



Data analysis IDEPR 3 environments

Year 2022

- 202268IDEPR_cere
- 202267IDEPR_repe
- 202266IDEPR_ciati (has not yet been harvested)

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Palmira, June 2022

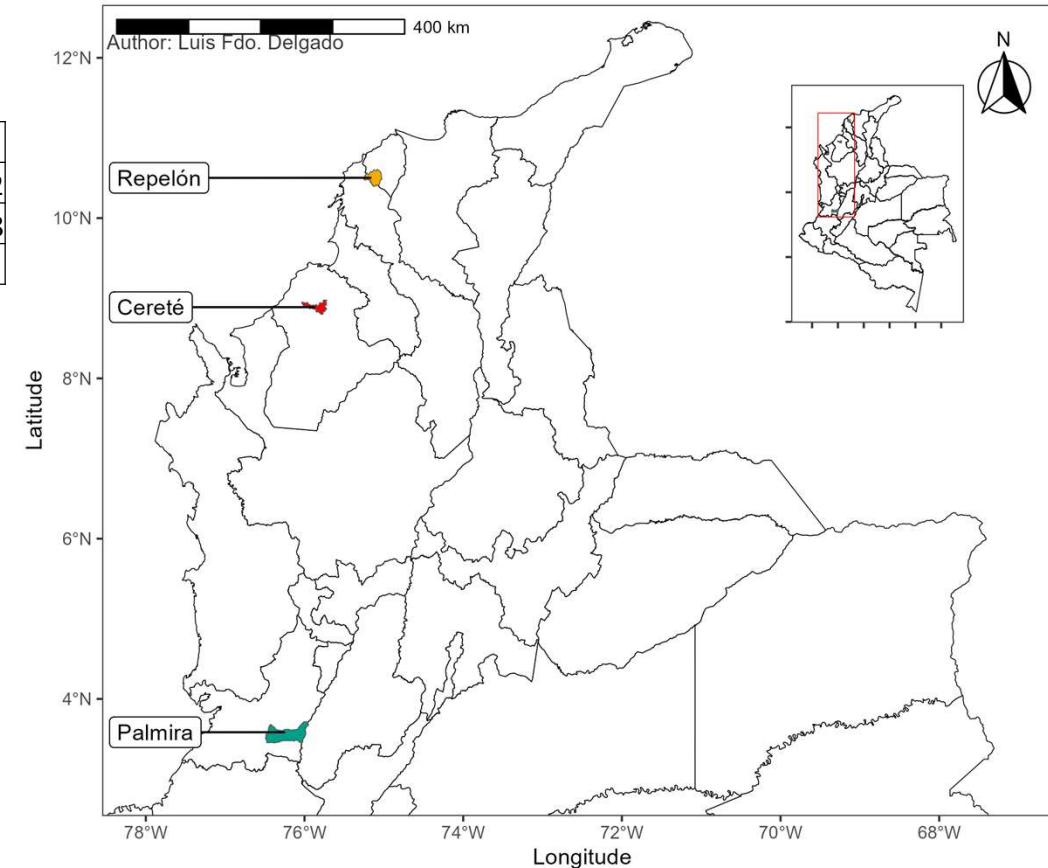


@BiovIntCIAT_eng
@BiovIntCIAT_esp

#Alliance4Science

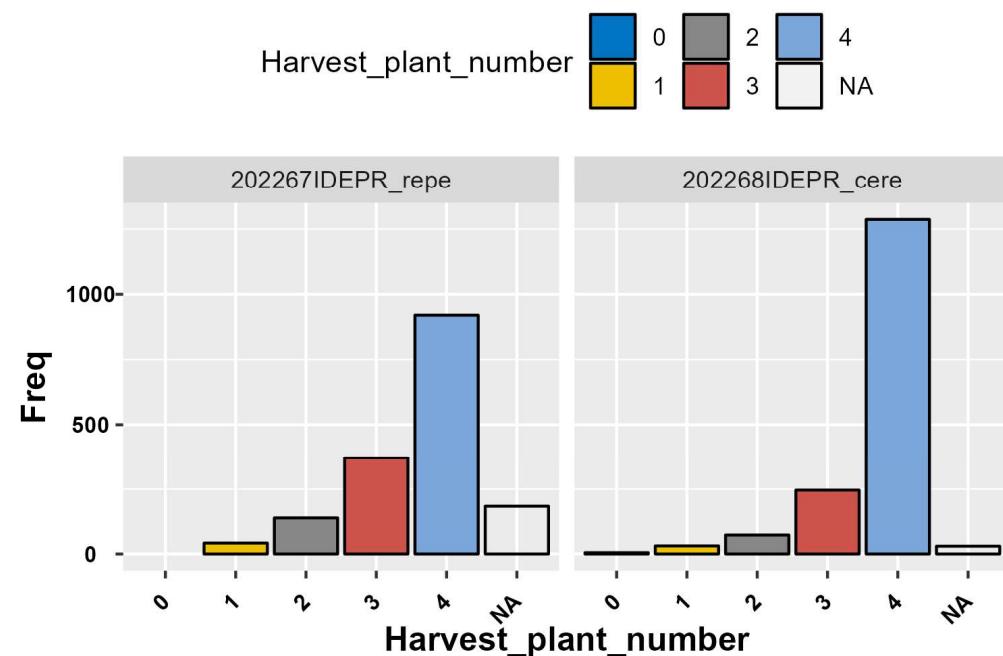
Resolvable row-col with randomized checks

use_trial_name	use_plant_date	use_harvest_date	harvesting_time	use_location	n_gen
202267IDEPR_repe	2022-July-25	2023-April-17	8month 23day	Repelon. Atlantico, Colombia	822
202268IDEPR_cere	2022-July-29	2023-April-18	8month 20day	Cerete. Cordoba, Colombia	828
202266IDEPR_ciat					



