



Data analysis 2022BCEPR2env-set2

- 202230BCEPR\_ciat- 202238BCEPR\_cere

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@BiovIntClAT\_eng
@BiovIntClAT\_esp

#Alliance4Science

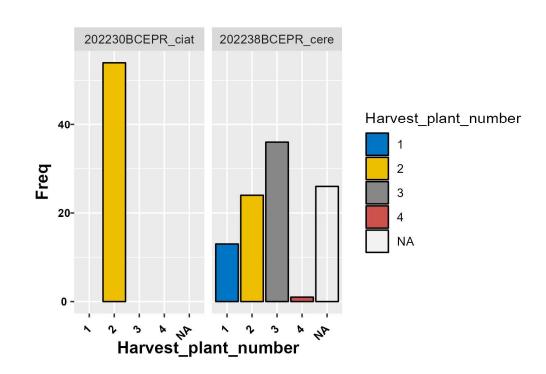
The Alliance of Bioversity International and the International Center for Tropical Agriculture (CIAT) is part of CGIAR, a global research partnership for a food-secure future

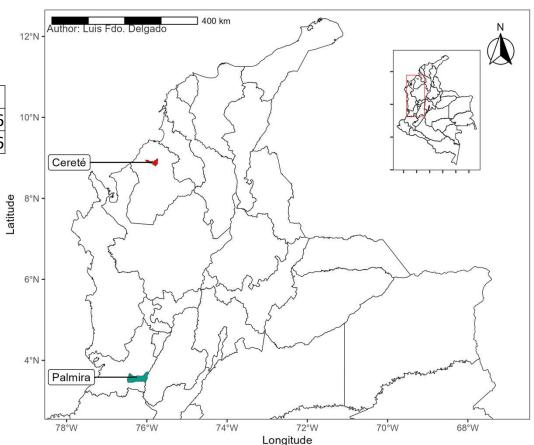
### Resolvable row-col with randomized checks

use_trial_name	use_plant_date	use_harvest_date	harvesting_time	use_location	n_gen
202230BCEPR_ciat	2022-July-07	2023-May-09	10month 2day	CIAT. Valle, Colombia	46
202238BCEPR_cere	2022-August-05	2023-May-10	9month 5day	Cerete. Cordoba, Colombia	46

### Plot size:

- 202230BCEPR\_ciat, 5 plants per plot, harvesting 2 plants for root\_type
- 202238BCEPR\_cere, 5 plants per plot, harvesting 4 plants for yield





