



Data analysis DVPRG 10 environments

**202050DVPRG_ciat, 202081DVPRG_momi,
202082DVPRG_pivi
202217DVPRG_momi, 202118DVPRG_momi,
202121DVPRG_repe, 202136DVPRG_ciat, 202218DVPRG_repe
202252DVPRG_stom, 202231DVPRG_ciat**

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Palmira, July 2022

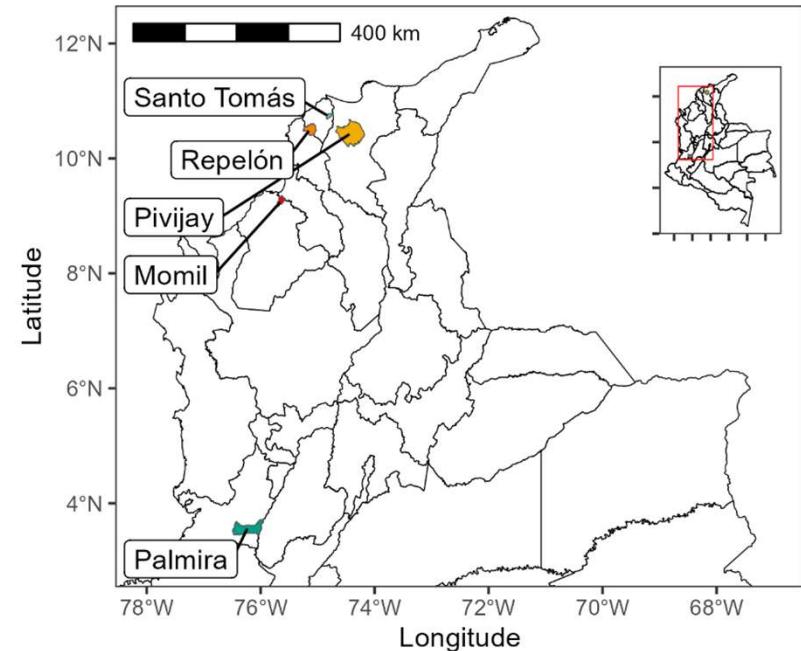


@BiovIntCIAT_eng
@BiovIntCIAT_esp

#Alliance4Science

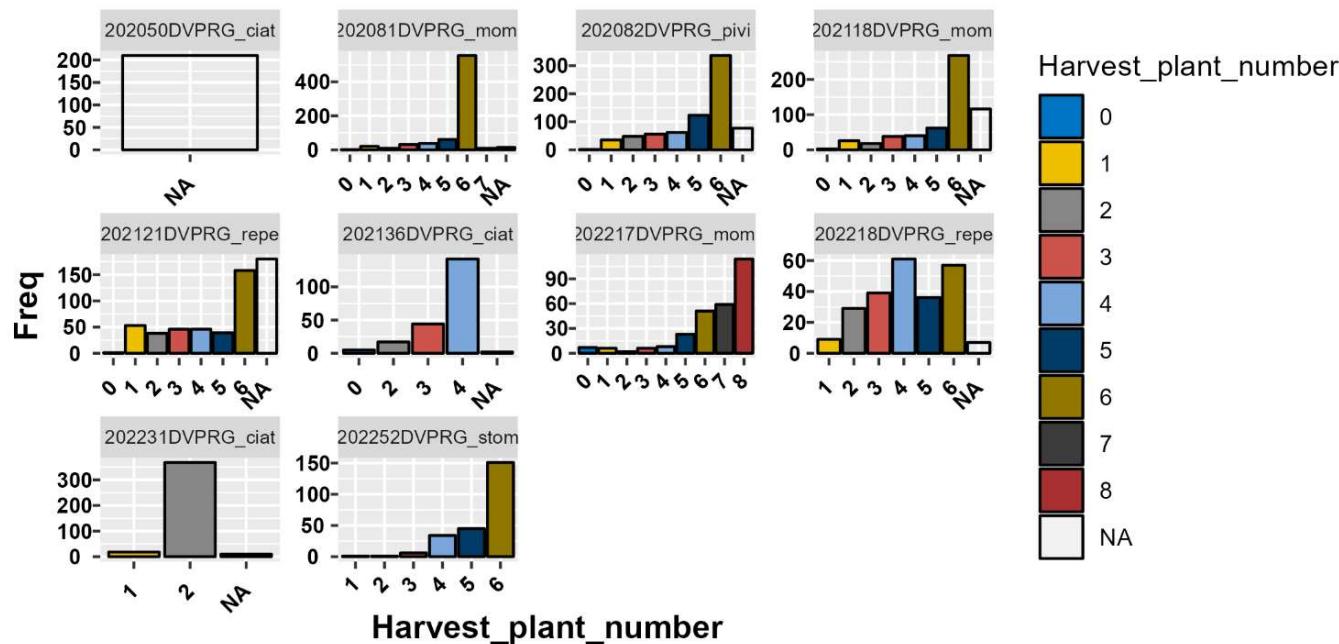
Resolvable row-col with randomized checks