Plot size:

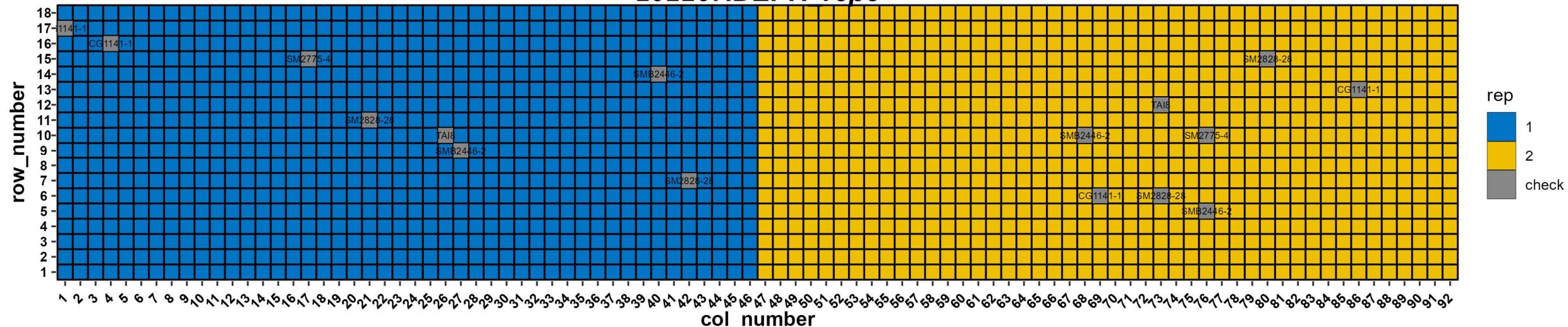
- 202267IDEPR_repe, 4 plants per plot, harvesting 4 plants for yield
- 202268IDEPR_cere, 4 plants per plot, harvesting 4 plants for yield



