



Data analysis MDEPR – 2 environments

Year 2023

202301MDEPR_tani
202304MDPYT_dona

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Palmira, October 2023



@BiovIntCIAT_eng

@BiovIntCIAT_esp

#Alliance4Science

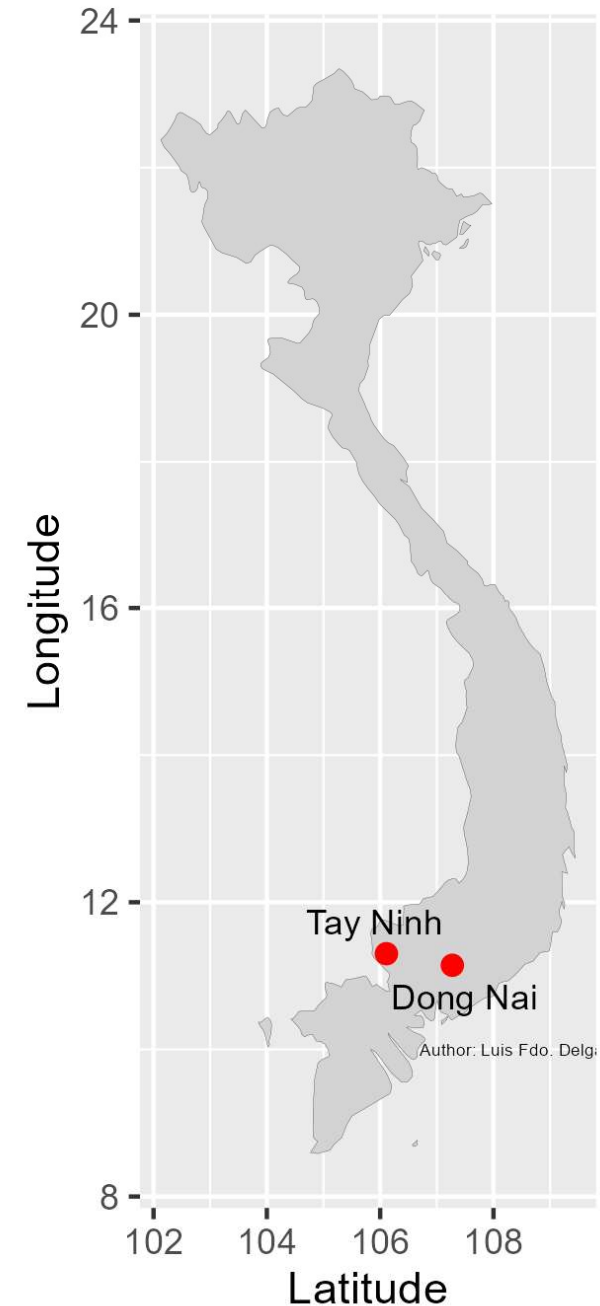
The Alliance of Bioversity International and the International Center for Tropical Agriculture (CIAT) is part of CGIAR, a global research partnership for a food-secure future

