



Data analysis DVGST 7 environments

Year 2022

- 202256DVGST_stom
- 202257DVGST_momi
- 202258DVGST_ciat (Hasn't yet been harvested)
- 202271DVGST_ciat

Year 2021

- 202151DVGST_ciat
- 202176DVGST_repe
- 202177DVGST_momi

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Palmira, June 2022



@BiovIntCIAT_eng
@BiovIntCIAT_esp

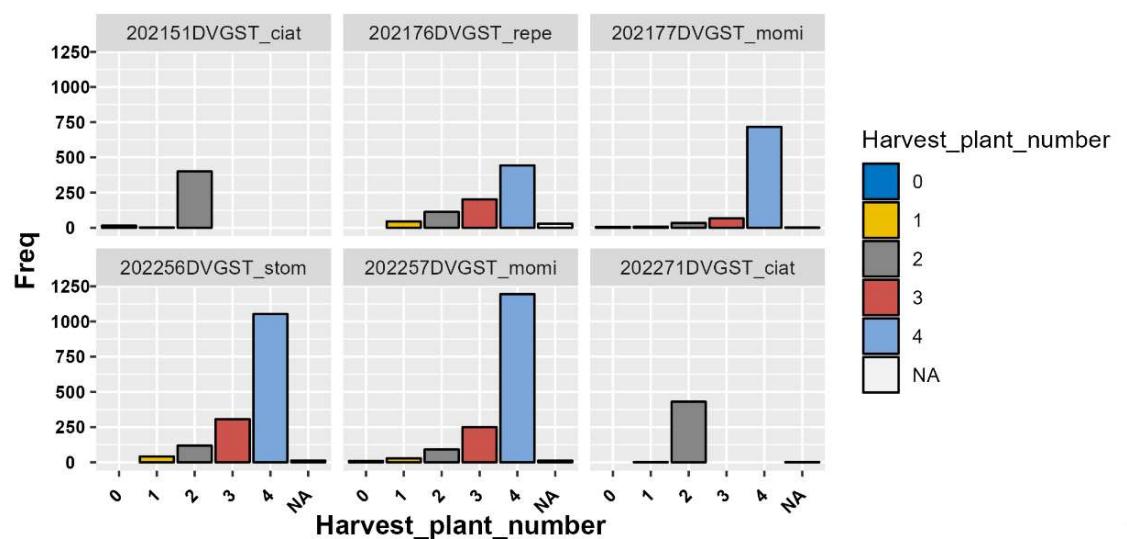
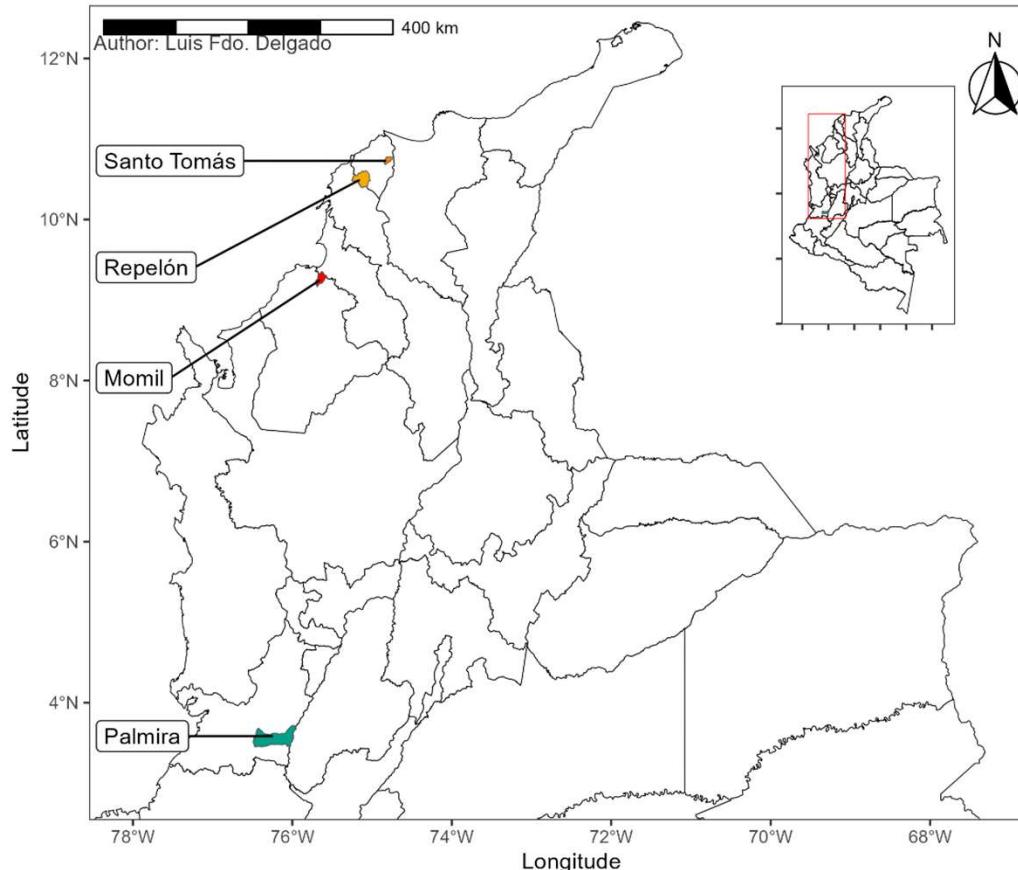
#Alliance4Science

Resolvable row-col with randomized checks

use_trial_name	use_plant_date	use_harvest_date	harvesting_time	use_location	n_gen
202151DVGST_ciat	2021-August-12	2022-June-30	10month 18day	CIAT. Valle, Colombia	407
202176DVGST_repe	2021-July-07	2022-April-04	8month 28day	Repelon. Atlantico, Colombia	411
202177DVGST_momi	2021-July-03	2022-March-30	8month 27day	Momil. Cordoba, Colombia	410
202256DVGST_stom	2022-July-15	2023-April-03	8month 19day	Santo Tomas. Atlantico, Colombia	758
202257DVGST_momi	2022-July-22	2023-April-17	8month 26day	Momil. Cordoba, Colombia	787
202271DVGST_ciat	2022-August-10	2023-June-20	10month 10day	CIAT. Valle, Colombia	398