use_trial_name	use_plant_date	use_harvest_date	harvesting_time	use_location	n_gen
202050DVPRG_ciat	2020-July-21	Not harvested		CIAT. Valle, Colombia	208
202081DVPRG_momi	2020-July-22	2021-May-03	9month 11day	Momil. Cordoba, Colombia	228
202082DVPRG_pivi	2020-July-08	2021-April-30	9month 22day	Pivijay. Magdalena, Colombia	226
202118DVPRG_momi	2021-May-20	2022-March-25	10month 5day	Momil. Cordoba, Colombia	181
202121DVPRG_repe	2021-June-01	2022-March-23	9month 22day	Repelon. Atlantico, Colombia	180
202136DVPRG_ciat	2021-July-29	2022-May-30	10month 1day	CIAT. Valle, Colombia	197
202217DVPRG_momi	2022-May-19	2023-March-02	9month 11day	Momil. Cordoba, Colombia	135
202218DVPRG_repe	2022-May-08	2023-February-21	9month 13day	Repelon. Atlantico, Colombia	117
202252DVPRG_stom	2022-June-30	2023-March-03	8month 3day	Santo Tomas. Atlantico, Colombia	117
202231DVPRG_ciat	2022-July-07	2023-May-19	10month 12day	CIAT. Valle, Colombia	345