Locations - Introduction

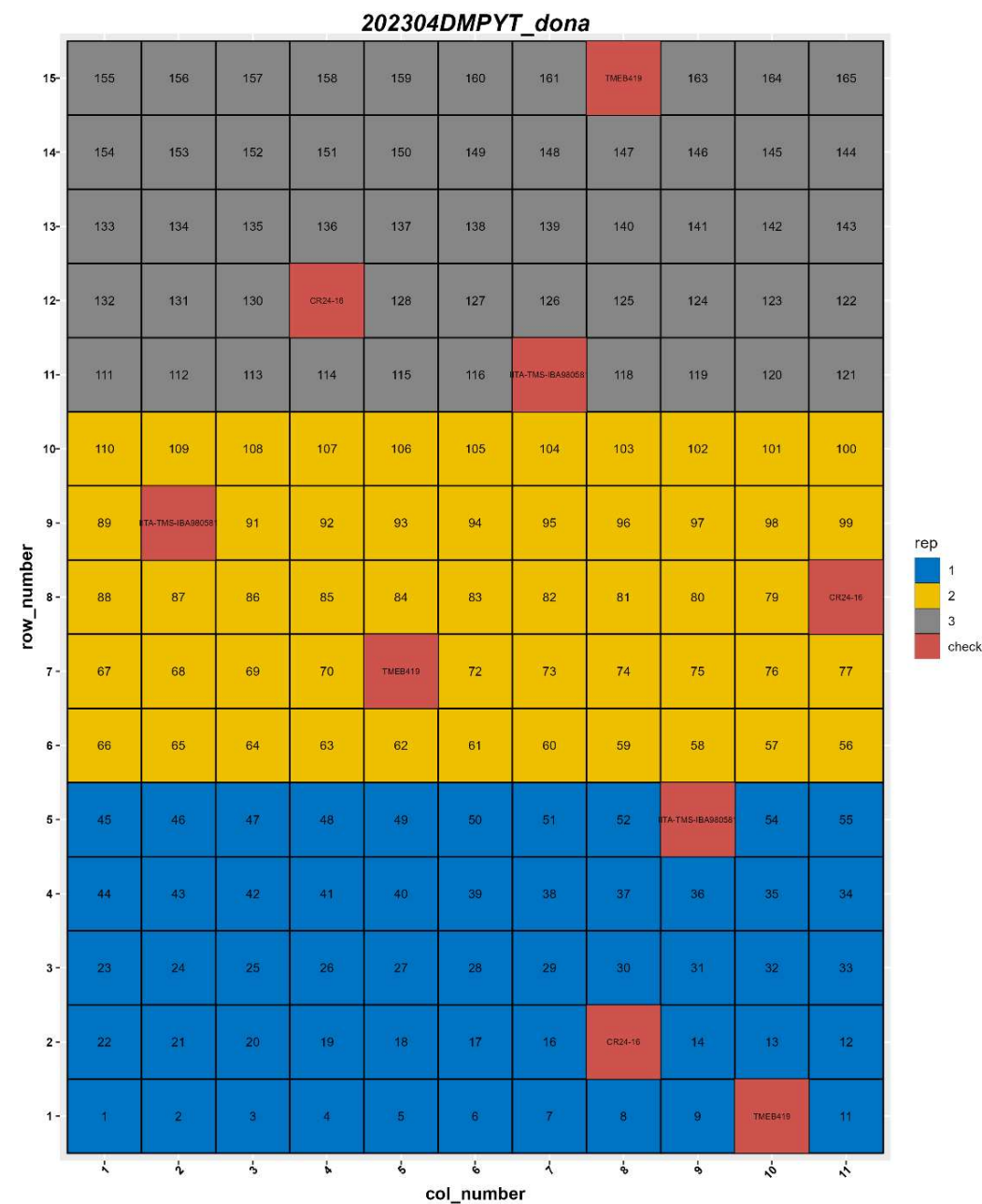
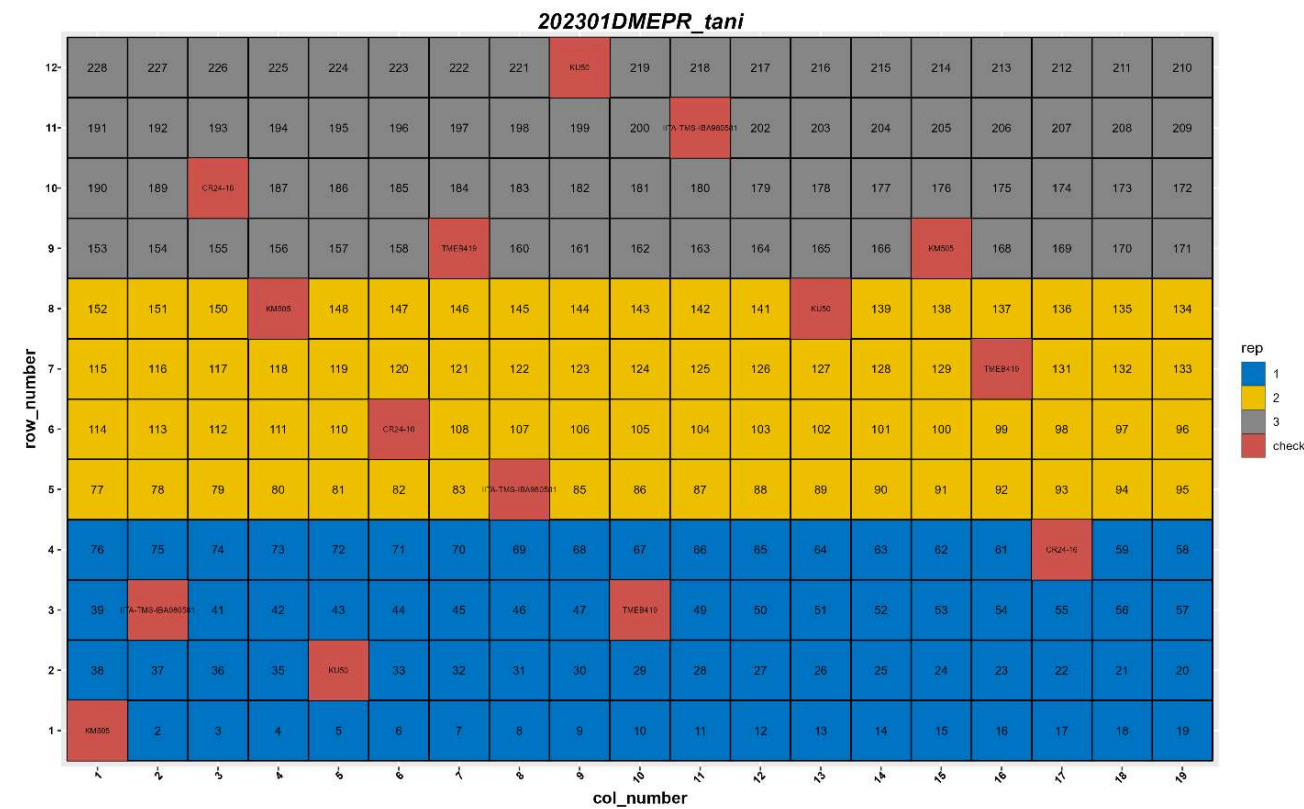
- Tay Ninh, Vietnam
- Dong Nai, Vietnam
- The preliminary trials of the pipeline - CMD-resistance cassava for starch and animal feed
- TPE: subhumid and semi-arid lowland tropics
- locations: Tay Ninh and Dong Nai, Vietnam
- breeding cycle: Cohort 1 of cycle 1
- Project: ACIAR, USAID
- Purpose:
 - 1) Improve breeding populations;
 - 2) Deliver variety candidates to NARES in Asia and Africa;
 - 3) Perform "training-by-doing"