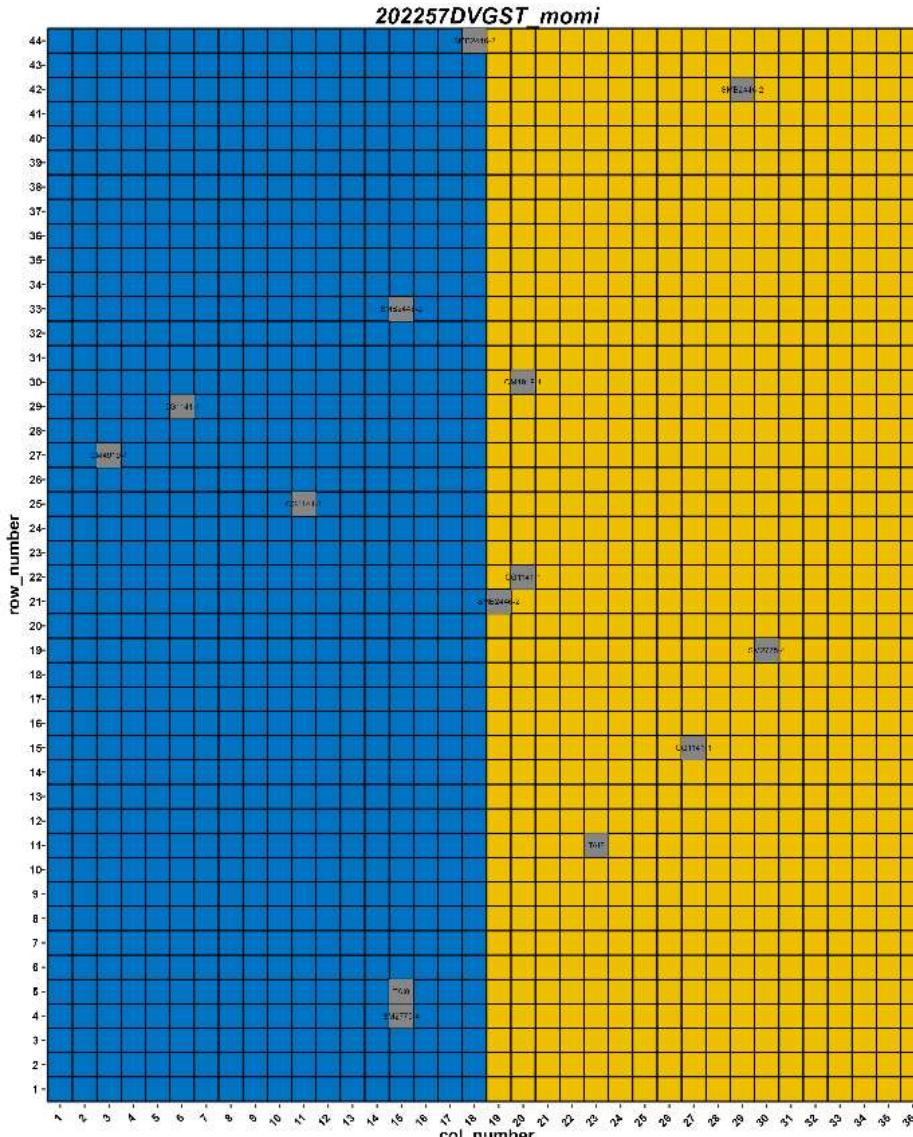
Plot size:

- 202151DVGST_ciat, **4** plants per plot, harvesting **2** plants for root_type
- 202176DVGST_repe, **4** plants per plot, harvesting **4** plants for yield
- 202177DVGST_momi, **4** plants per plot, harvesting **4** plants for yield
- 202256DVGST_stom, **5** plants per plot, harvesting **4** plants for yield
- 202257DVGST_momi, **5** plants per plot, harvesting **4** plants for yield
- 202171DVGST_ciat, **5** plants per plot, harvesting **2** plants for root_type

