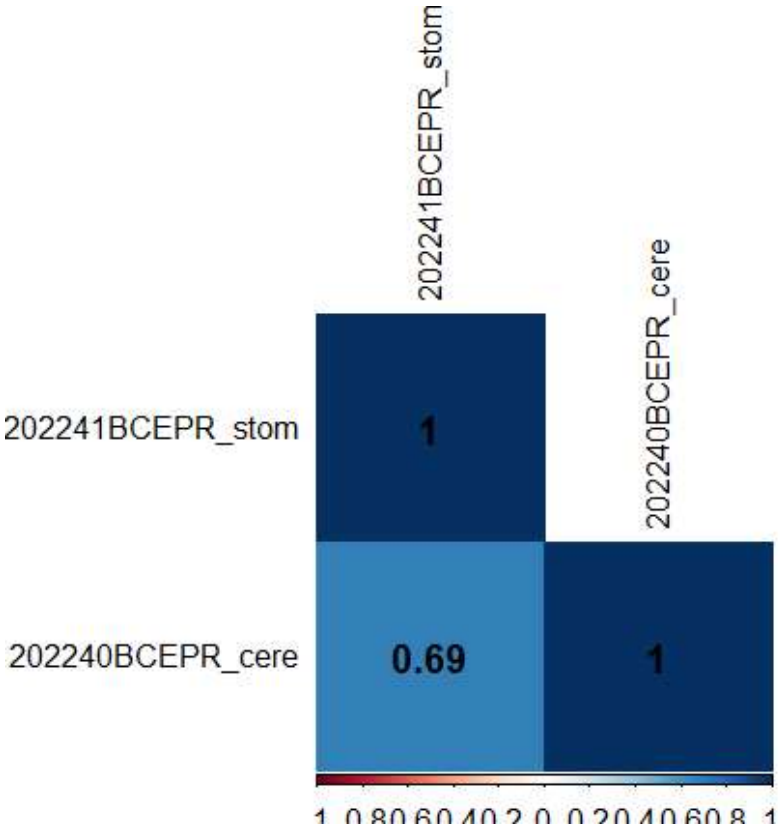| trait	h2
DM_gravity	0.91
root_skin_color1_3	0.81
height_1st_branch	0.72
germinated_number_plot	0.69
germination_perc	0.69
DM_yield_ha	0.6
root_number_commercial	0.44
root_type1_5	0.16
root_weight_plot	0
yield_ha	0
vigor1_5	0