Locations in Vietnam

Tay Ninh and Dong Nai

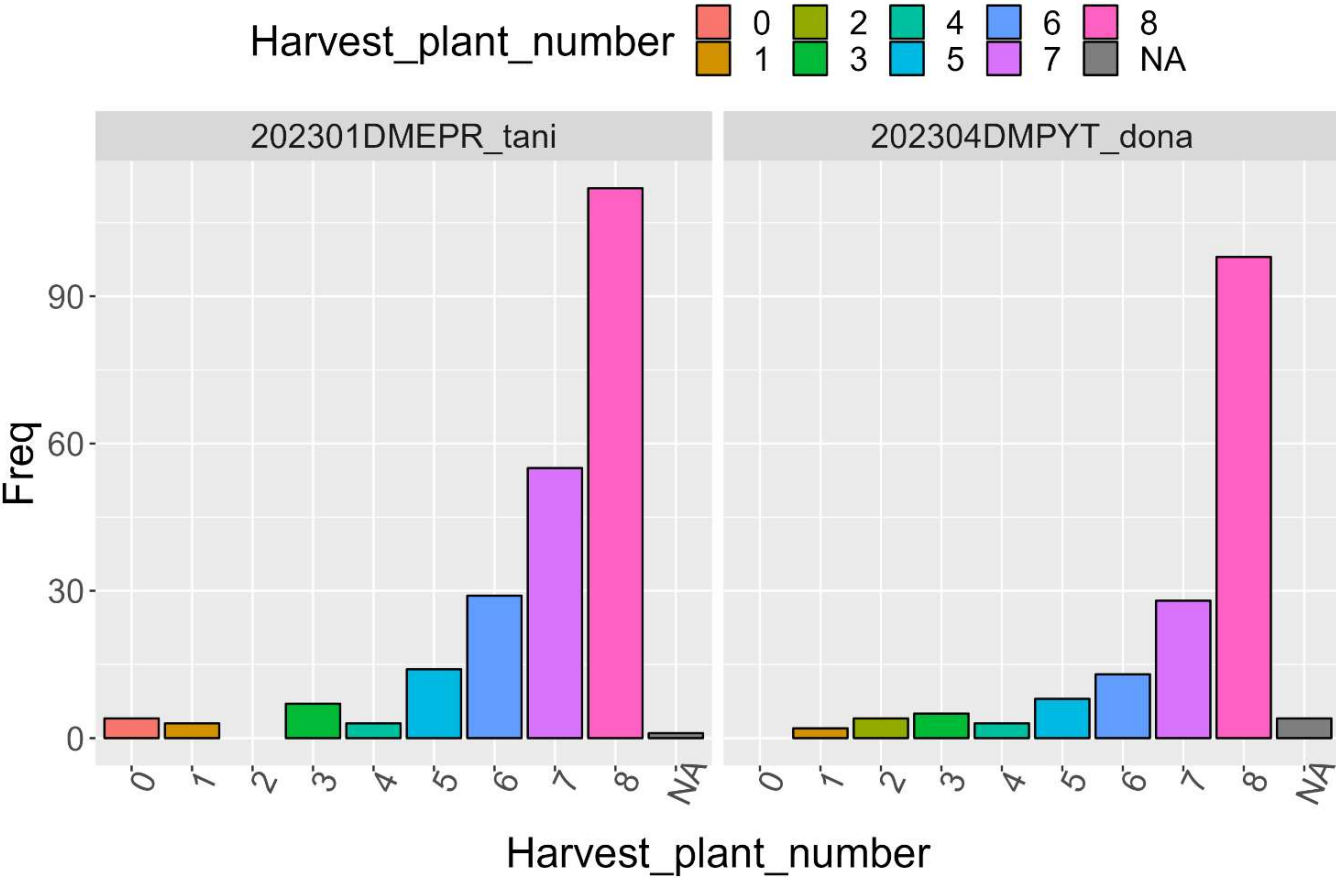


Year 2023: Trial Design – Resolvable Row col



Resolvable row-col with randomized checks

use_trial_name	use_plant_date	use_harvest_date	harvesting_time	use_location	n_gen
202301DMEPR_tani	2023-February-09	2023-December-08	9month 29day	Tay Ninh	76
202304DMPYT_dona	2023-March-02	2023-December-08	9month 6day	Dong Nai	55



Check genotypes

KU50_is_KM94

CR24-16

IITA-TMS-IBA980581

KM505

TMEB419



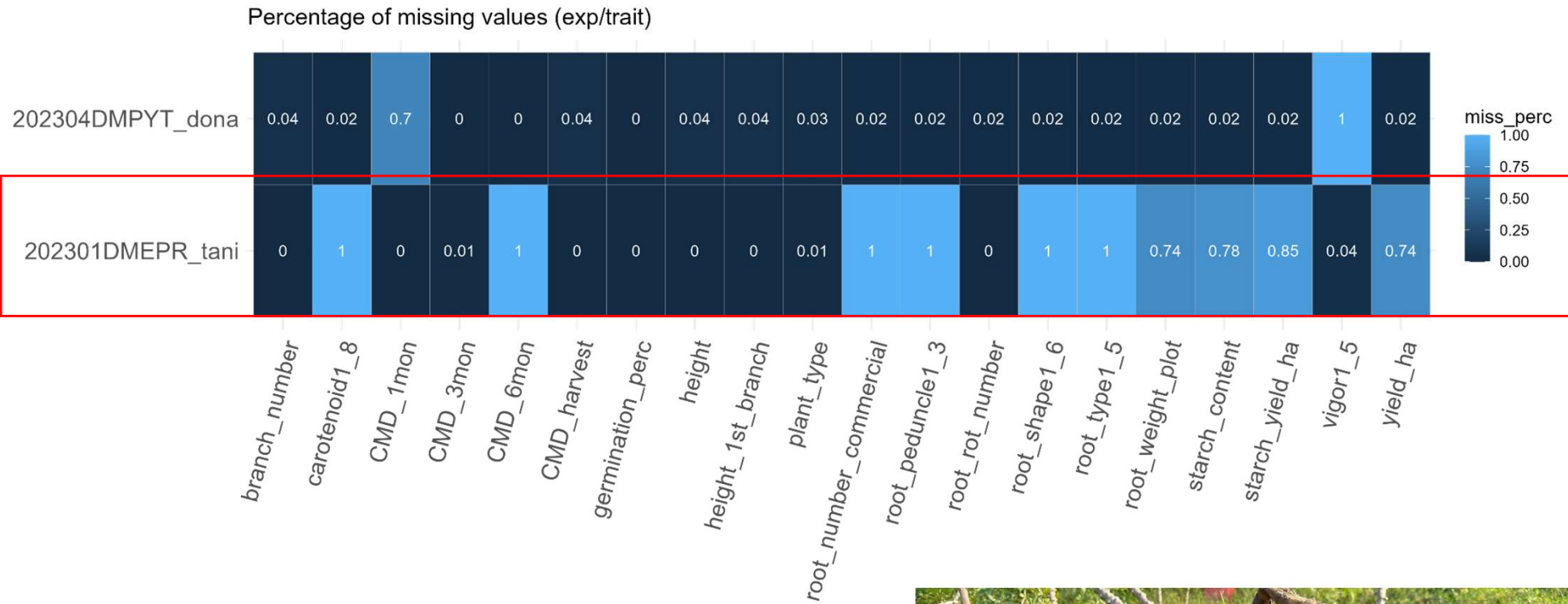
3 - Unloading cassava. Women processors, Korogho Côte d'Ivoire. Patricio Mendez del Villar / 3 - Déchargement de manioc Femmes transformatrices, Korogho Cote d'Ivoire. Patricio Mendez del Villar