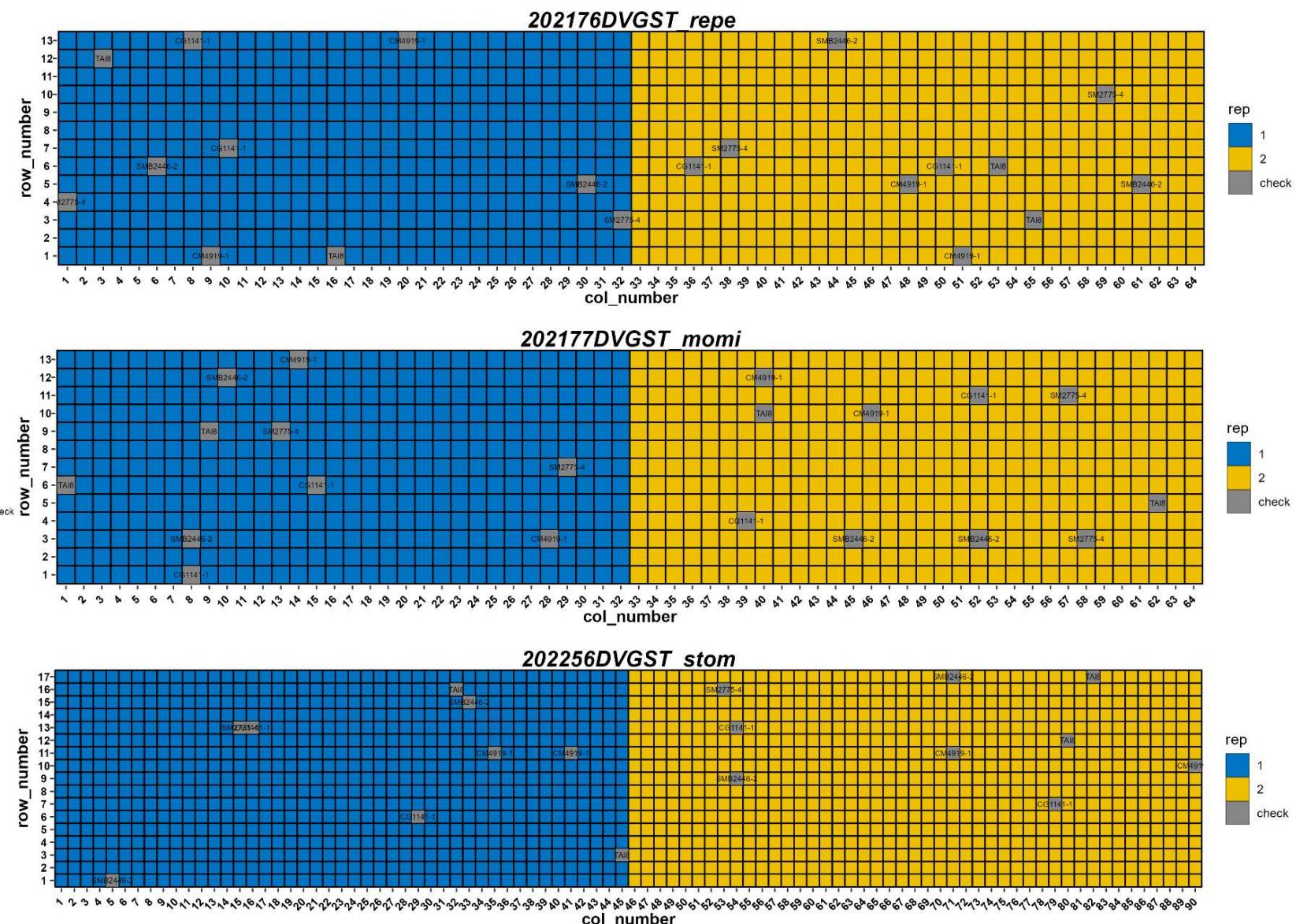


Trial Design in Nort Cost: Resolvable

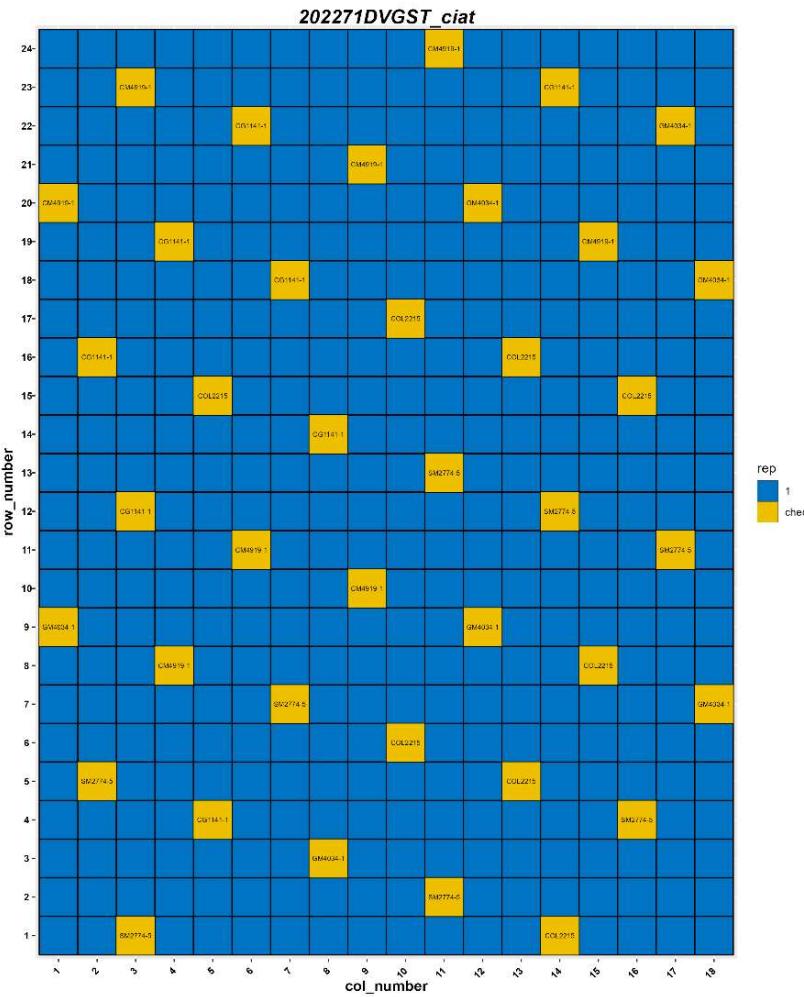
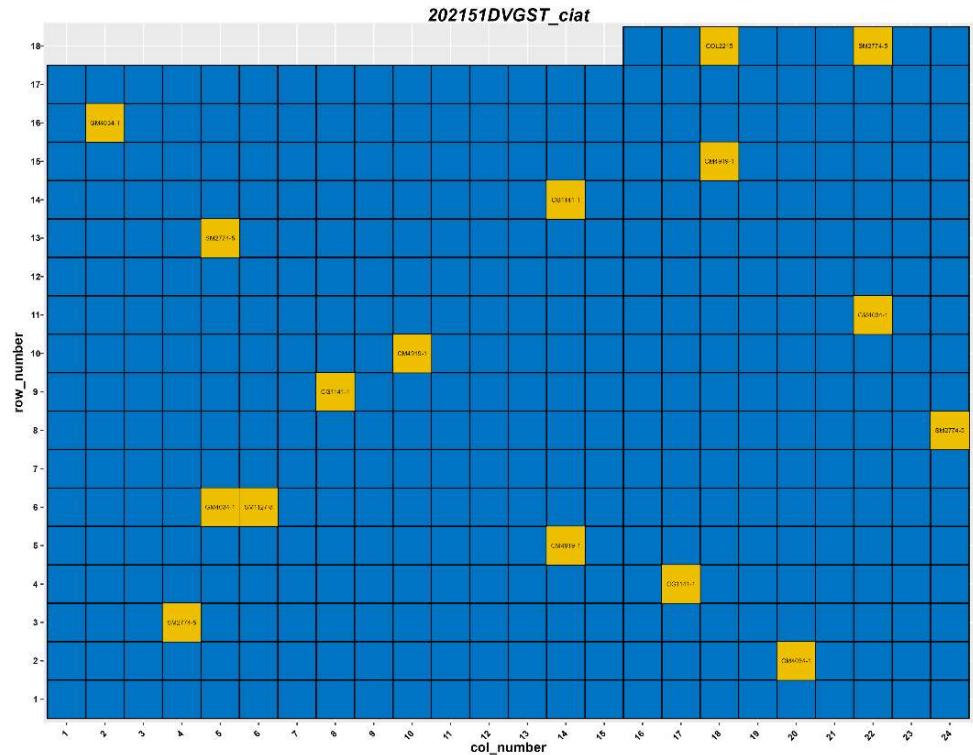
Row col