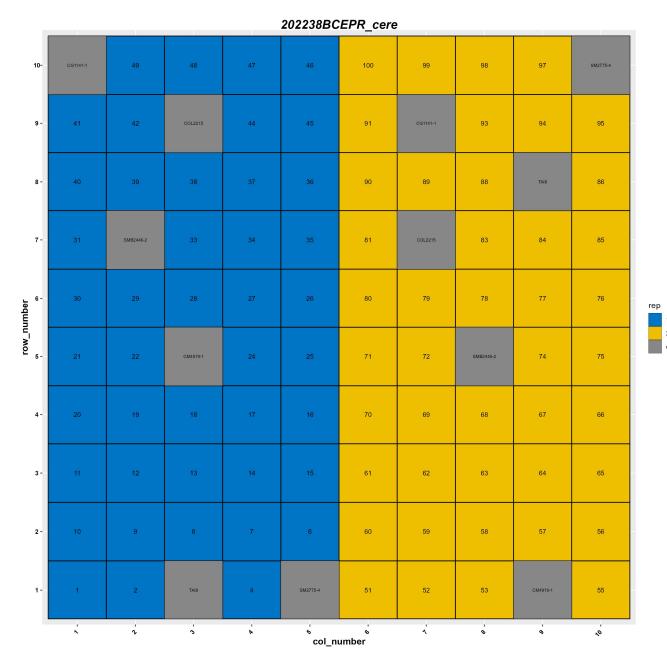


### **Trial Design – Row col**

# 202230BCEPR\_ciat

col\_number

### **Check varieties are completely randomized**

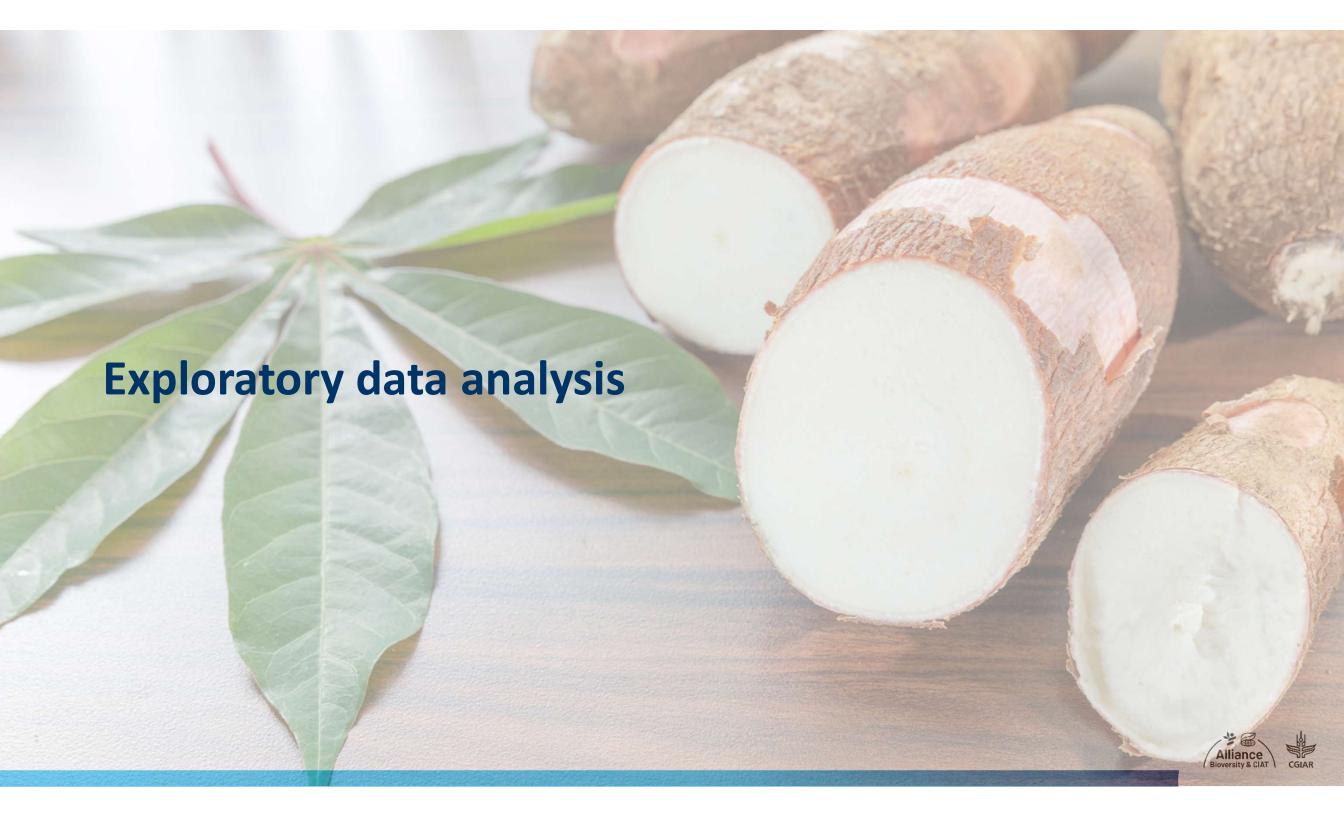




### **Check genotypes**

- 1. CG1141-1\_is\_Costena
- 2. CM4919-1\_is\_Veronica
- 3. COL2215\_is\_Venezolana
- 4. SM2775-4\_is\_Bellotti
- 5. SMB2446-2\_is\_Caiseli
- 6. TAI8\_is\_TAI