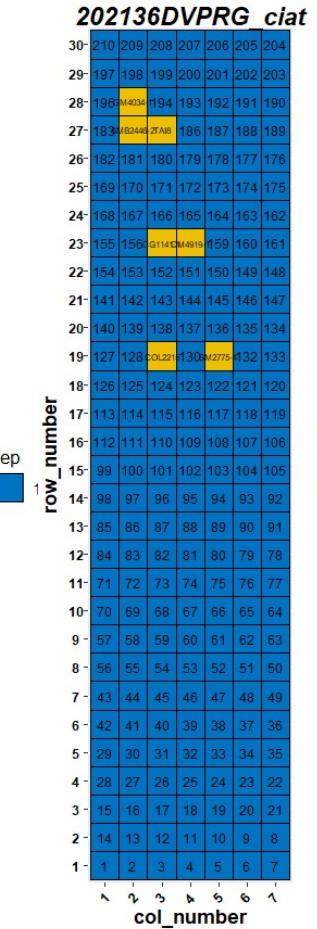
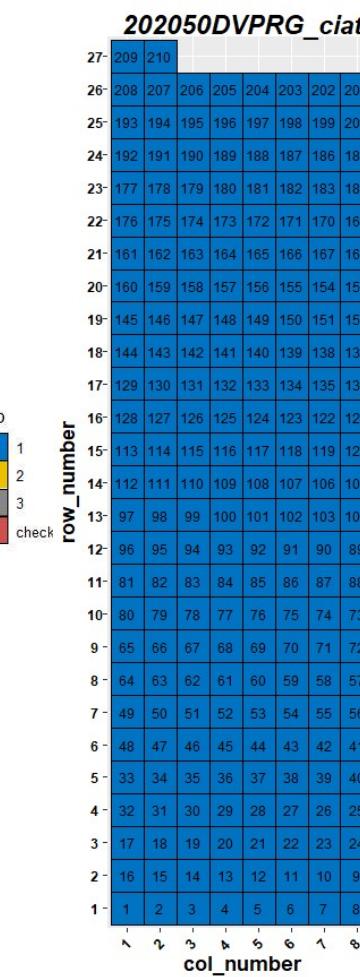
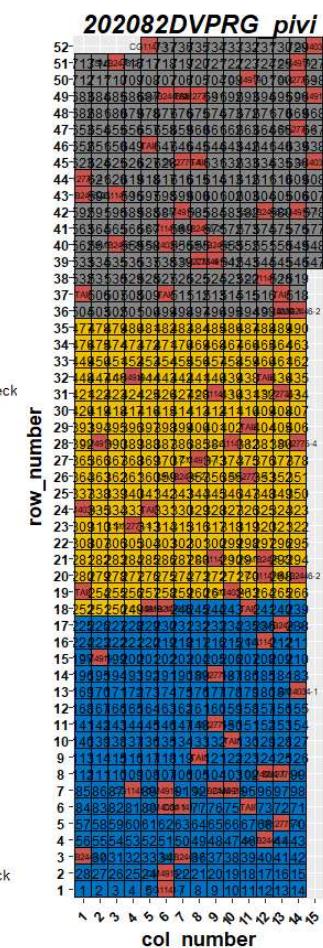