Check varieties are completely randomized

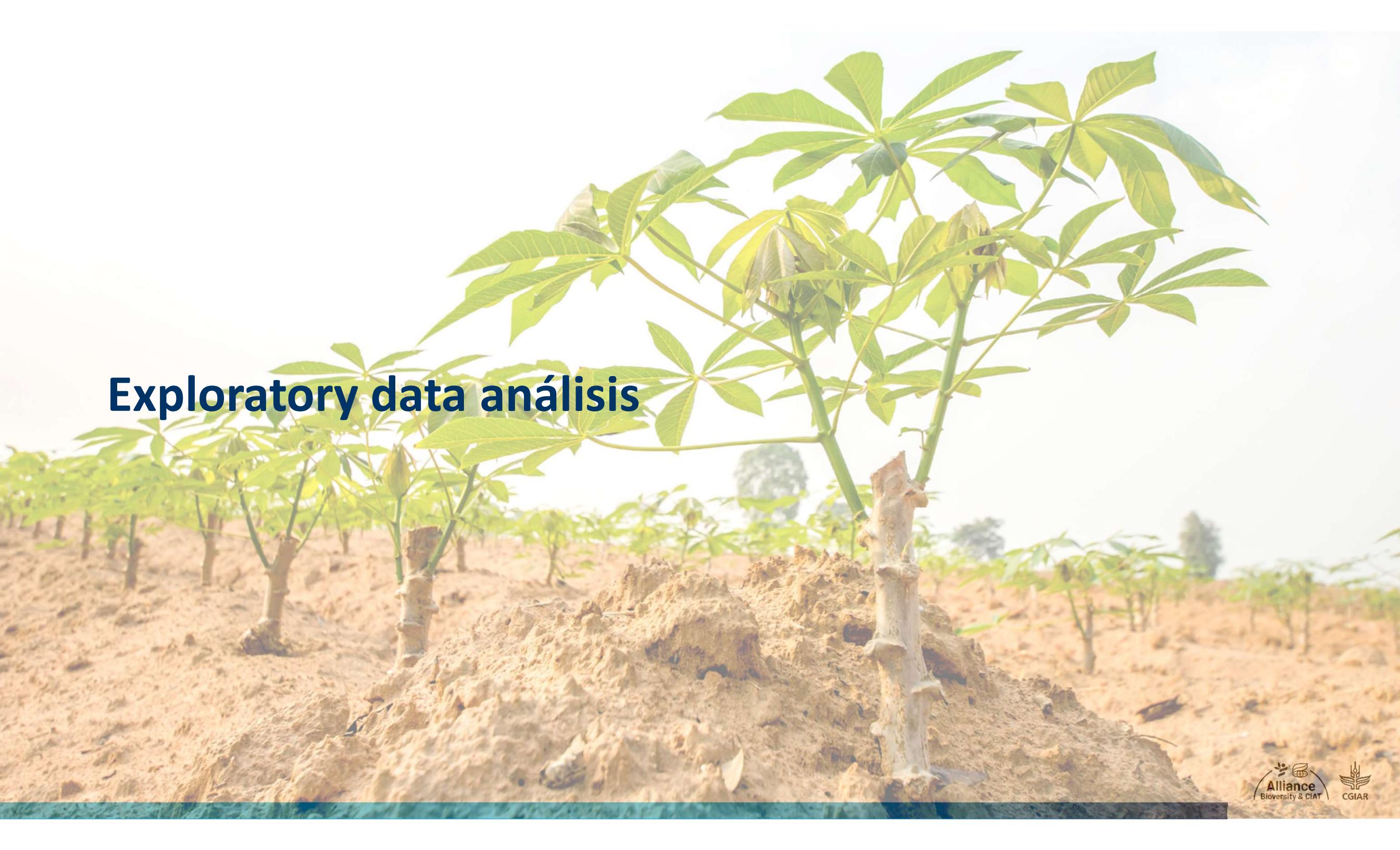


Trial Design in Palmira: Row - col



Check genotypes

1. CG1141-1_is_Costena
2. CM4919-1_is_Veronica
3. COL2215_is_Venezolana
4. HMC1P12_is_HMC1
5. SM1127-8_is_Cubana
6. SM2775-4_is_Bellotti
7. SMB2446-2_is_Caiseli
8. TAI8_is_TAI
9. GM4034-1_is_Reina_wx
10. CM6438-14_is_Vergara