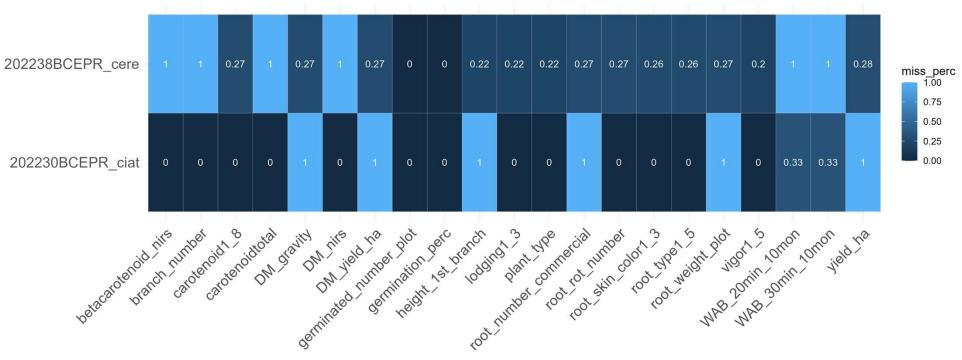


### **Traits evaluated**

betacarotenoid_nirs
branch_number
carotenoid1_8
carotenoidtotal
DM_gravity
DM_nirs
DM_yield_ha
germinated_number_plot
germination_perc
height_1st_branch
lodging1_3
plant_type
root_number_commercial
root_rot_number
root_skin_color1_3
root_type1_5
root_weight_plot
vigor1_5
WAB_20min_10mon
WAB_30min_10mon
yield_ha

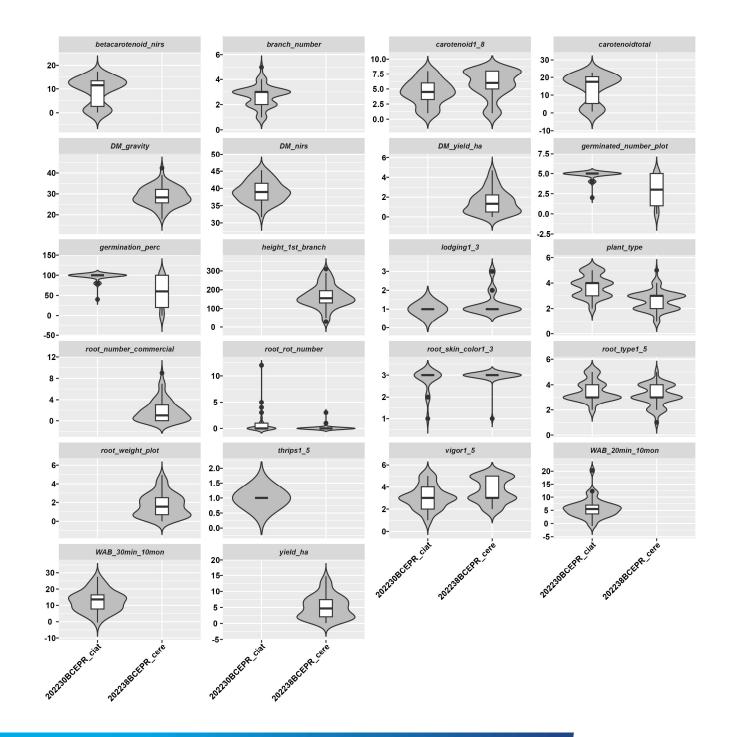
### Missing values across trials

Percentage of missing values (exp/trait)