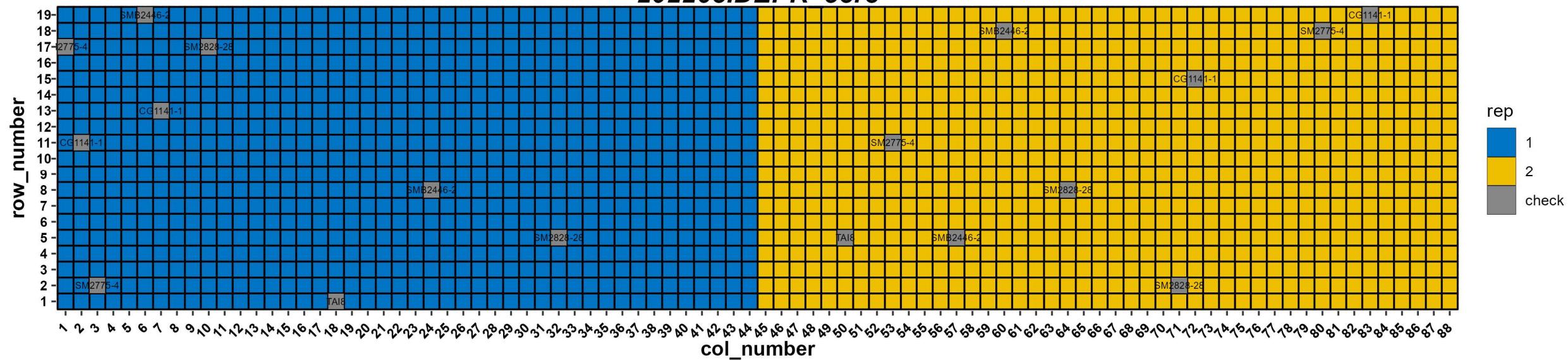
Trial Design – Row col

Check varieties are completely randomized

202267 IDEPR repe



202268 IDEPR cere



Check genotypes

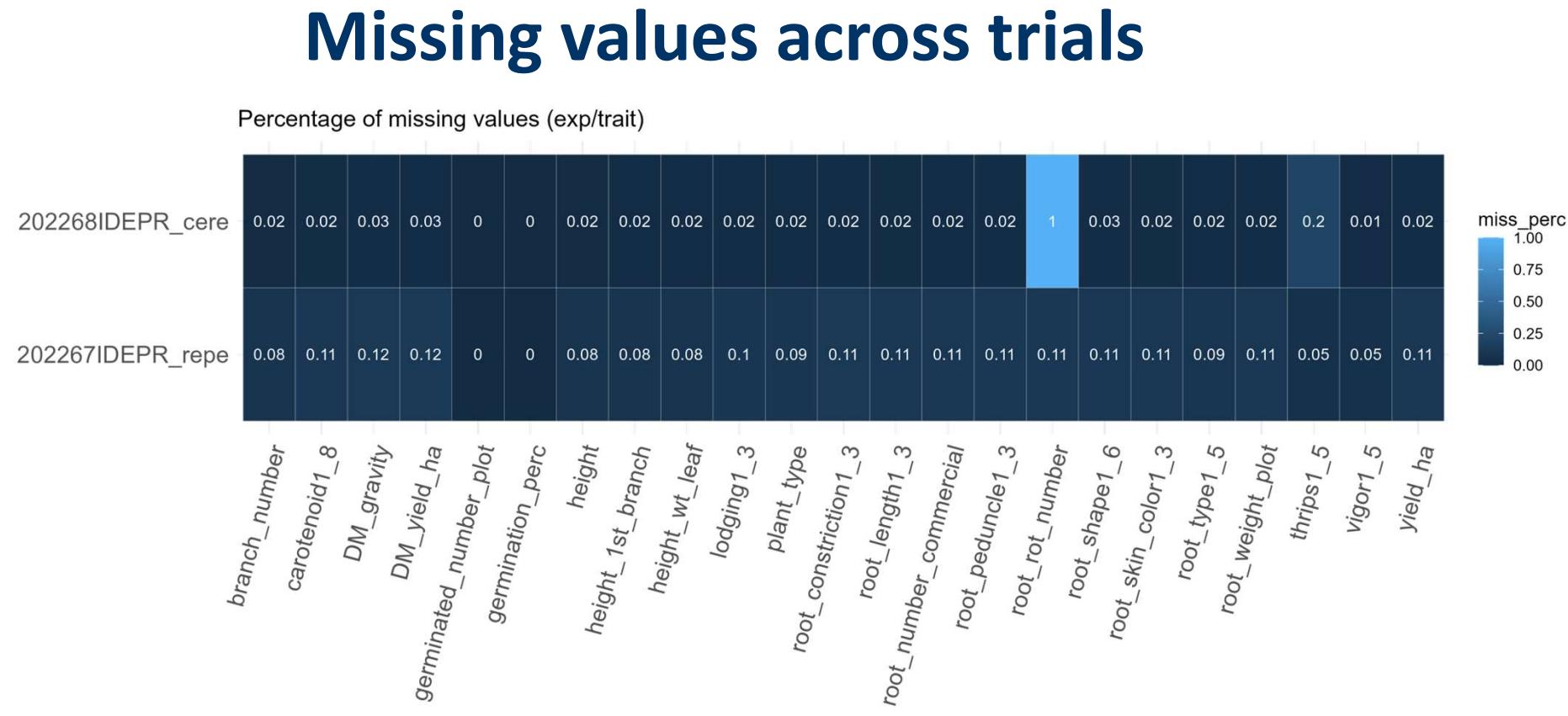
1. CG1141-1_is_Costena
2. SM2775-4_is_Bellotti
3. SMB2446-2_is_Caiseli
4. TAI8_is_TAI