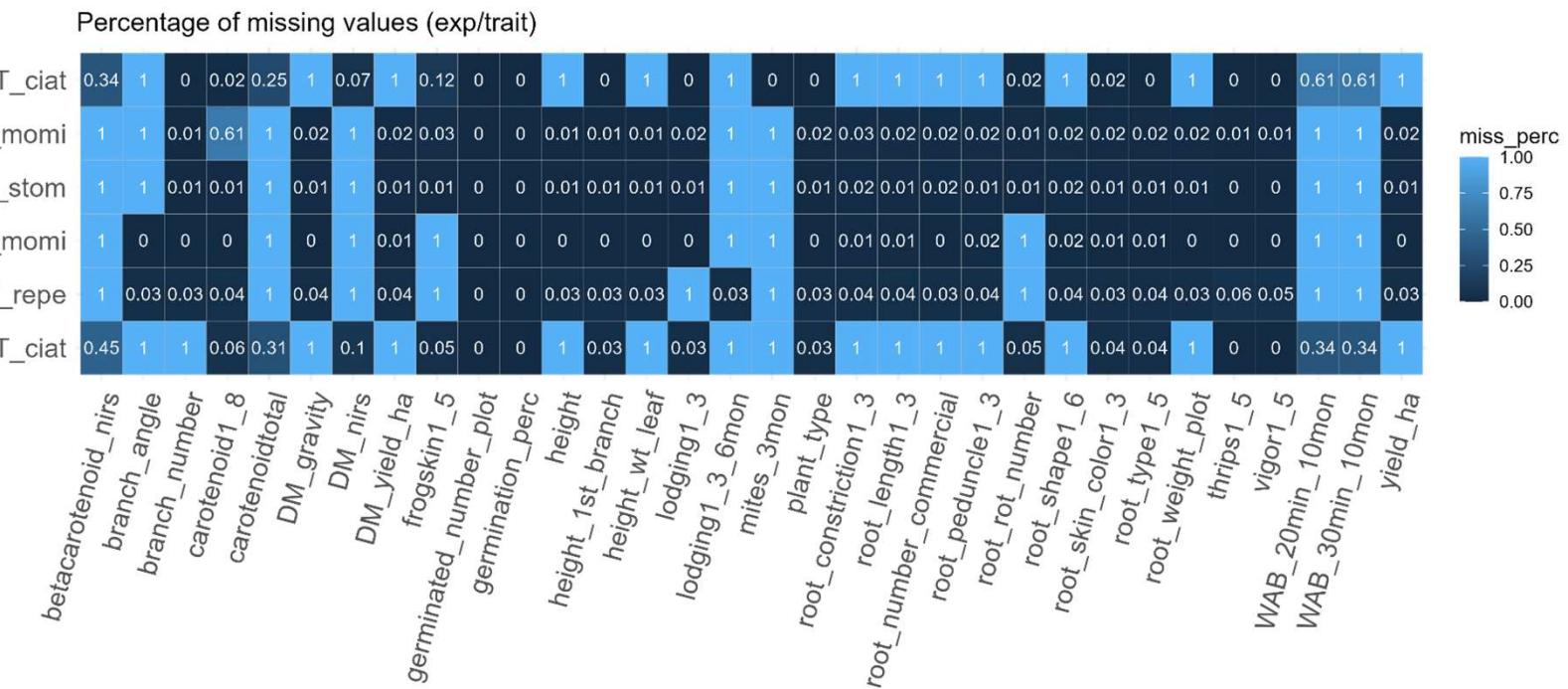
Exploratory data análisis

Traits evaluated

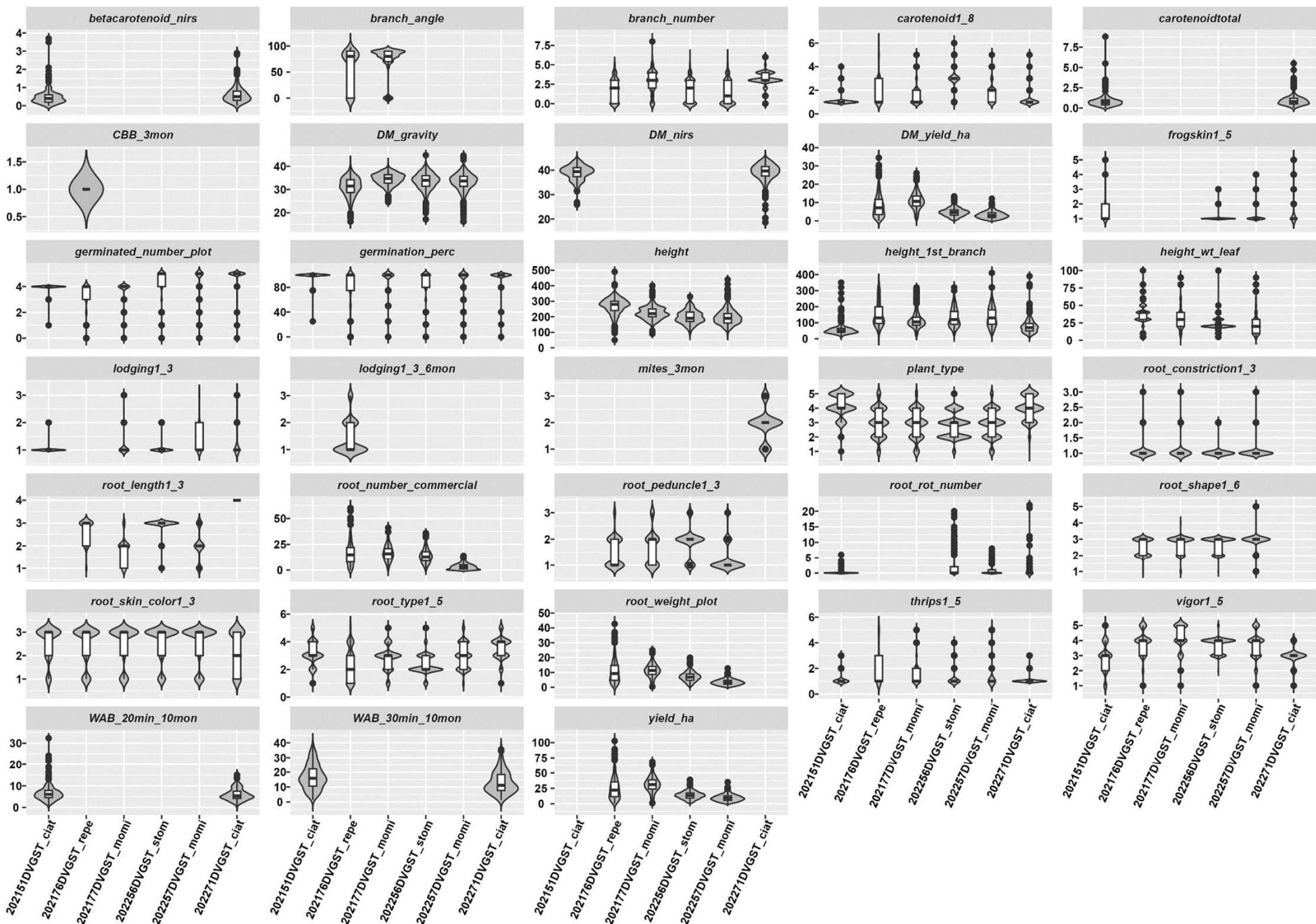
Assessed agronomic traits

WAB_20min_12mon
WAB_30min_12mon
branch_angle
branch_number
DM_gravity
DM_nirs
height_1st_branch
yield_ha
germination_perc
DM_yield_ha
root_weight_plot
frogskin1_5
vigor1_5
lodging1_3
lodging1_3_6mon
root_number_commercial
plant_type
height
height_wt_leaf
root_skin_color1_3
root_constriction1_3
root_type1_5
root_length1_3
root_rot_number
germinated_number_plot
root_peduncle1_3
root_shape1_6
thrips1_5
carotenoid1_8

Missing values across trials



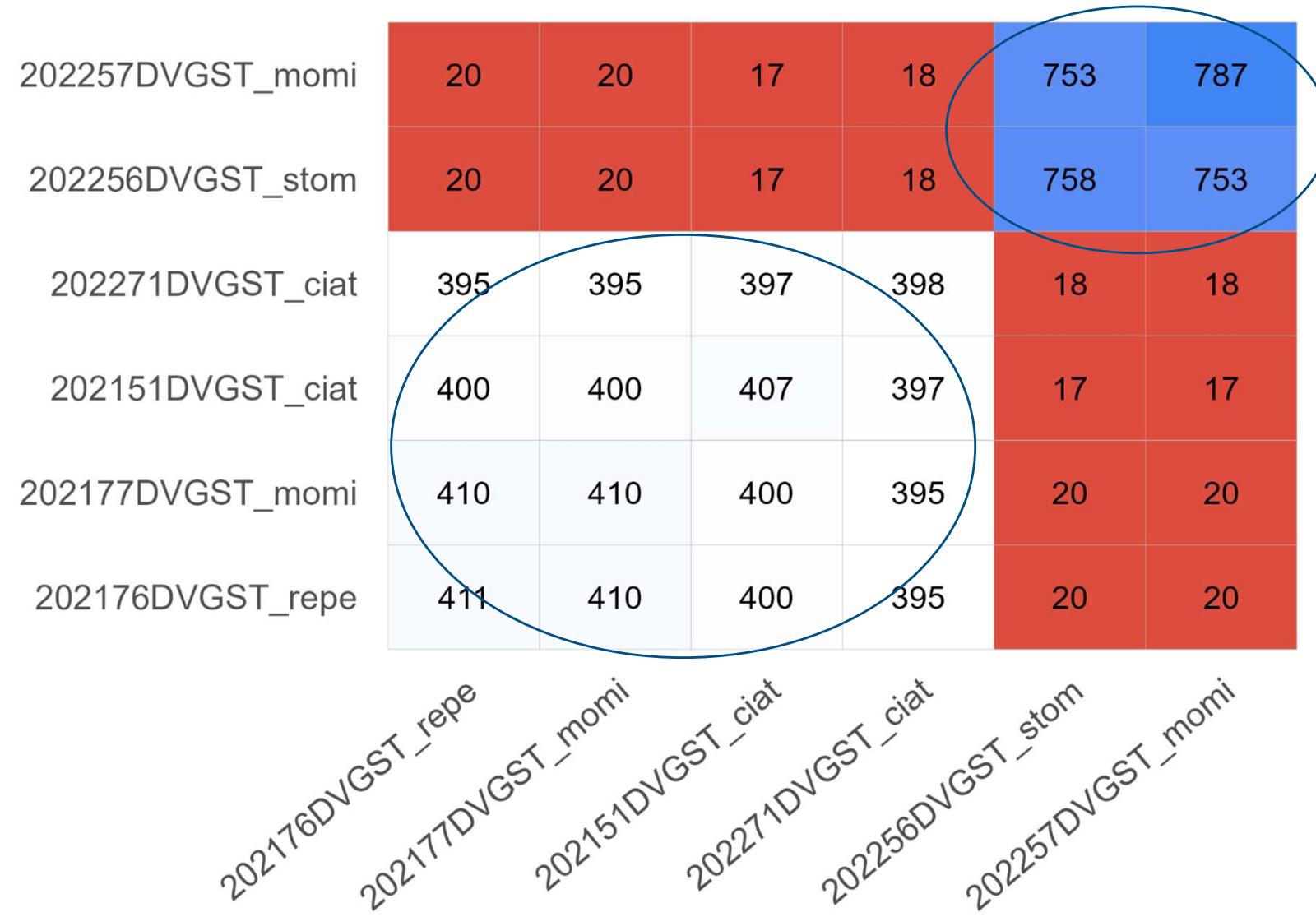
Trait variation across trials (phenotypic value)



Shared genotypes

2 common genotype groups found.