# Trait variation across trials (phenotypic value)

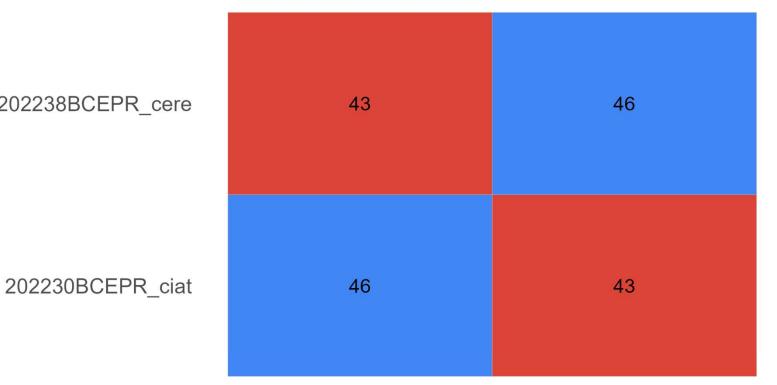


### **Shared genotypes**

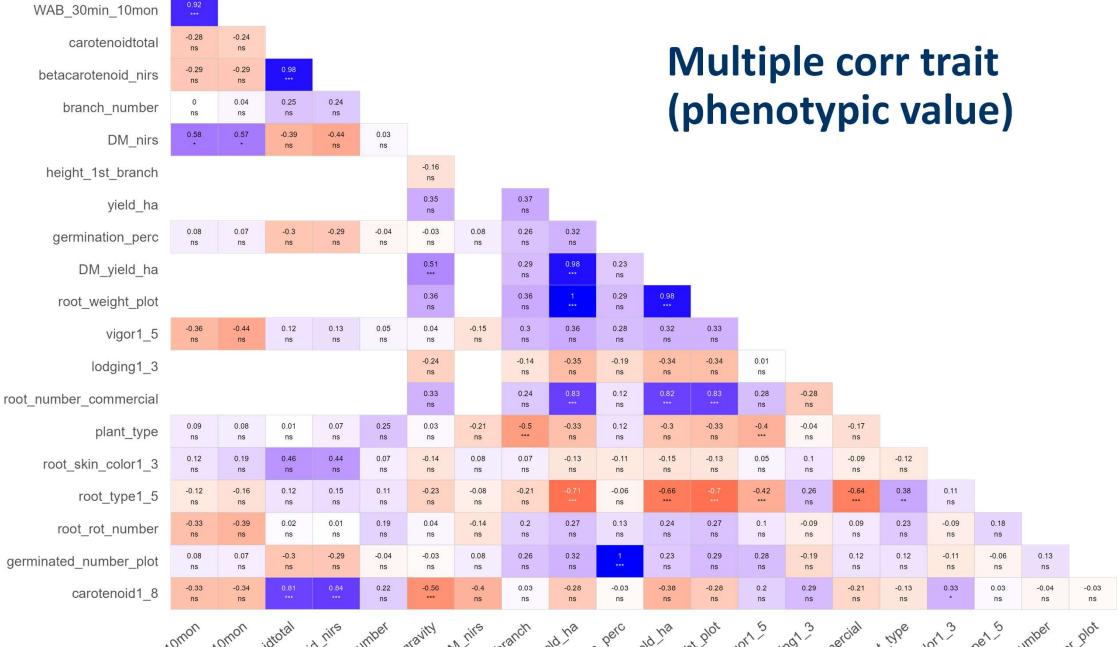
**Connectivity Matrix** 

**43 -46** shared genotypes found.

202238BCEPR\_cere



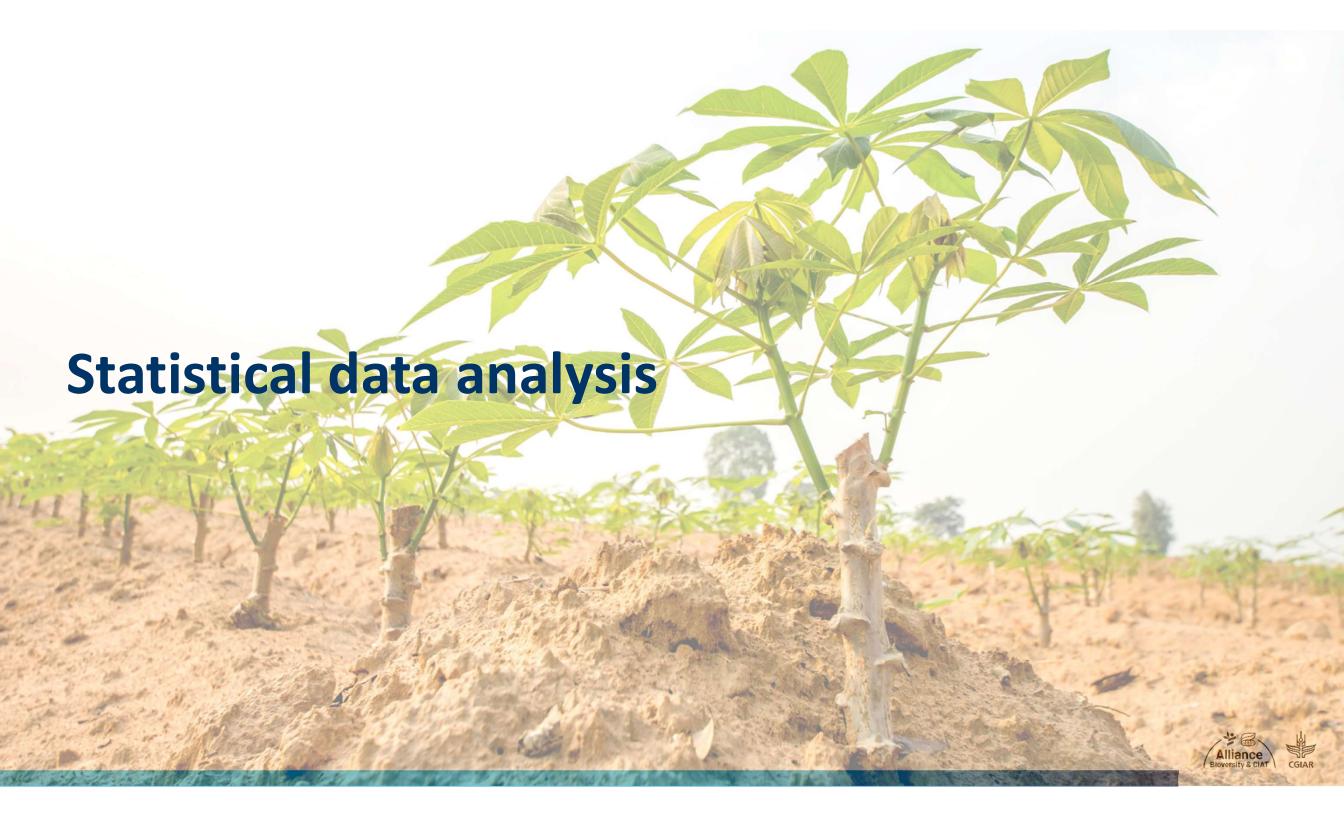




plant type colors, 3 types, 5 rot in gerninated number plot root, jot, number



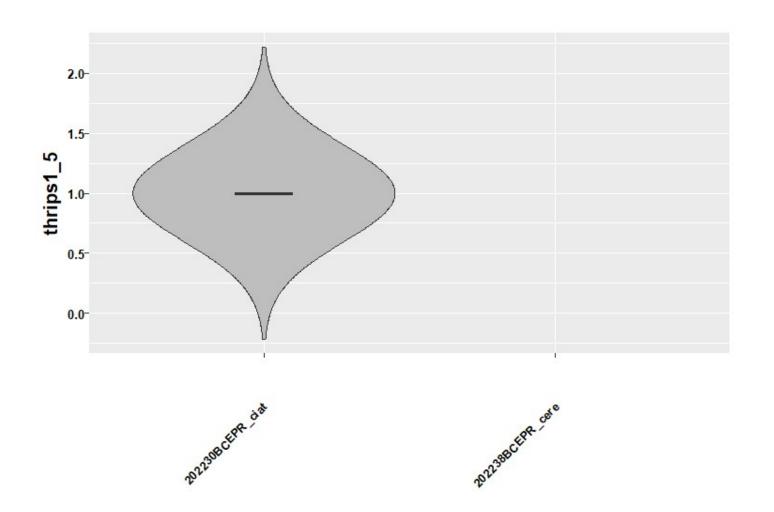




### No variation dropped traits

- thrips1\_5

thrips1\_5 trait
was removed
from the analysis
because its
mean\_of\_sd = 0





### Single heritability

### **Moderate** to **low** heritability among two locations.

4																				
						DM				lodg	gi				1					
	betacarote	e branch_ '	caroten	caroten	DM_g	ٰ nir_ٰ,	DM_yi	germinated_r	germinati <sup>)</sup>	neight_1s ng¹	plant	root_number	root_rot	root_skin	root_t	root_wei	vigo	WAB_20m	WAB_30m	yield
trial	noid_nirs	number	oid1_8	oidtotal	ravity	<u> S</u>	eld_ha	umber_plot	on_perc	t_branch 3	_type	e_commercial	_number	_color1_3	ype1_5	ght_plot <sup>ا</sup>	r1_5	_in_10mon	in_10mon	_ha
202230BC					<del>_</del> ′		<u> </u>													,
EPR_ciat	1	1 0.74	1	4 7	<b>4</b> "	0.97	<b>/</b>				0.88	<u>'</u>	0.99	0.84	0.64	<u> </u>	0.88	0.24	0.41	<u> </u>
202238BC						4								<u>'</u>				4		
EPR_cere	1	, r	0.89	<b>_</b> '	0.81	4′	0.6	0.81	0.81	0.76 0	0.55	5 0.54	0.36	<u> </u>	0.36	6 0.58	<u>ر</u> ک	<u> </u>	<u>,                                     </u>	0.56

Below single heritability is too high to be true (202230BCEPR\_ciat trial)

trait	trial	heritability
carotenoidtotal	202230BCEPR_ciat	1
betacarotenoid_nirs	202230BCEPR_ciat	1
DM_nirs	202230BCEPR_ciat	0.97
root_rot_number	202230BCEPR_ciat	0.99
carotenoid1_8	202230BCEPR_ciat	1

Without the information on random variability and experimental error provided by replication, single heritability may be **overestimated** because these sources of variation are not accounted for. Therefore, it is important to interpret heritability results from trials without **replications** with **caution** and to consider the possibility that replication controls may influence the results.





## Thank you!