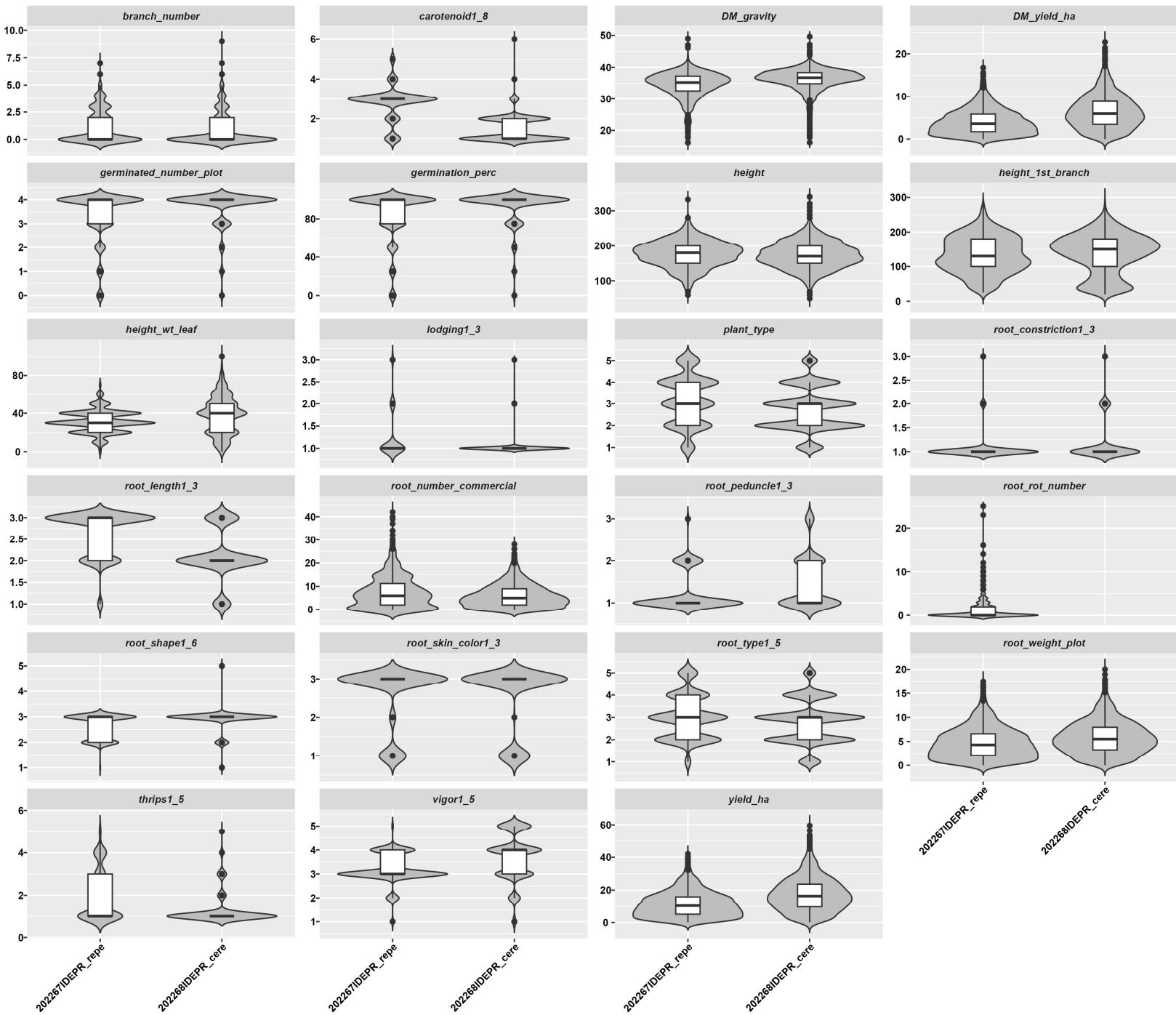
Exploratory data análisis

Traits evaluated

Agronomic traits
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
root_length1_3
root_rot_number
germinated_number_plot
root_peduncle1_3
root_shape1_6
thrips1_5
carotenoid1_8

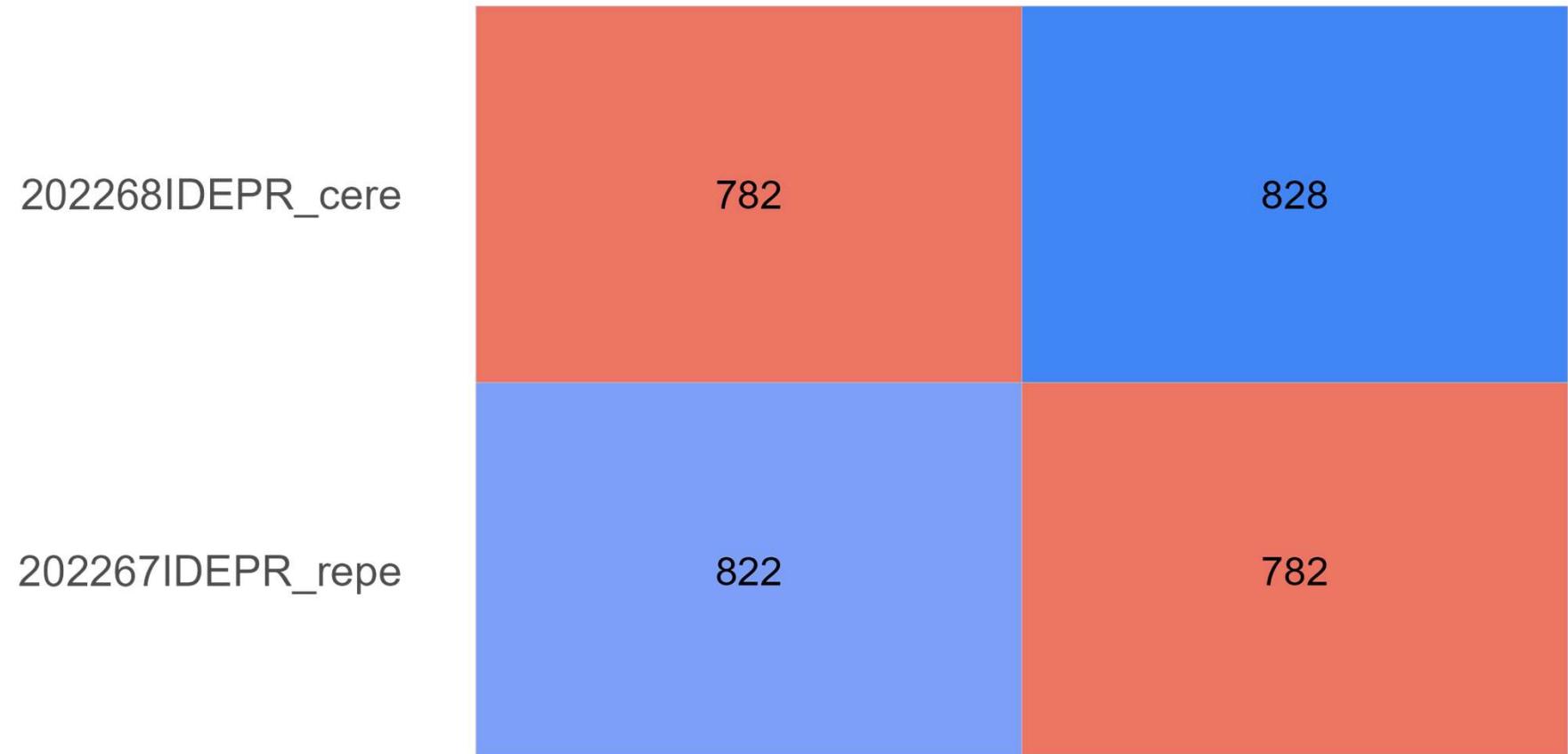


Trait variation across trials (phenotypic value)



Shared genotypes

Connectivity Matrix



202267IDEPR_repe
202268IDEPR_cere

Multiple corr trait (phenotypic value)