Connectivity Matrix



Multiple corr trait (phenotypic value)

Statistical data analysis

Dropped traits

CBB_3mon



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

Single heritability

Moderate to high heritability among two locations.

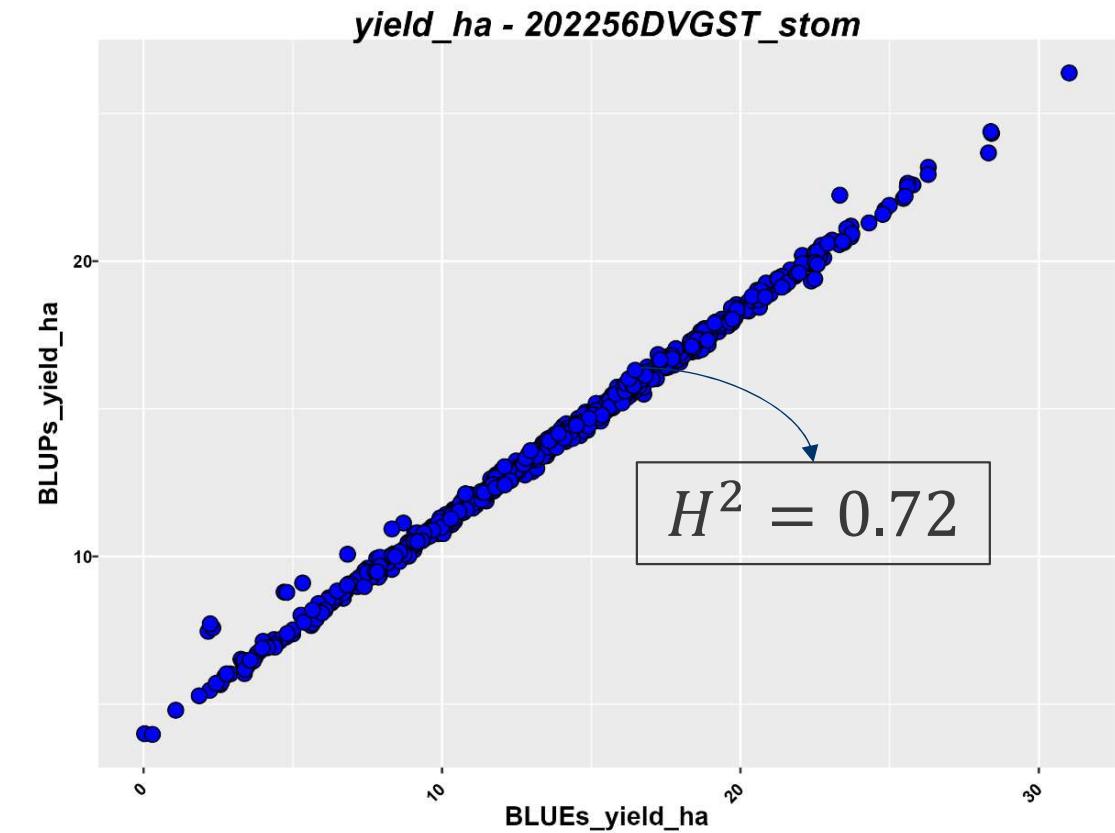
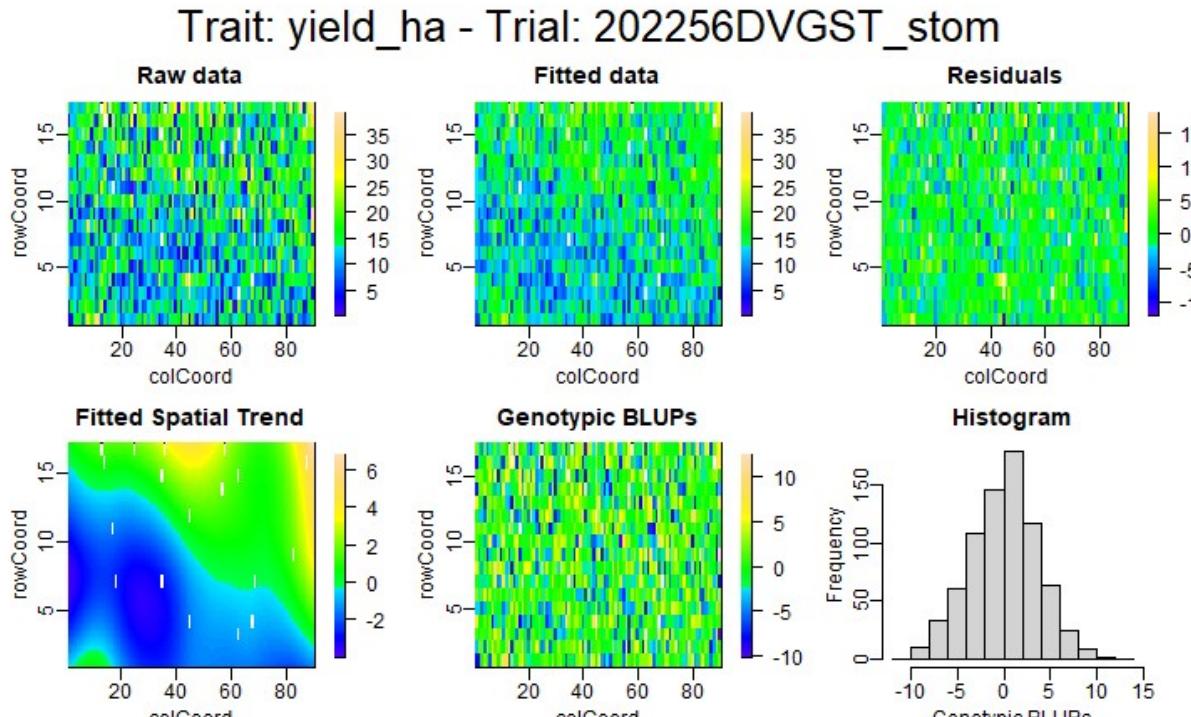
trial	branch_angle	branch_number	caroteno_id1_8	DM_gravity	DM_yield_id_ha	frogskin_n1_5	germinated_number_plot	germination_n_perc	height_ht	height_1st_branch	height_wt_leaf	lodging_g1_3	lodging1_3_6mon	plant_type	root_constriction1_3	root_length_gth1_3	root_number_commercial	root_peduncle1_3	root_rotation_number	root_shape1_6	root_skin_color1_3	root_type1_5	root_weight_ht_plot	thrips_vigor1_5	vigor1_5	yield_ha	
202176DVG ST_repe	0.82	0.87	0.61	0.74	0.72		0.69	0.69	0.86	0.82	0.58		0.57	0.72	0.25	0.42	0.62	0.41		0.35	0.96	0.64	0.72	0.1	0.07	0.72	
202177DVG ST_momi	0.83	0.77	0.58	0.86	0.83		0.54	0.54	0.8	0.85	0.58	0.5		0.63	0.51	0.54	0.67	0.76		0.67	0.96	0.69	0.82	0.49	0.53	0.82	
202256DVG ST_stom		0.87	0.67	0.82	0.71	0.81		0.68	0.68	0.88	0.86	0.53	0.37		0.66	0.04	0.42	0.07	0.61	0.36	0.03	0.96	0.62	0.71	0.88	0.52	0.72
202257DVG ST_momi		0.79		0.71	0.69	0.3		0.69	0.69	0.63	0.73	0.52	0.01		0.01	0.04	0.28	0.49	0.16	0.15	0.19	0.95	0.58	0.7	0.58	0.7	