🚧 For traits with low heritability, please be **careful**. (blue square)
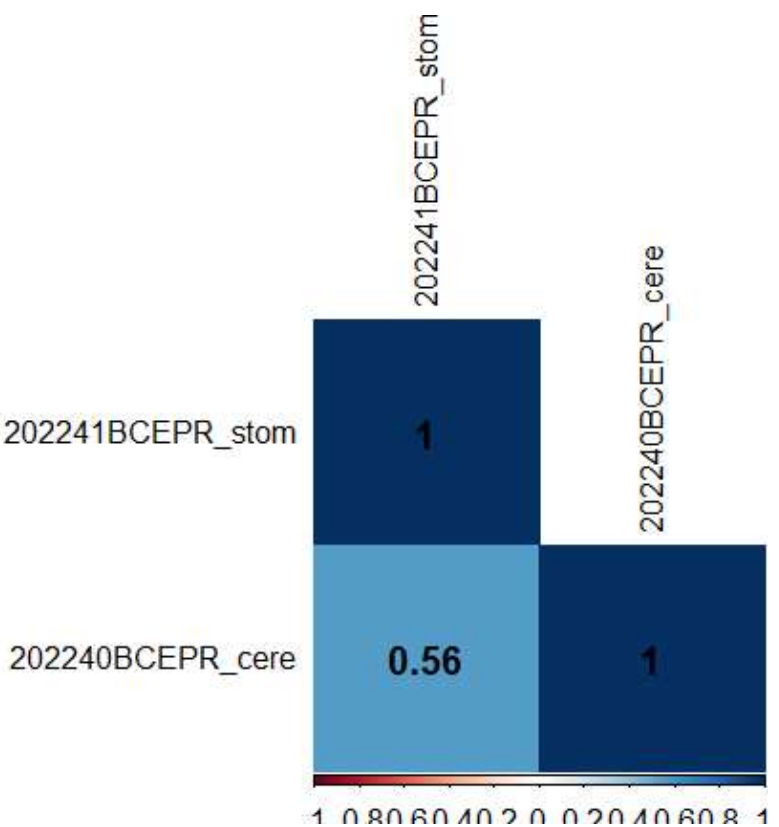
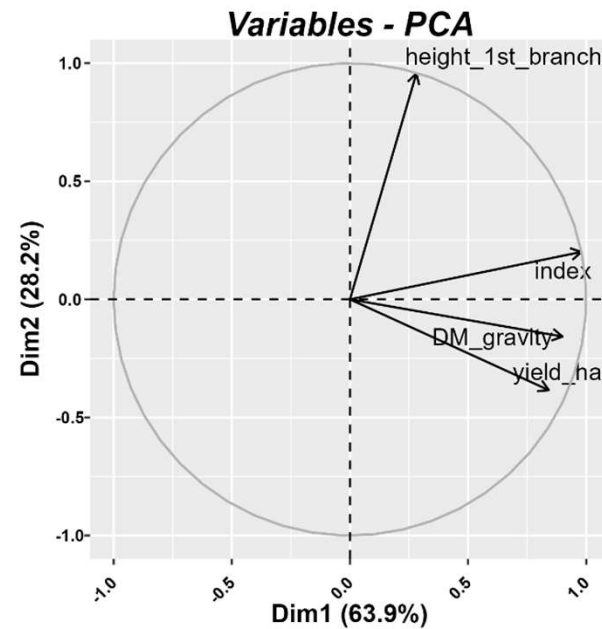# Genotypic Correlation: Locations

Genotypic Correlation: Trials

Selection comments

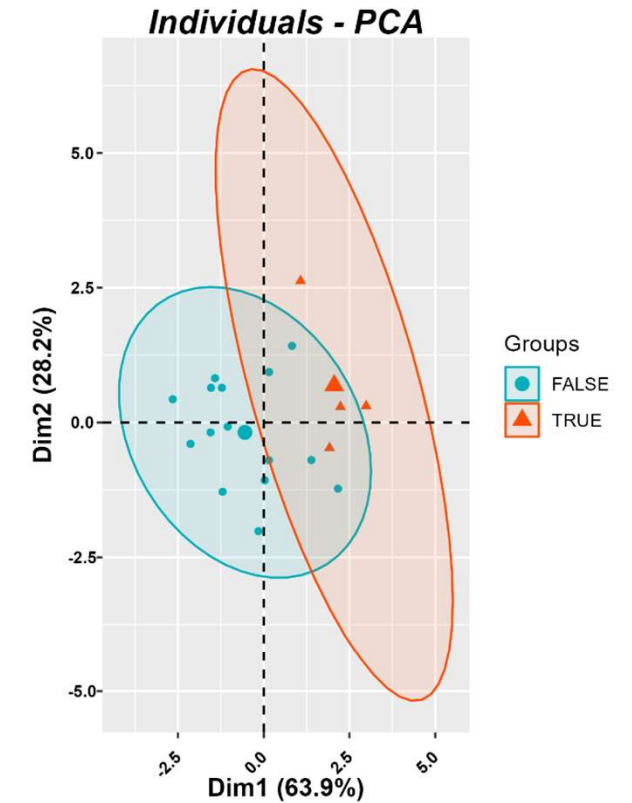1) **DM_gravity**, **plant_type** & **yield_ha** were used to calculate index selection.

2) Scores given were:
   - DM_gravity = 10
   - height_1st_branch = 10
   - yield_ha = 10

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

Thank you!