Exploratory data analysis

Traits evaluated – missing values



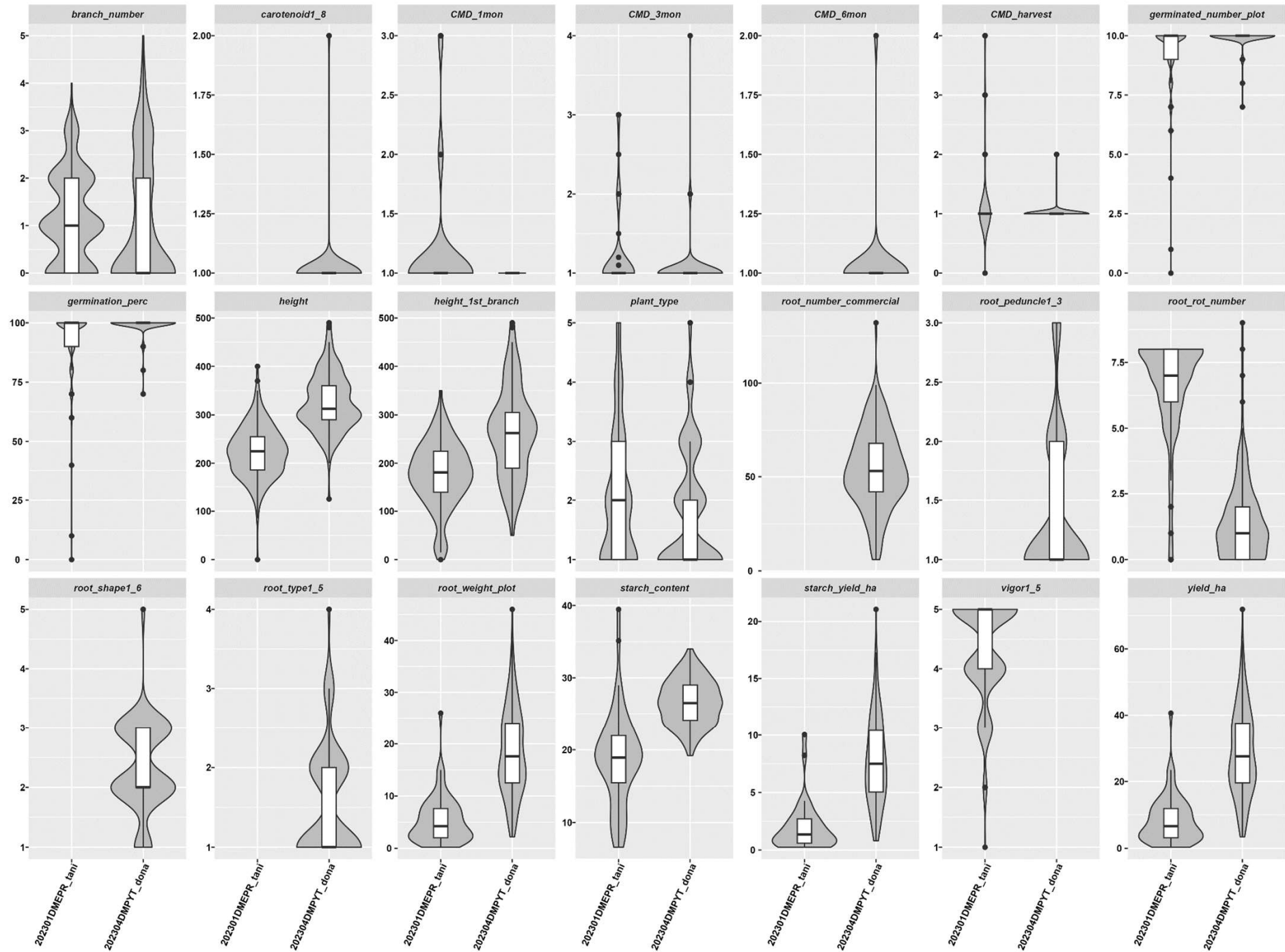
Agronomic traits	
CMD_harvest	
branch_number	
CMD_1mon	
CMD_3mon	
CMD_6mon	
height_1st_branch	
yield_ha	
root_weight_plot	
vigor1_5	
root_number_commercial	
plant_type	
height	
root_type1_5	
root_rot_number	
starch_content	
root_peduncle1_3	
root_shape1_6	
carotenoid1_8	
germination_perc	
starch_yield_ha	



The field in Tay Ninh was flooded for a week due to several days of consecutive rainfall.