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

GxE analysis was performed without following traits - trials:

- **lodging1_3**: 202257DVGST_momi
- **plant_type**: 202257DVGST_momi
- **lodging1_3_6mon**: (only one trait to fit).
- **root_constriction1_3**: 202257DVGST_momi & 202256DVGST_stom
- **root_number_commercial**: 202256DVGST_stom
- **root_shape1_6**: 202256DVGST_stom
- **vigor1_5**: 202176DVGST_repe

Single heritability - yield_ha - 202256DVGST_stom



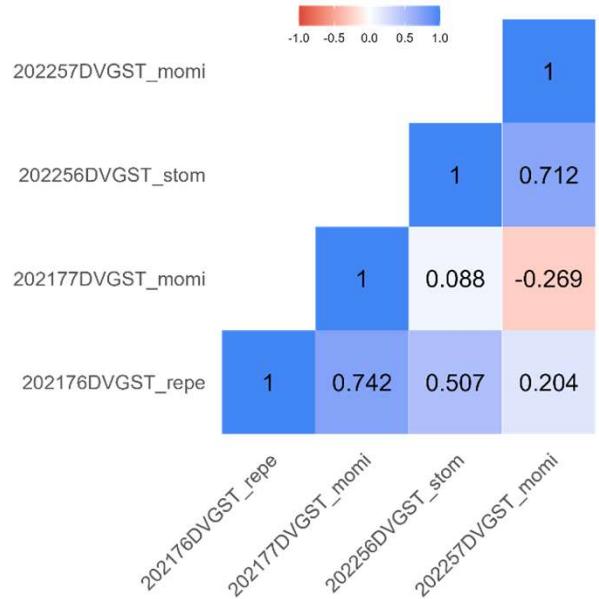
Heritability gxe all trials

trait	h2
root_skin_color1_3	0.97
height	0.84
branch_angle	0.84
DM_gravity	0.75
germinated_number_plot	0.73
germination_perc	0.72
frogskin1_5	0.71
height_1st_branch	0.71
branch_number	0.65
carotenoid1_8	0.61
thrips1_5	0.61
root_peduncle1_3	0.51
vigor1_5	0.47
height_wt_leaf	0.44
plant_type	0.43
root_length1_3	0.4
lodging1_3	0.26
DM_yield_ha	0.17
root_type1_5	0.17
root_weight_plot	0.15
yield_ha	0.12
root_shape1_6	0
root_constriction1_3	0
root_number_commercial	0
root_rot_number	0

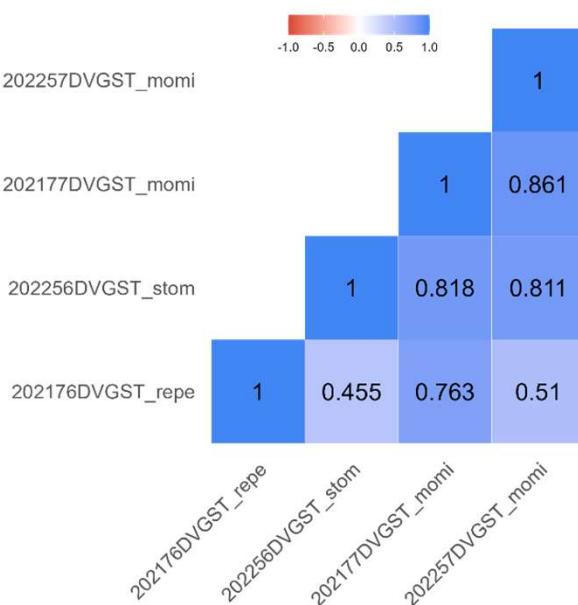
For traits with low heritability, please be **careful.** (blue square)