	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	root_length1_3	root_rot_number	germinated_number_plot	root_peduncle1_3	root_shape1_6	carotenoid1_8	
DM_gravity		-0.12 ***																					
height_1st_branch		-0.7 ***	0.2 ***																				
yield_ha		0.02 ns	0.5 ***	0.18 ***	0.36 ***																		
germination_perc		-0.11 ***	0.24 ***	0.18 ***	0.36 ***																		
DM_yield_ha		0 ns	0.56 ***	0.19 ***	0.99 ***	0.35 ***																	
root_weight_plot		0.04 ns	0.49 ***	0.2 ***	0.98 ***	0.37 ***	0.97 ***																
vigor1_5		0.1 ***	0.32 ***	0.14 ***	0.62 ***	0.33 ***	0.62 ***	0.58 ***															
lodging1_3		0.19 ***	-0.31 ***	-0.12 ***	-0.22 ***	-0.08 ***	-0.22 ***	-0.2 ***	-0.11 ***														
root_number_commercial		0.07 **	0.39 ***	0.16 ***	0.75 ***	0.26 ***	0.74 ***	0.82 ***	0.39 ***	-0.12 ***													
plant_type		0.22 ***	-0.37 ***	-0.51 ***	-0.45 ***	-0.24 ***	-0.45 ***	-0.46 ***	-0.42 ***	0.29 ***	-0.35 ***												
height		0.24 ***	0.14 ***	0.35 ***	0.39 ***	0.19 ***	0.37 ***	0.42 ***	0.46 ***	0.05 ns	0.37 ***	-0.5 ***											
height_wt_leaf		-0.16 ***	0.22 ***	0.46 ***	0.3 ***	0.18 ***	0.29 ***	0.28 ***	0.3 ***	-0.08 ***	0.16 ***	-0.53 ***	0.51 ***										
root_skin_color1_3		0.18 ***	-0.01 ns	-0.09 ***	0.06 ns	-0.03 ns	0.05 ns	0.06 ns	0.08 ***	0.07 +	0.03 ns	-0.02 ns	0.19 ***	0.13 ***									
root_constriction1_3		0.02 ns	-0.07 *	-0.01 ns	-0.09 ***	-0.01 ns	-0.1 ***	-0.11 ***	0 ns	-0.01 ns	-0.14 ***	-0.01 ns	0.01 ns	0.05 ns	-0.07 *								
root_type1_5		-0.03 ns	-0.47 ***	-0.18 ***	-0.75 ***	-0.31 ***	-0.74 ***	-0.77 ***	-0.47 ***	0.24 ***	-0.69 ***	0.42 ***	-0.37 ***	-0.27 ***	-0.11 ***	0.14 ***							
root_length1_3		0.17 ***	0.08 **	0.05 ns	0.22 ***	0.07 *	0.2 ***	0.3 ***	0.17 ***	0.04 ns	0.37 ***	-0.17 ***	0.34 ***	0.1 ***	0.14 ***	-0.07 **	-0.37 ***						
root_rot_number		0.03 ns	-0.04 ns	-0.01 ns	0 ns	0.14 ***	-0.01 ns	0 ns	0.17 ***	-0.03 ns	0.02 ns	-0.06 ns	0.09 *	0.01 ns	0.01 ns	0.03 ns	-0.07 ns	0.02 ns					
germinated_number_plot		-0.11 ***	0.24 ***	0.18 ***	0.36 ***	1 ***	0.35 ***	0.37 ***	0.33 ***	-0.08 ***	0.26 ***	-0.24 ***	0.19 ***	0.18 ***	-0.03 ns	-0.01 ns	-0.31 ***	0.07 *	0.14 ***				
root_peduncle1_3		0.08 ***	-0.05 ns	-0.05 ns	-0.02 ns	0.02 ns	-0.02 ns	-0.06 ns	0.1 ***	0.04 ns	-0.11 ***	-0.02 ns	0.08 ***	0.09 ***	0.06 ns	0.18 ***	0.14 ***	-0.03 ns	0.06 ns	0.02 ns			
root_shape1_6		0 ns	0.07 **	0.03 ns	0.12 ***	0.04 ns	0.12 ***	0.08 ***	0.12 ***	-0.09 ***	0.01 ns	-0.08 ns	0.04 ns	0.06 ns	-0.01 ns	0.07 **	-0.07 *	0.08 **	-0.04 ns	0.04 ns	0.13 ***		
thrips1_5		-0.06 ns	-0.28 ***	-0.06 ns	-0.28 ***	-0.1 ***	-0.29 ***	-0.26 ***	-0.32 ***	0.12 ***	-0.18 ***	0.37 ***	-0.23 ***	-0.3 ***	-0.02 ns	-0.05 ns	0.25 ***	0.02 ns	-0.05 ns	-0.1 ***	-0.05 ns	-0.03 ns	
carotenoid1_8		0.04 ns	-0.29 ***	-0.02 ns	-0.32 ***	-0.12 ***	-0.33 ***	-0.23 ***	-0.25 ***	0.22 ***	-0.02 ns	0.19 ***	-0.04 ns	-0.21 ***	-0.11 ***	-0.09 ***	0.16 ***	0.27 ***	0.07 ns	-0.12 ***	-0.18 ***	-0.19 ***	0.28 ***

A large pile of harvested cassava roots, showing many long, brown, tapered tubers with white, fibrous ends. Some roots have small green tags attached.

Statistical data analysis

Single heritability

Moderate to high heritability among two locations.

trial	branch_number	carotenoid1_8	DM_gravity	DM_id_ha	DM_yield	germinated_number_plot	germinated_on_perc	height	height_1st_branch	height_wt_leaf	lodging1_3	plant_type	root_constraint1_3	root_length1_3	root_number_commercial	root_peduncle1_3	root_number	root_shape1_6	root_skin_color1_3	root_type1_5	root_weight_per_plot	thrip_s1_5	vigor1_5	yield_ha	
202267IDEPR_repe	0.86	0.29	0.64	0.77		0.79	0.79	0.82	0.81	0.65	0.56	0.78	0.15	0.51		0.67	0.15	0.32	0.14	0.97	0.73	0.78	0.9	0.66	0.78
202268IDEPR_cere	0.83	0.4	0.71	0.78		0.78	0.78	0.66	0.75	0.68	0.01	0.66	0.12	0.41		0.67	0.24		0	0.98	0.64	0.79	0.5	0.67	0.78

Traits with heritability <0.1 were removed from the next GxE analysis.