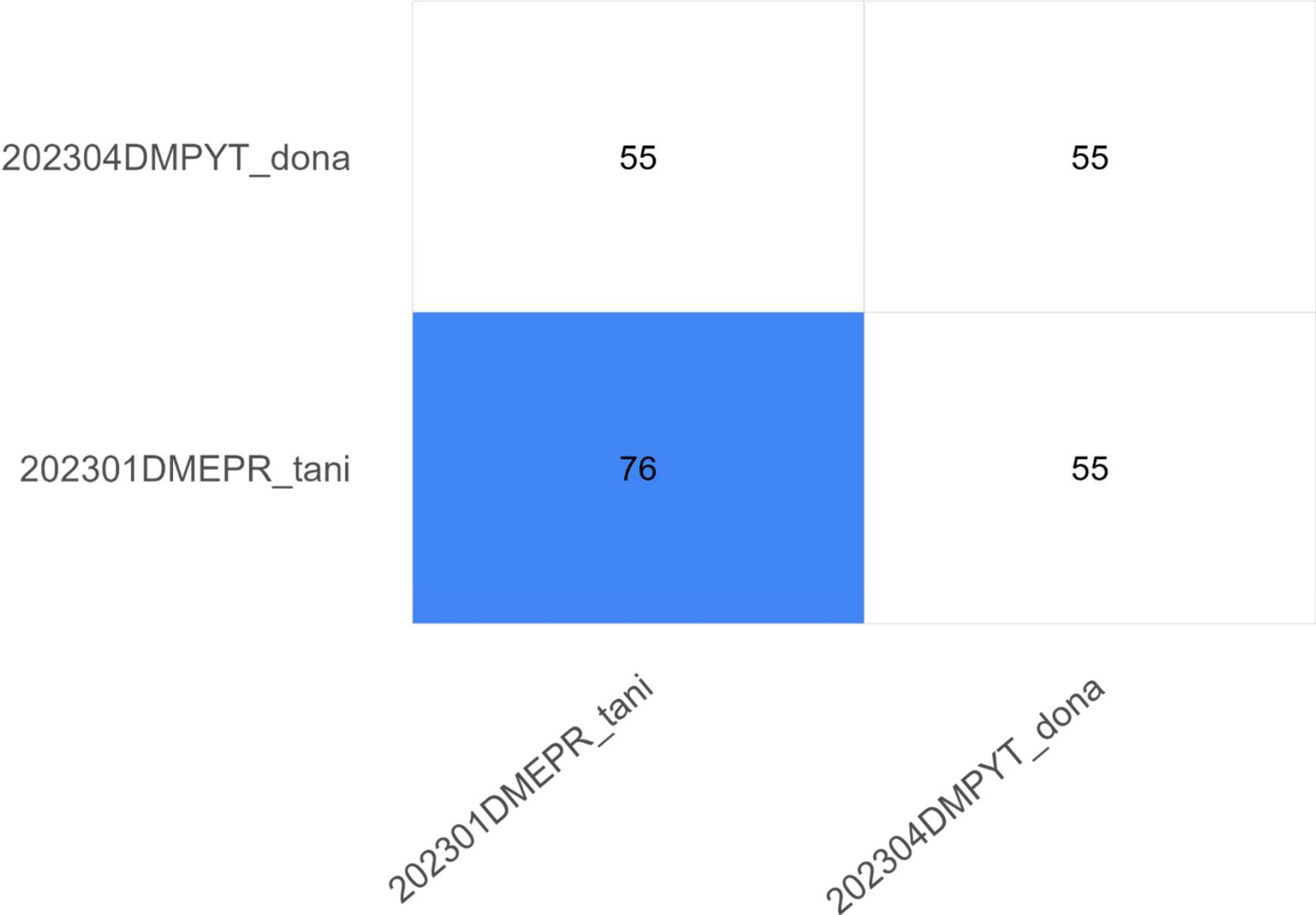


Trait variation across trials (phenotypic value)



Shared clones among trials

Connectivity Matrix



Multiple corr trait (phenotypic value)

branch_number	-0.03 ns																			
CMD_1mon	0.39 ***	-0.01 ns																		
CMD_3mon	0.48 ***	-0.05 ns	0.35 ***																	
CMD_6mon	0.7 ***	-0.16 ns		0.53 ***																
height_1st_branch	-0.07 ns	-0.53 ***	-0.02 ns	0 ns	0.2 ns															
yield_ha	-0.14 ns	-0.01 ns	-0.21 ns	-0.02 ns	0.11 ns	0.14 ns														
root_weight_plot	-0.14 ns	-0.01 ns	-0.21 ns	-0.02 ns	0.11 ns	0.14 ns	1 ***													
vigor1_5	-0.17 ns	0.06 ns	-0.16 ns	-0.07 ns		0.2 ns	-0.05 ns	-0.05 ns												
root_number_commercial	0.19 ns	-0.07 ns		0.13 ns	0.1 ns	-0.08 ns	0.89 ***	0.89 ***												
plant_type	-0.01 ns	0.53 ***	-0.06 ns	-0.03 ns	-0.13 ns	-0.55 ***	0.03 ns	0.03 ns	-0.04 ns	-0.11 ns										
height	-0.14 ns	-0.02 ns	-0.06 ns	-0.08 ns	0.1 ns	0.71 ***	0.28 **	0.28 **	0.3 ***	-0.23 ns	-0.15 ns									
root_type1_5	-0.11 ns	0.12 ns		-0.07 ns	-0.06 ns	0.04 ns	-0.59 ***	-0.59 ***		-0.56 ***	0.09 ns	0.16 ns								
root_rot_number	0.13 ns	0.01 ns	0.04 ns	0.12 ns	-0.04 ns	-0.38 ***	-0.49 ***	-0.49 ***	0.38 ***	-0.03 ns	0.1 ns	-0.55 ***	0.06 ns							
starch_content	-0.11 ns	0.03 ns	-0.21 ns	-0.14 ns	0.3 *	0.17 ns	0.45 ***	0.45 ***	0.07 ns	0.24 ns	0.04 ns	0.34 ***	-0.18 ns	-0.43 ***						
root_peduncle1_3	-0.08 ns	0.09 ns		-0.1 ns	-0.12 ns	-0.02 ns	-0.2 ns	-0.2 ns		-0.22 ns	0.08 ns	0.12 ns	0.4 ***	-0.01 ns	-0.25 ns					
root_shape1_6	0.06 ns	0.08 ns		-0.07 ns	-0.13 ns	-0.02 ns	-0.12 ns	-0.12 ns		-0.19 ns	-0.04 ns	-0.01 ns	0.19 ns	0.21 ns	-0.12 ns	0.28 *				
carotenoid1_8	-0.02 ns	-0.01 ns		-0.02 ns	-0.03 ns	0.01 ns	0.03 ns	0.03 ns		0.1 ns	-0.11 ns	0.04 ns	-0.04 ns	-0.07 ns	-0.01 ns	-0.01 ns	-0.12 ns			
germination_perc	-0.27 ***	-0.01 ns	-0.17 ns	-0.2 *	0.04 ns	0.15 ns	0.29 **	0.29 **	0.34 ***	0.25 ns	-0.04 ns	0.22 **	-0.21 ns	-0.06 ns	0.26 *	-0.06 ns	-0.16 ns	0.03 ns		
starch_yield_ha	-0.03 ns	0.01 ns	-0.25 ns	0.05 ns	0.19 ns	0.08 ns	0.98 ***	0.98 ***	0.21 ns	0.86 ***	0.04 ns	0.17 ns	-0.57 ***	-0.37 ***	0.58 ***	-0.23 ns	-0.13 ns	0.01 ns	0.3 **	
	CMD_harvest	branch_number	CMD_1mon	CMD_3mon	CMD_6mon	height_1st_branch	yield_ha	root_weight_plot	vigor1_5	root_number_commercial	plant_type	height	root_type1_5	root_rot_number	starch_content	root_peduncle1_3	root_shape1_6	carotenoid1_8	germination_perc	starch_yield_ha

Statistical data analysis

Single heritability

trial	branch_n umber	carotenoi d1_8	CMD_1m on	CMD_3m on	CMD_6m on	CMD_har vest	germinati on_perc	height	height_1s t_branch	plant_typ e	root_nu mber_co mmercial	root_ped uncle1_3	root_rot_ number	root_sha pe1_6	root_type 1_5	root_wei ght_plot	starch_co ntent	starch_yi eld_ha	vigor1_5	yield_ha
202301DMEPR_t ani	0.62		0.59	0.94		0.46	0.2	0.48	0.39	0.45			0.63						0.58	
202304DMPYT_d ona	0.95	0.58		0.37	0.86		0.61	0.79	0.87	0.75	0.82	0.58	0.31	0.7	0.71	0.86	0.89	0.87		0.86