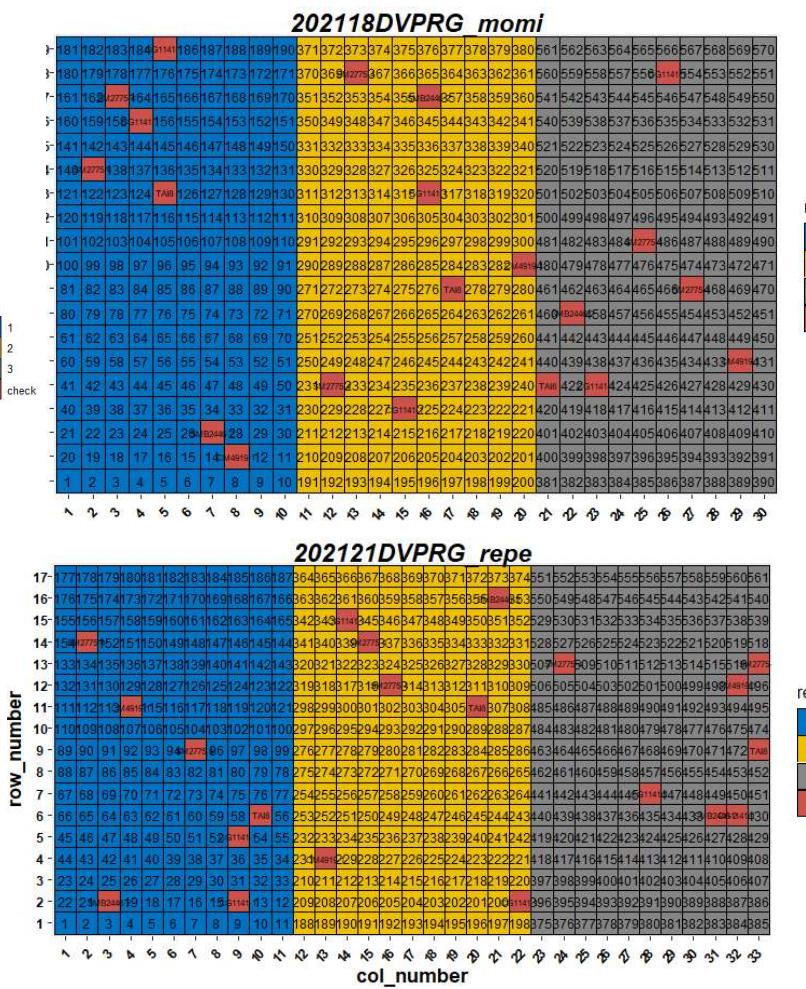
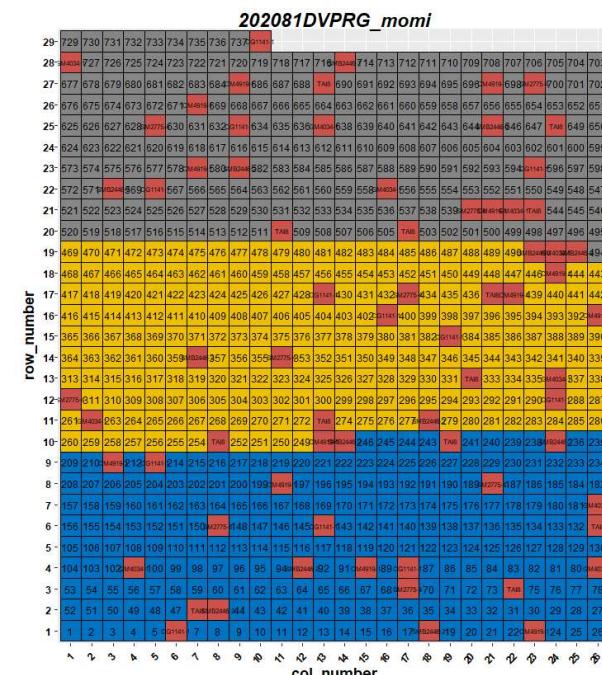