GxE analysis was performed without following traits - trials:

trial	traits	heritability
202268IDEPR_cere	lodging1_3	0.01
202268IDEPR_cere	root_rot_number	NA
202268IDEPR_cere	root_shape1_6	0

Heritability gxe all trials

trait	h2
root_skin_color1_3	0.99
branch_number	0.89
germinated_number_plot	0.84
germination_perc	0.84
root_weight_plot	0.83
yield_ha	0.83
DM_yield_ha	0.82
thrips1_5	0.82
height_1st_branch	0.82
height	0.8
DM_gravity	0.78
root_type1_5	0.77
plant_type	0.73
vigor1_5	0.72
root_number_commercial	0.71
height_wt_leaf	0.64
root_length1_3	0.53
carotenoid1_8	0.48
root_peduncle1_3	0.17
root_constriction1_3	0

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

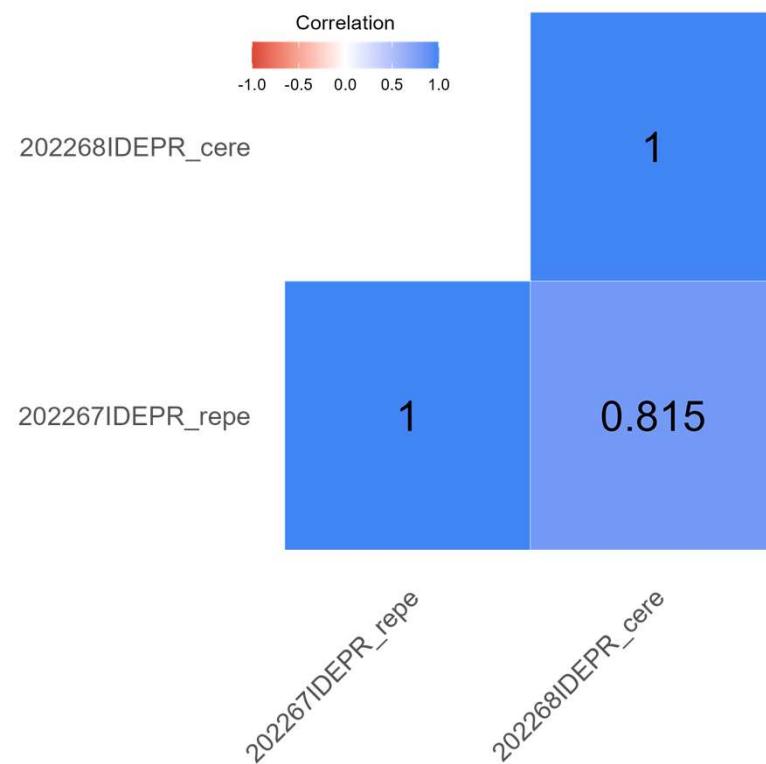
Genotypic Correlation: Locations

trial:trial	trait	cor
202267IDEPR_repe:202268IDEPR_cere	root_skin_color1_3	0.995493
202267IDEPR_repe:202268IDEPR_cere	carotenoid1_8	0.901905
202267IDEPR_repe:202268IDEPR_cere	DM_gravity	0.894594
202267IDEPR_repe:202268IDEPR_cere	germinated_number_plot	0.887895
202267IDEPR_repe:202268IDEPR_cere	germination_perc	0.887895
202267IDEPR_repe:202268IDEPR_cere	thrips1_5	0.887092
202267IDEPR_repe:202268IDEPR_cere	branch_number	0.879649
202267IDEPR_repe:202268IDEPR_cere	root_type1_5	0.849532
202267IDEPR_repe:202268IDEPR_cere	root_peduncle1_3	0.840964
202267IDEPR_repe:202268IDEPR_cere	DM_yield_ha	0.817766
202267IDEPR_repe:202268IDEPR_cere	root_weight_plot	0.816244
202267IDEPR_repe:202268IDEPR_cere	yield_ha	0.815351
202267IDEPR_repe:202268IDEPR_cere	height	0.804747
202267IDEPR_repe:202268IDEPR_cere	vigor1_5	0.796952
202267IDEPR_repe:202268IDEPR_cere	height_1st_branch	0.782504
202267IDEPR_repe:202268IDEPR_cere	root_number_commercial	0.778959
202267IDEPR_repe:202268IDEPR_cere	root_length1_3	0.762572
202267IDEPR_repe:202268IDEPR_cere	plant_type	0.663216
202267IDEPR_repe:202268IDEPR_cere	height_wt_leaf	0.639289
202267IDEPR_repe:202268IDEPR_cere	root_constriction1_3	0.032436