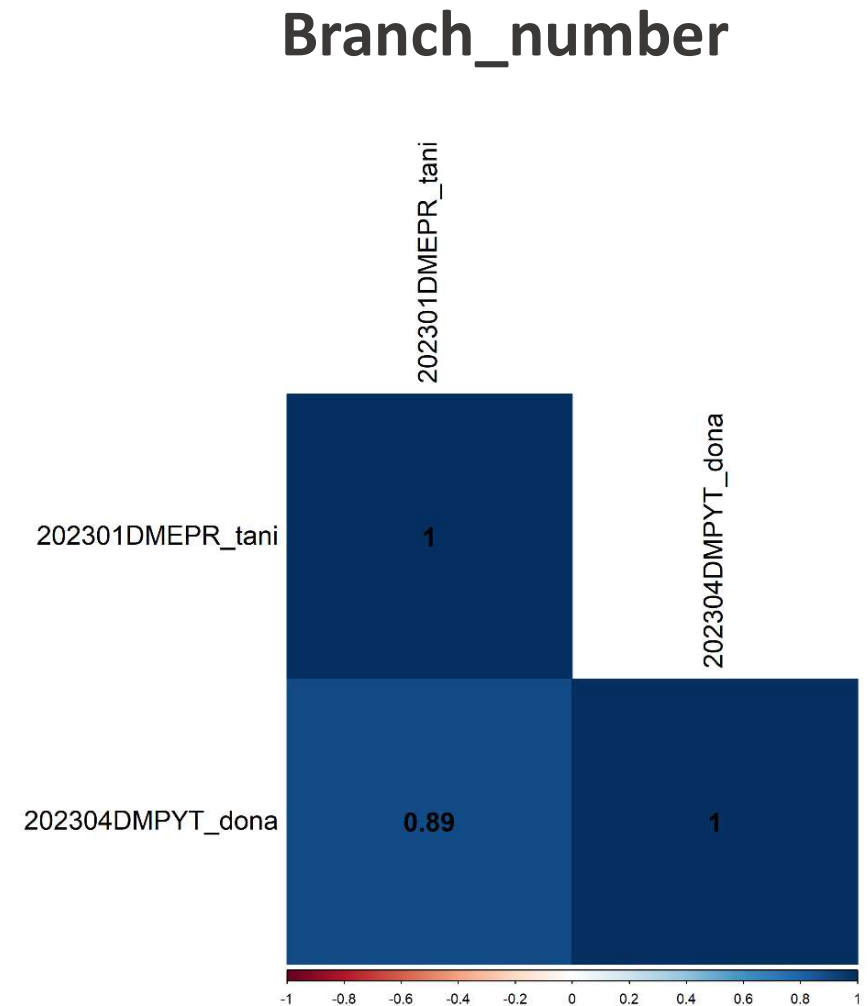
Traits with heritability
< 0.1 were remove
them from the GxE
analysis.

- GxE analysis will be perform
using the following traits:
- CMD_3mon
 - branch_number
 - height
 - plant_type
 - height_1st_branch

Heritability gxe all trials

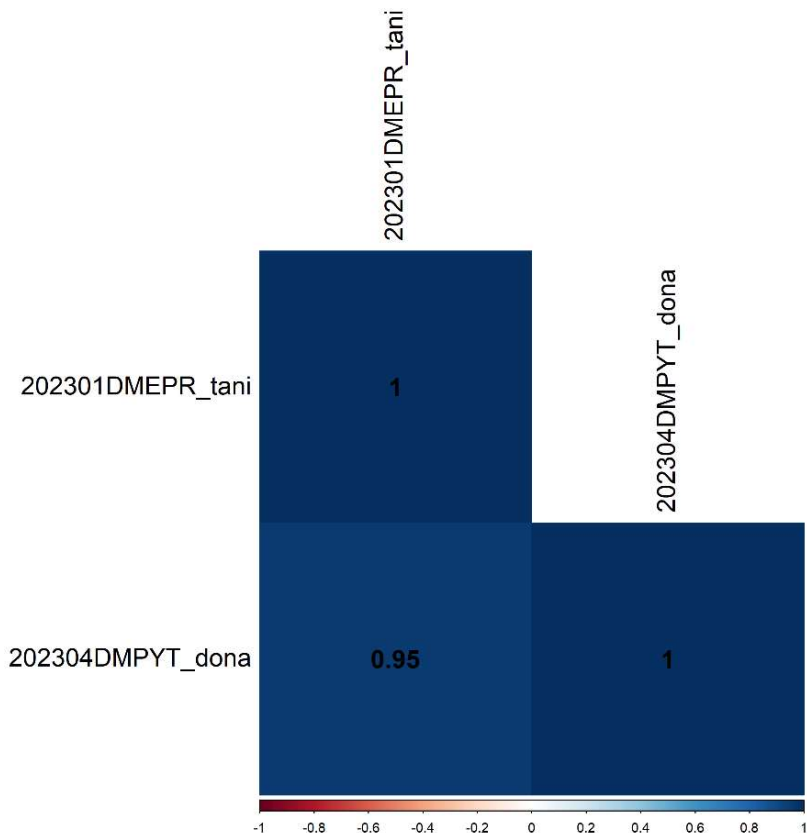
Genotypic Correlation: Locations

trait	h2
CMD_3mon	0.92
branch_number	0.8
height	0.68
plant_type	0.67
height_1st_branch	0.49