Plot size:

- 202081DVPRG_momi: **10** plants per plot, harvesting **6** plants for yield
- 202082DVPRG_pivi: **10** plants per plot, harvesting **6** plants for yield
- 202118DVPRG_momi: **10** plants per plot, harvesting **6** plants for yield
- 202121DVPRG_repe: **10** plants per plot, harvesting **6** plants for yield
- 202217DVPRG_momi: **10** plants per plot, harvesting **8** plants for yield
- 202218DVPRG_repe: **10** plants per plot, harvesting **6** plants for yield
- 202252DVPRG_stom: **10** plants per plot, harvesting **6** plants for yield
- 202231DVPRG_ciat: **5** plants per plot, harvesting **2** plants for yield



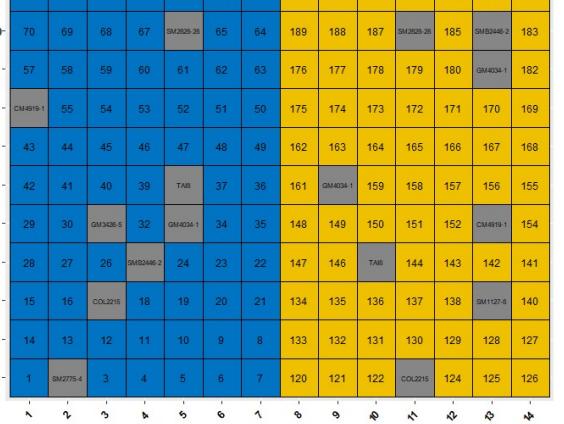
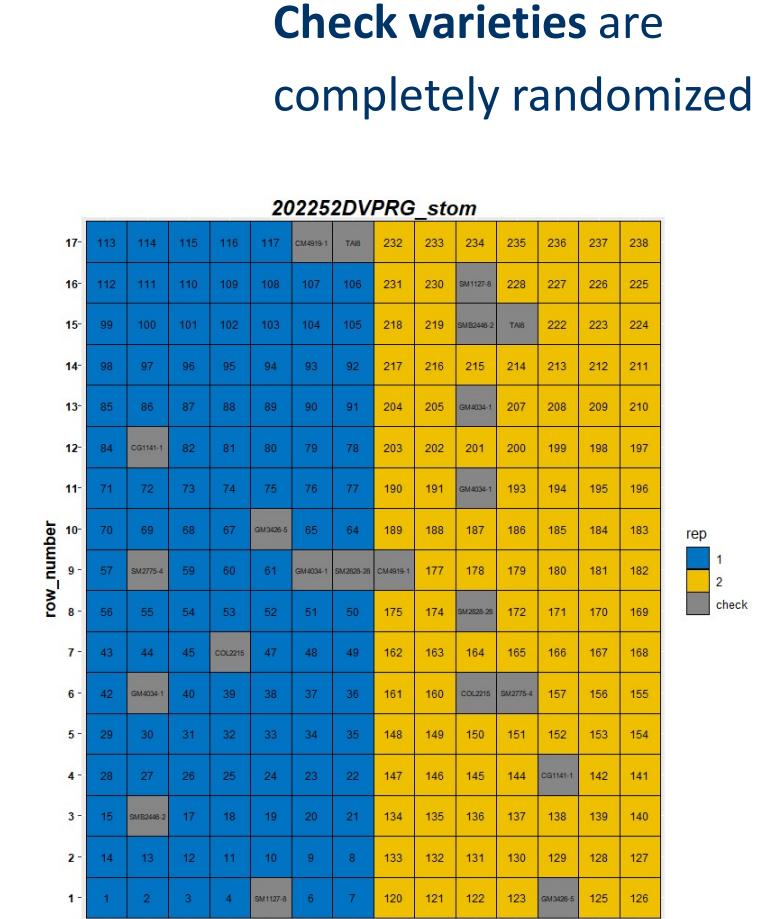
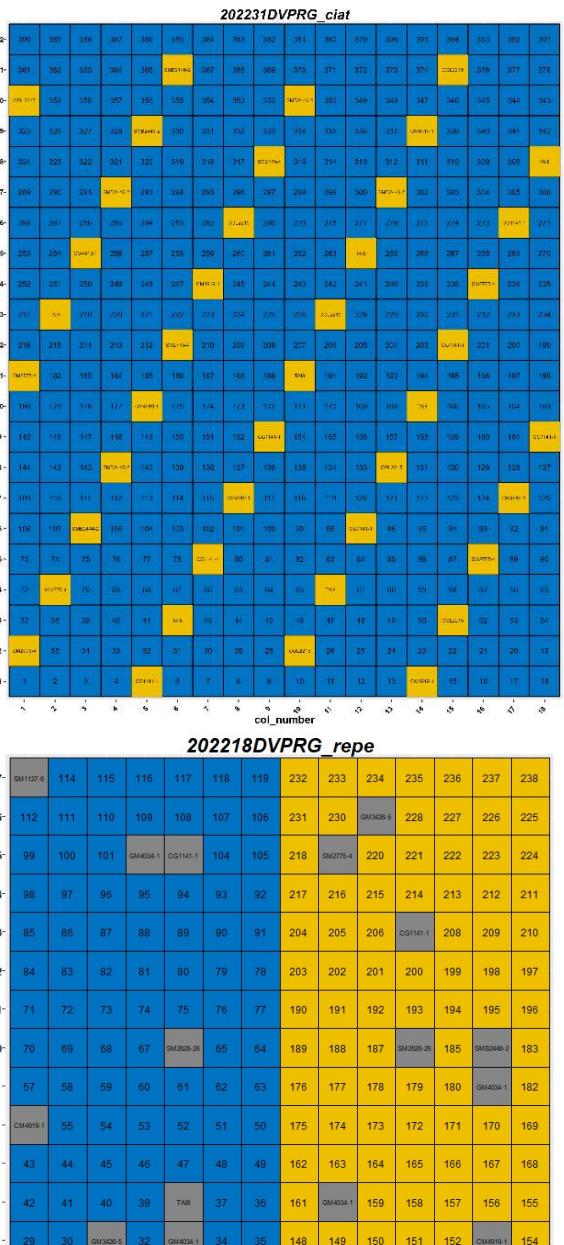
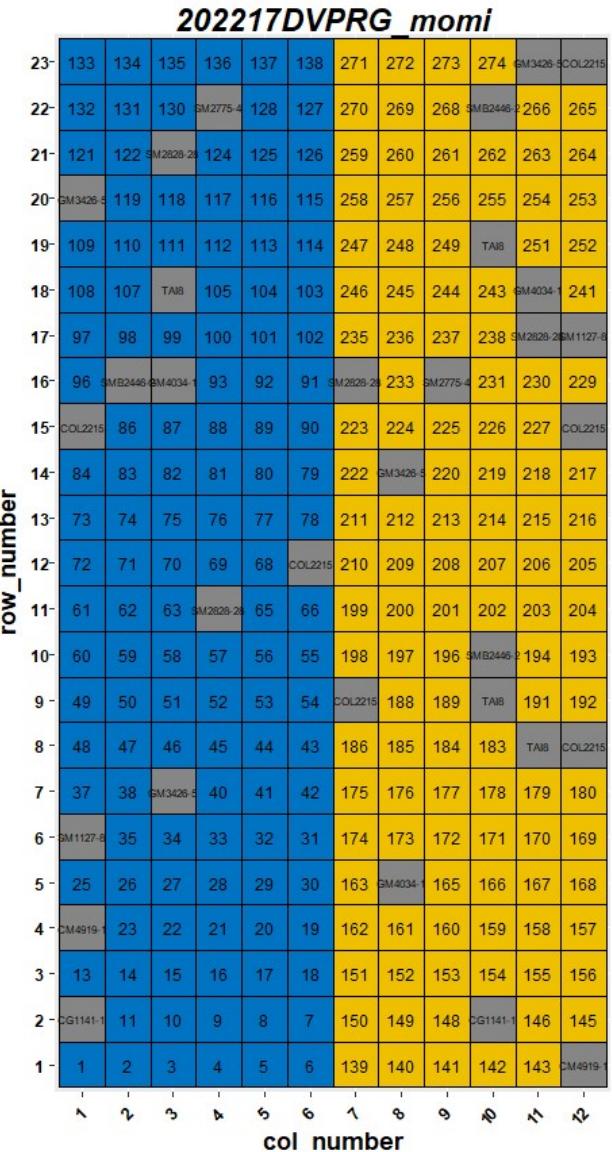
Trial Design – Row col