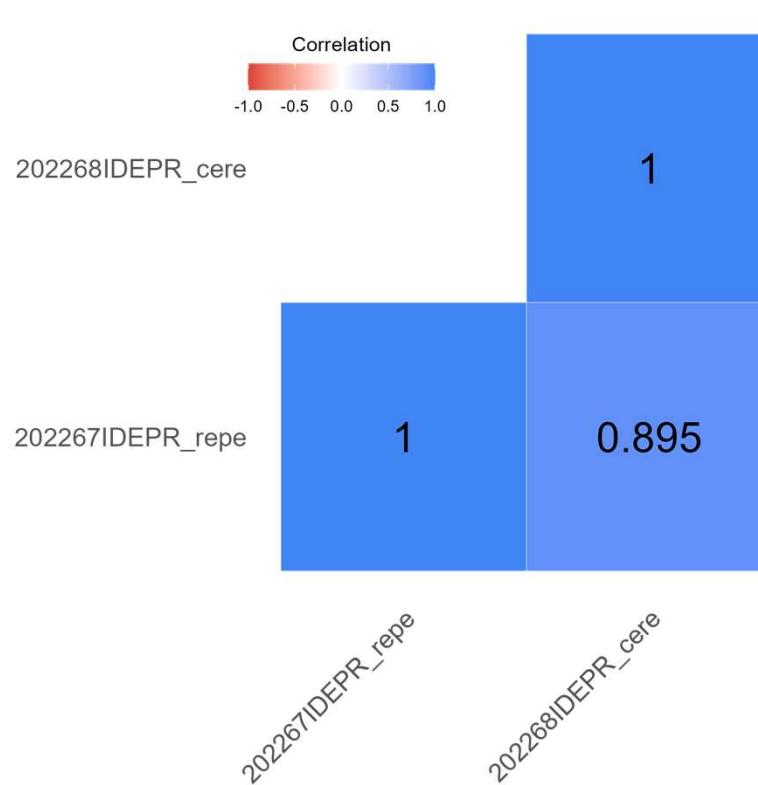
Moderate to high genotypic correlation among two locations, except for root_constriction1_3 trait (cor = 0.03)