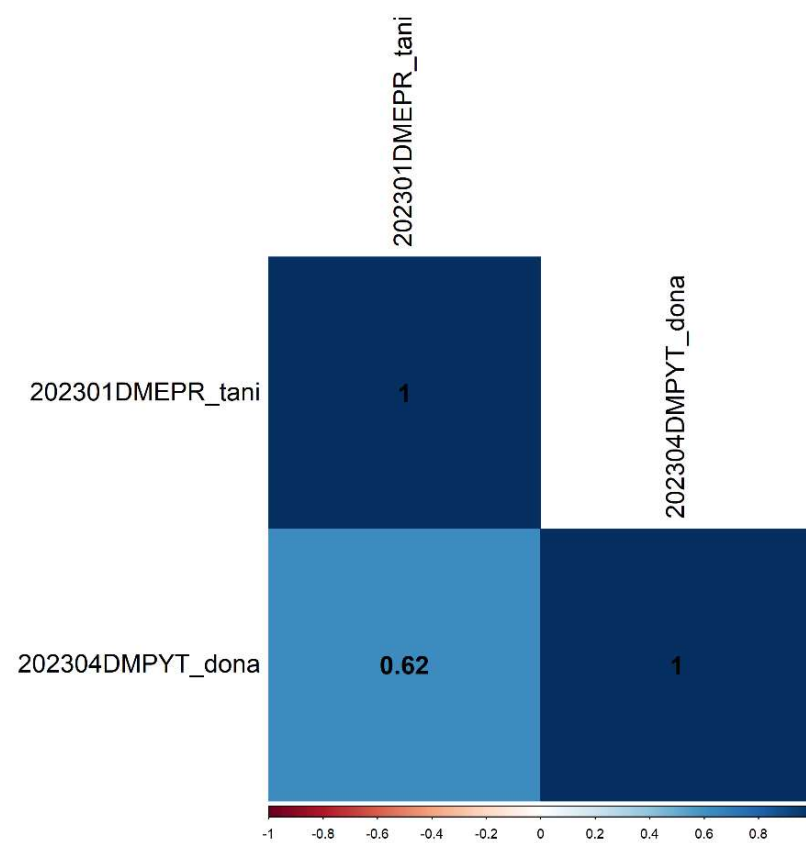


Genotypic Correlation: Locations

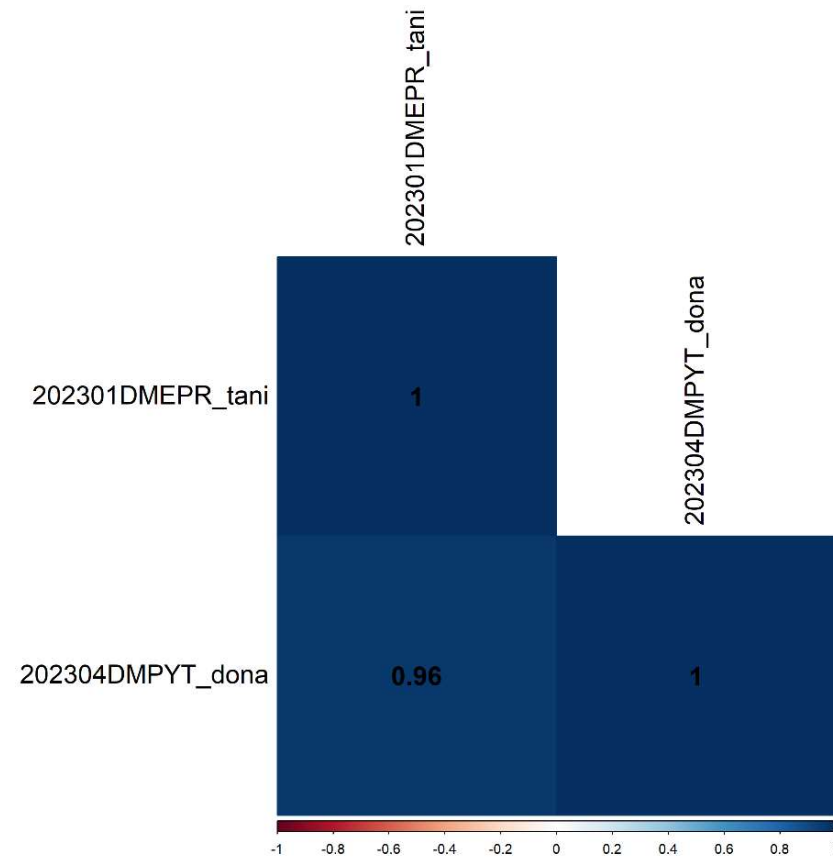
CMD_3mon



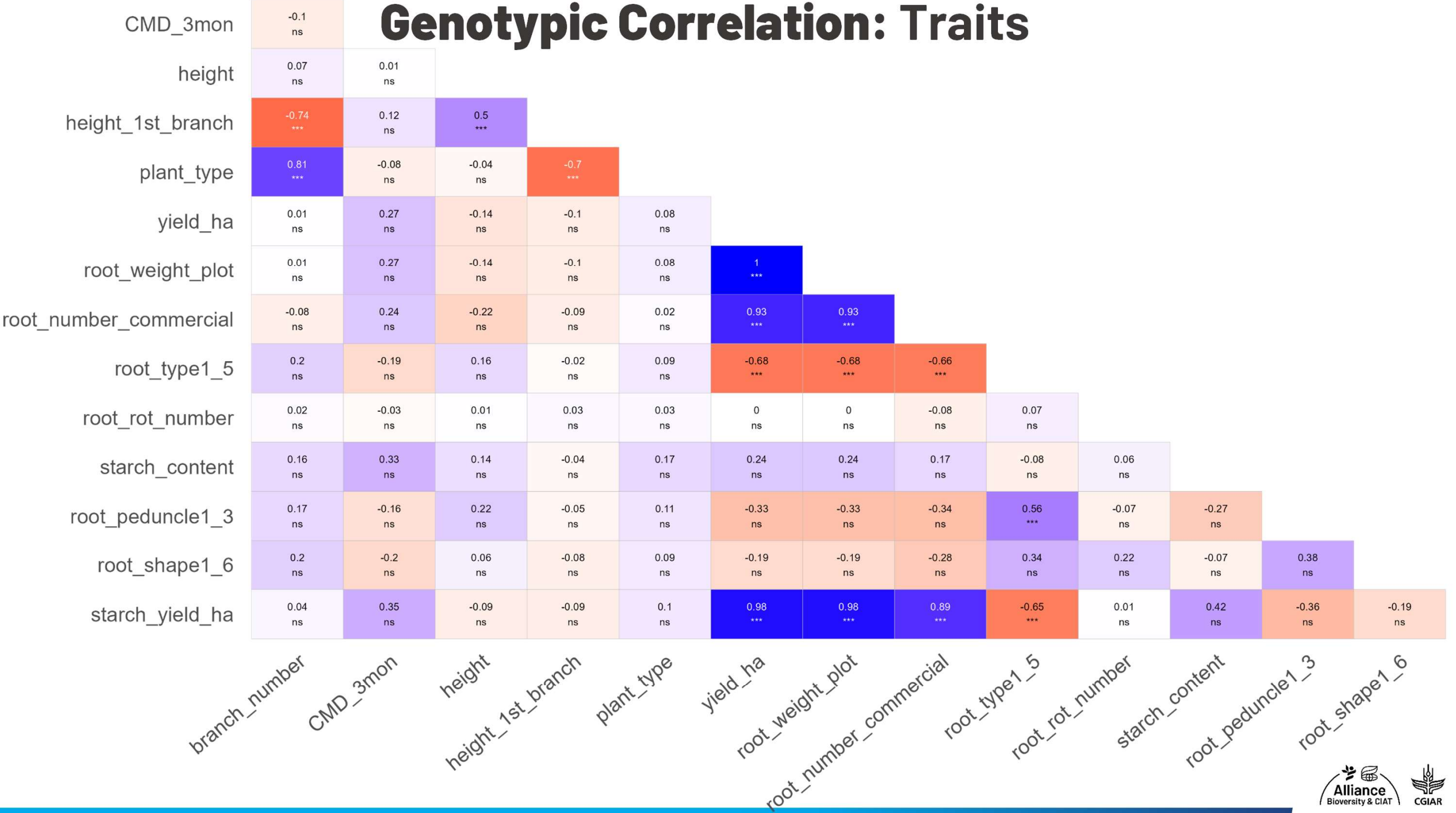
Height_first_branch



Plant_type



Genotypic Correlation: Traits



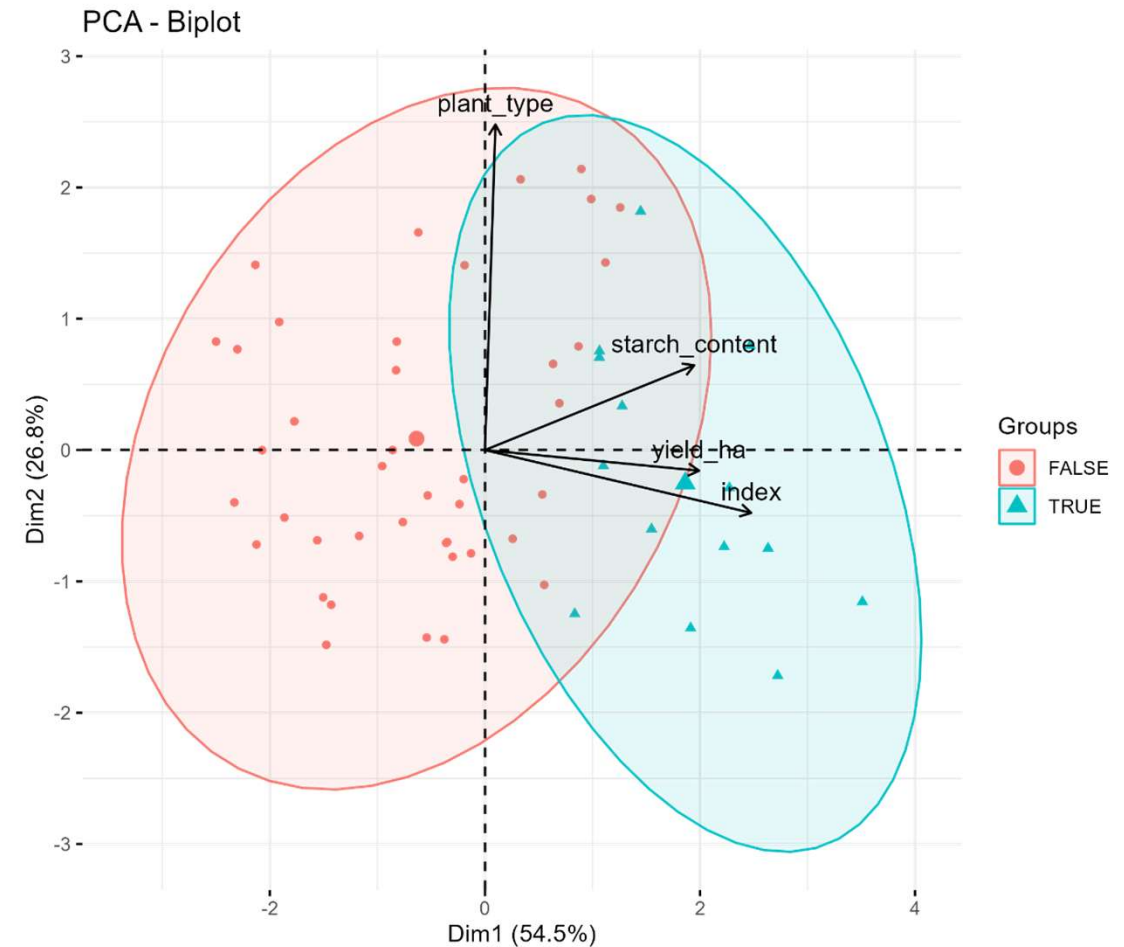
Index Selection

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


2) Scores given were:

- **Starch_content = 10**
- **yield_ha = 10**
- **plant_type = -5**

3) Percentage to be selected: **25%**





GitHub repo

 Ifdelgadam Location map added 7b89026 · now 8 Commits

data	first commit and tidy data done	18 hours ago
images	data analysis done	11 hours ago
output	data analysis done	11 hours ago
.gitignore	first commit and tidy data done	18 hours ago
2023MDEPR2env.Rproj	first commit and tidy data done	18 hours ago
README.md	Location map added	now
statistical_analysis.R	data analysis done	11 hours ago
tidying_data_up.R	first commit and tidy data done	18 hours ago

README

2023MDEPR2env

The preliminary trials of the pipeline - CMD-resistance cassava for starch and animal feed

TPE: subhumid and semi-arid lowland tropics

locations: Tay Nihn and Dong Nai, Vietnam

breeding cycle: Cohort 1 of cycle 1

Project: ACIAR, USAID

Purpose: 1) Improve breeding populations; 2) Deliver variety candidates to NARES in Asia and Africa; 3) Perform "training-by-doing"



<https://github.com/Cassava2050/2023MDEPR2env.git>



Thank you!