Genotypic Correlation: Locations

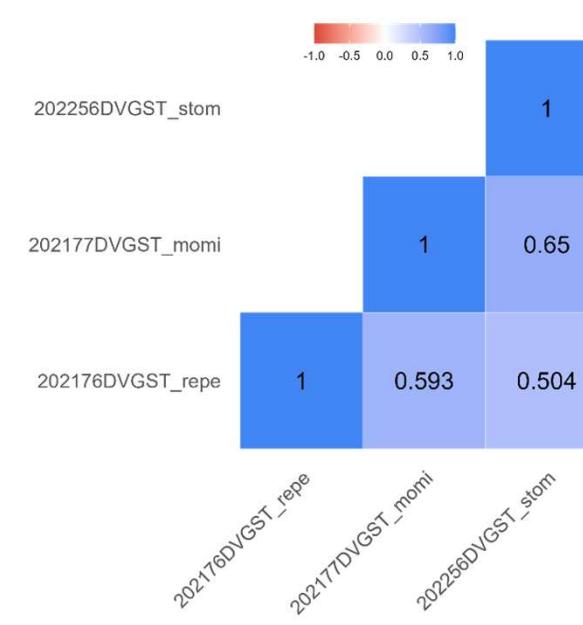
Yield



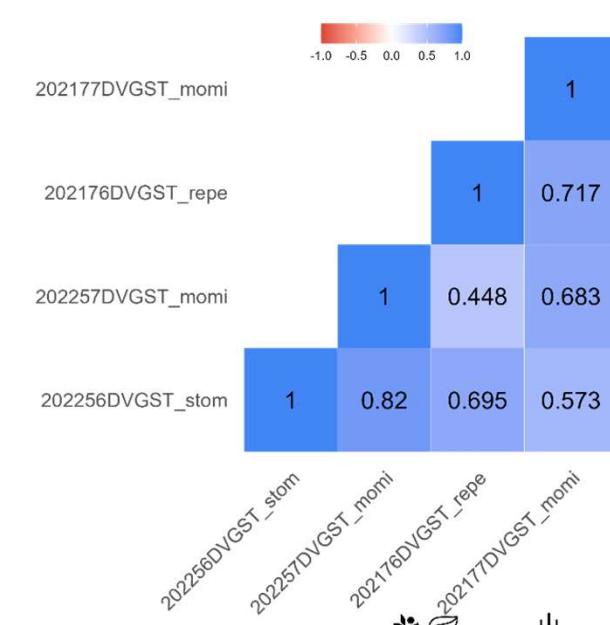
Dry Matter



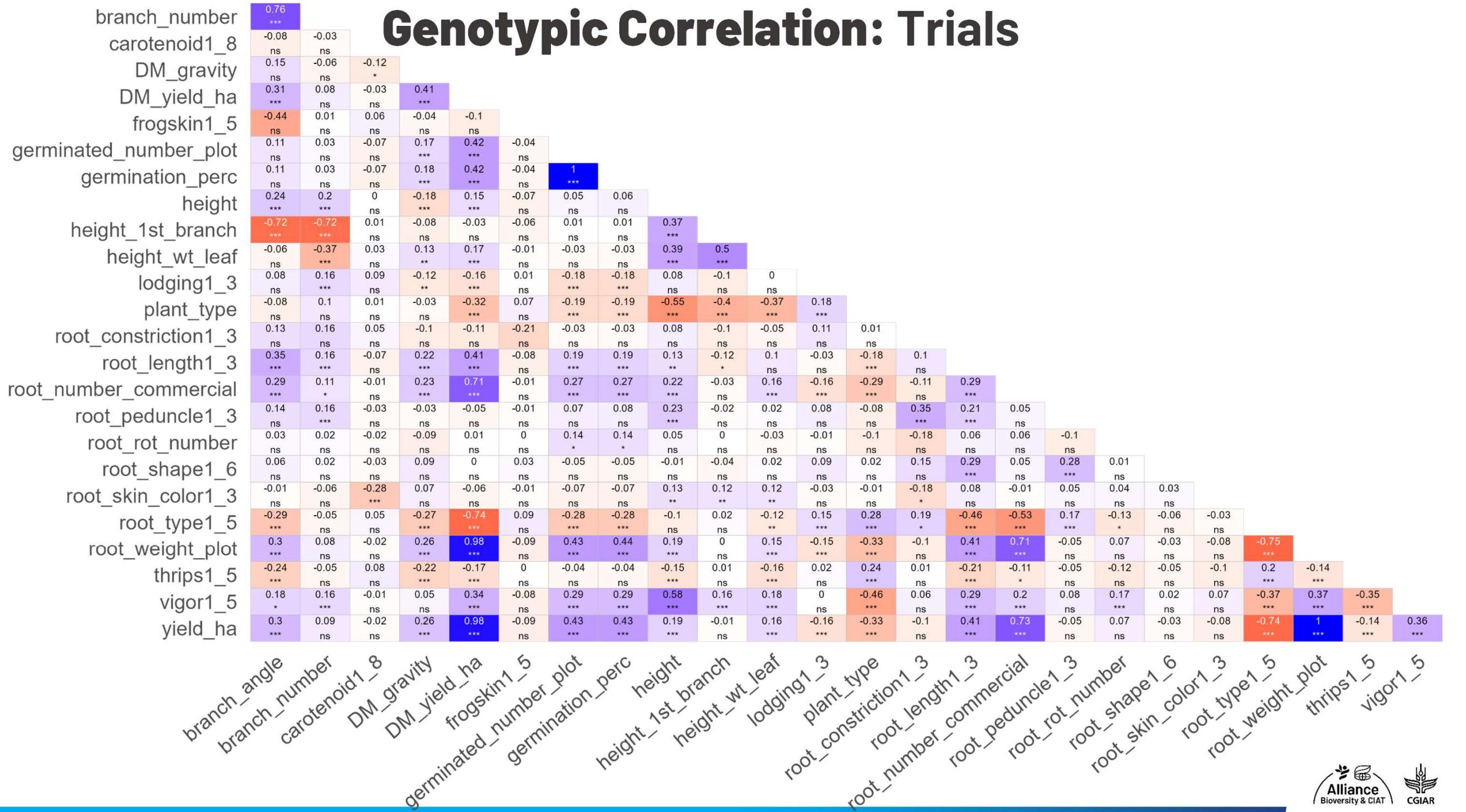
Plant type



height_1st_branch



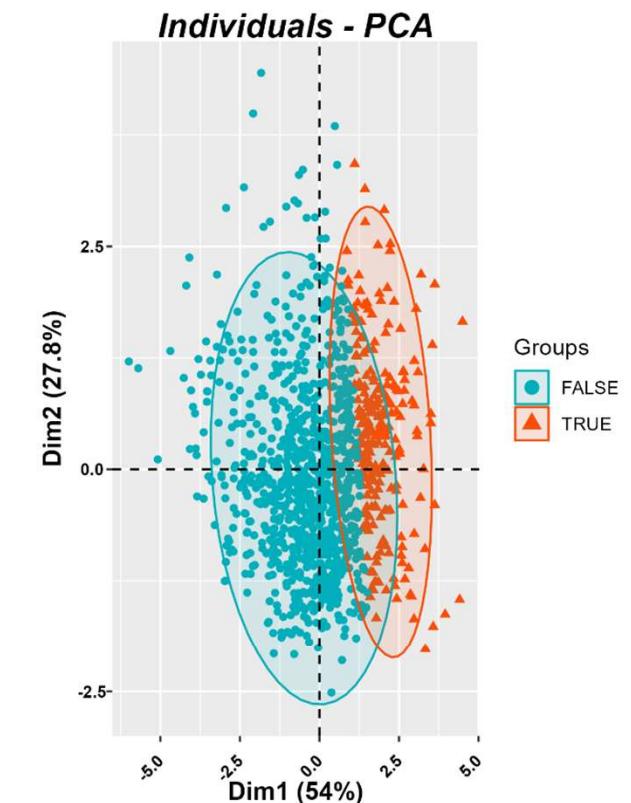
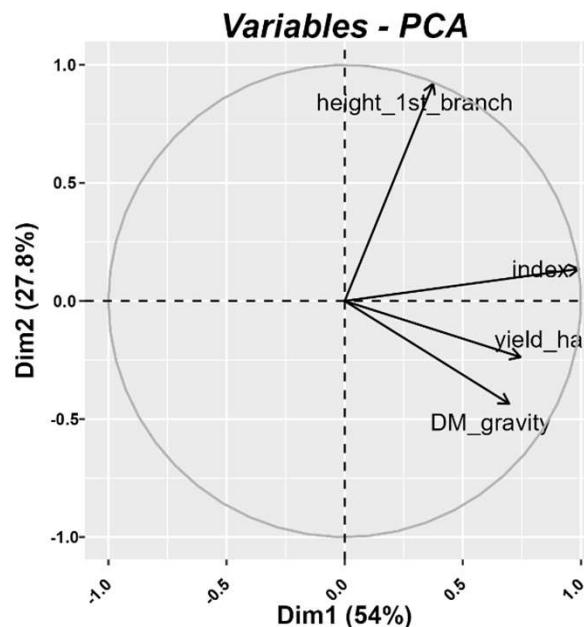
Genotypic Correlation: Trials



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!