Genotypic Correlation: Locations

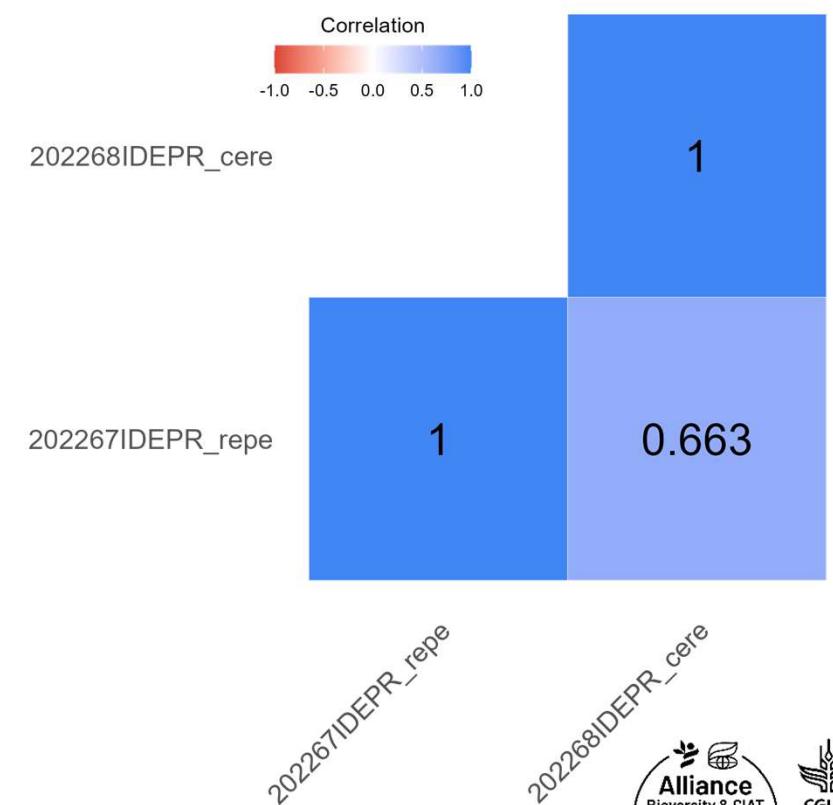
Yield



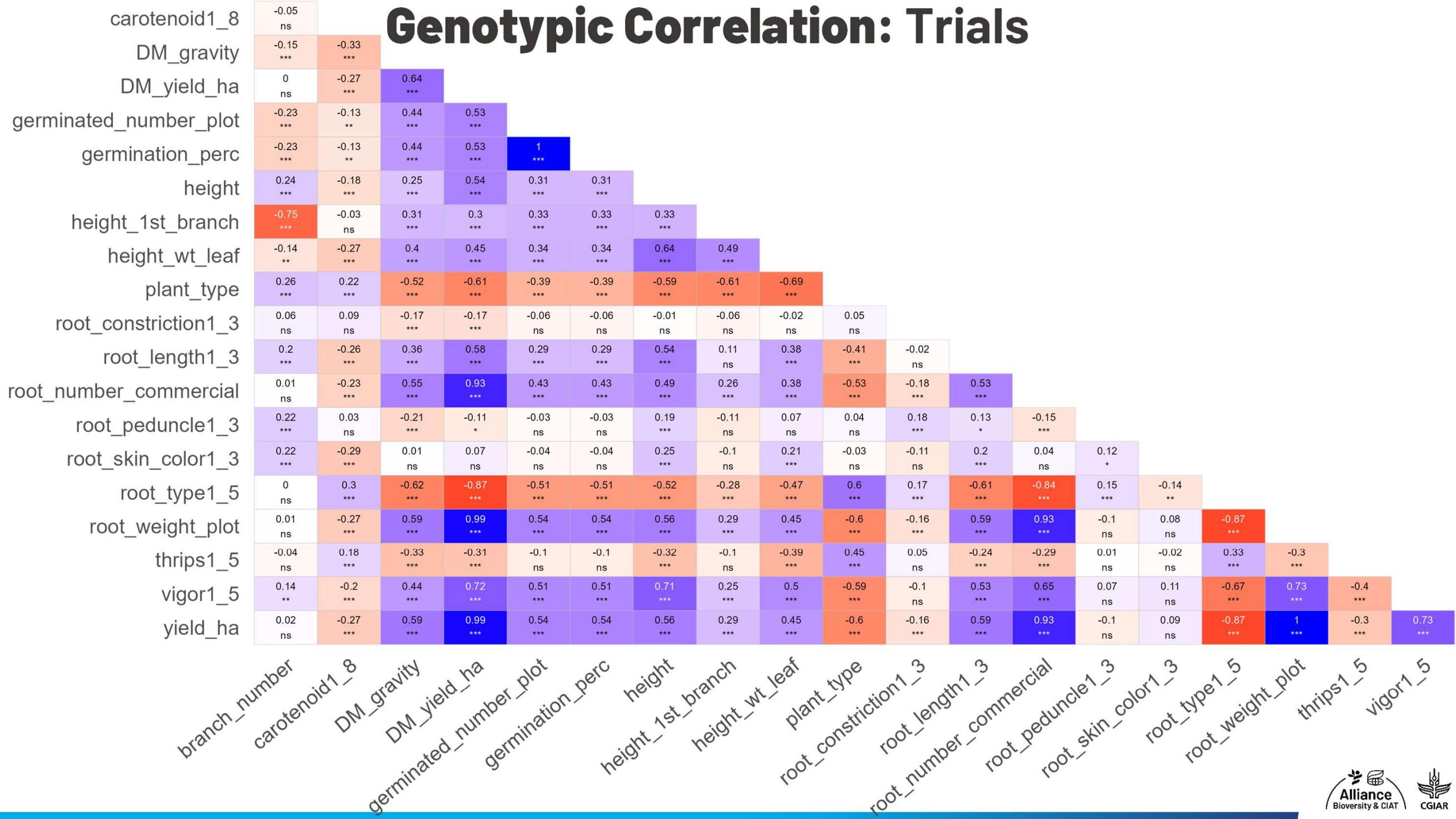
Dry Matter



Plant type



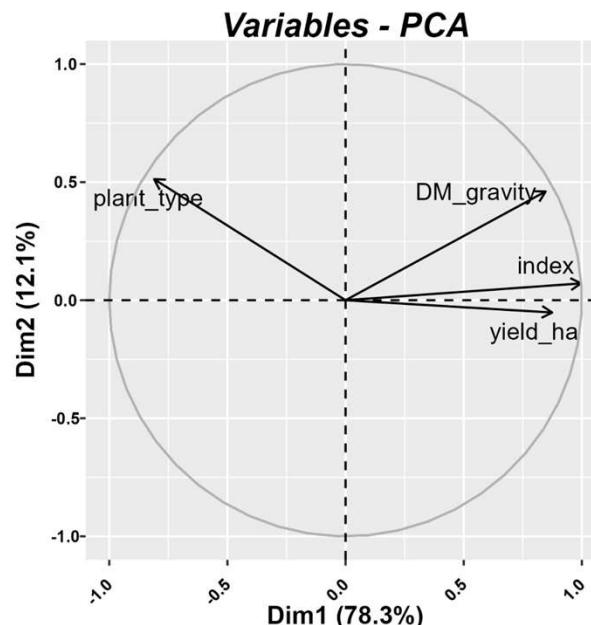
Genotypic Correlation: Trials



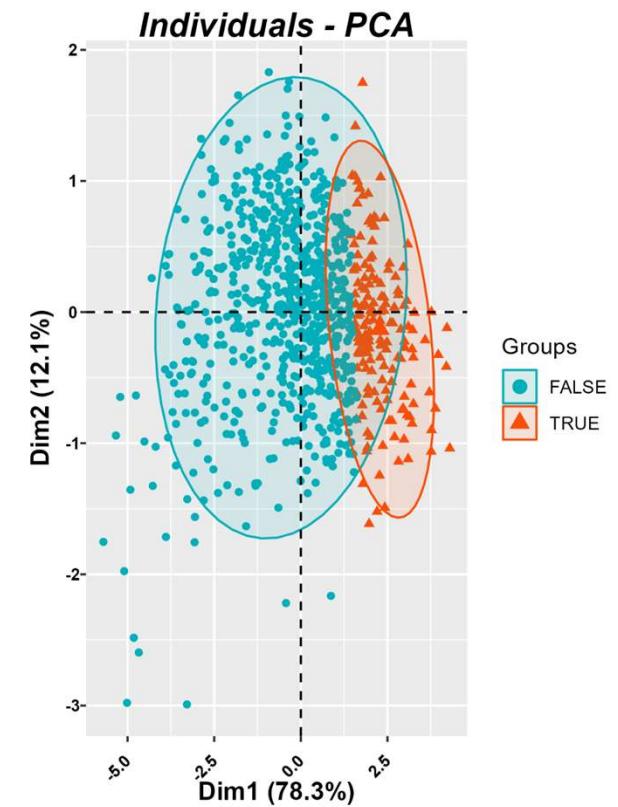
Selection comments

- 1) **DM_gravity, plant_type & yield_ha** were used to calculate index selection.
- 2) Scores given were:
 - DM_gravity = 10
 - plant_type = -5
 - yield_ha = 10
- 3) Percentage to be selected: **20%**
- 4) Main results can be found in the spreadsheet “**BLUEs_BLUPs_MET**” of master_result file.

A



B





Thank you!