Group 1

Check varieties are completely randomized

Trial Design – Row Group 2



Check genotypes

1. CG1141-1_is_Costena
2. CG489-31_is_NAT31
3. CM4919-1_is_Veronica
4. CM523-7_is_Catumare
5. CM6438-14_is_Vergara
6. CM6740-7_is_Reina
7. COL2215_is_Venezolana
8. GM4034-1_is_Reina_wx
9. HMC1P12_is_HMC1
10. SM1127-8_is_Cubana

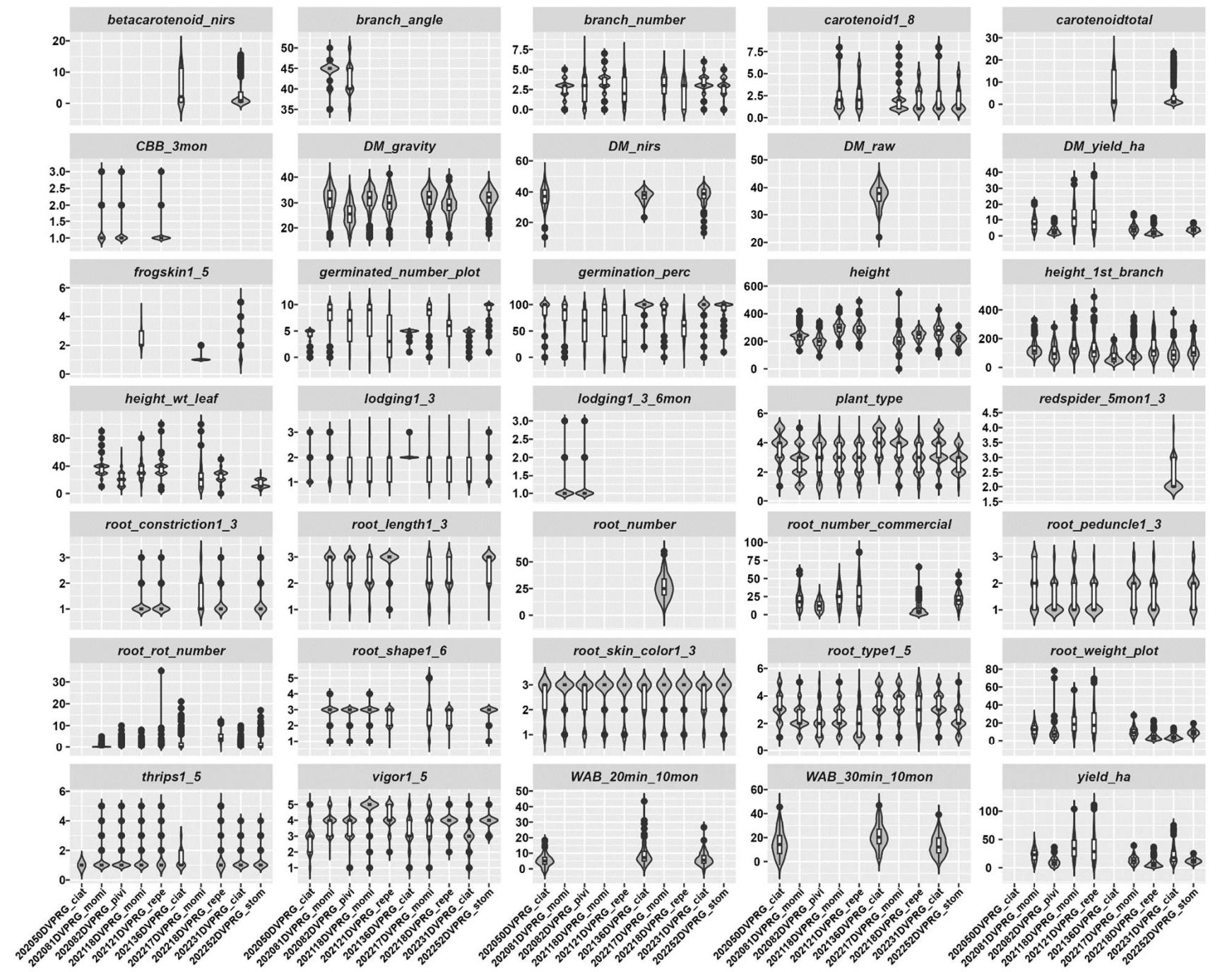


Exploratory data análisis

Traits evaluated

Traits evaluated	
betacarotenoid_nirs	lodging1_3_6mon
branch_angle	plant_type
branch_number	root_constriction1_3
carotenoid1_8	root_length1_3
carotenoidtotal	root_number
CBB_3mon	root_number_commercial
DM_gravity	root_peduncle1_3
DM_nirs	root_rot_number
DM_raw	root_shape1_6
DM_yield_ha	root_skin_color1_3
frogskin1_5	root_type1_5
germinated_number_plot	root_weight_plot
germination_perc	thrips1_5
height	vigor1_5
height_1st_branch	WAB_20min_10mon
height_wt_leaf	WAB_30min_10mon
lodging1_3	yield_ha

Trait variation across trials (phenotypic value)



Shared genotypes

Connectivity Matrix

202136DVPRG_ciat	15	15	15	196	157	157	196	192	189	197
202050DVPRG_ciat	15	15	15	188	159	158	200	194	208	189
202082DVPRG_pivi	16	16	16	206	177	176	222	226	194	192
202081DVPRG_momi	16	16	16	207	181	180	228	222	200	196
202121DVPRG_repe	13	13	13	164	180	180	180	176	158	157
202118DVPRG_momi	13	13	13	164	181	180	181	177	159	157
202231DVPRG_ciat	133	115	115	345	164	164	207	206	188	196
202252DVPRG_stom	117	117	117	115	13	13	16	16	15	15
202218DVPRG_repe	117	117	117	115	13	13	16	16	15	15
202217DVPRG_momi	135	117	117	133	13	13	16	16	15	15

Due to the common number of genotypes, two trial groups were made.

Group 1:

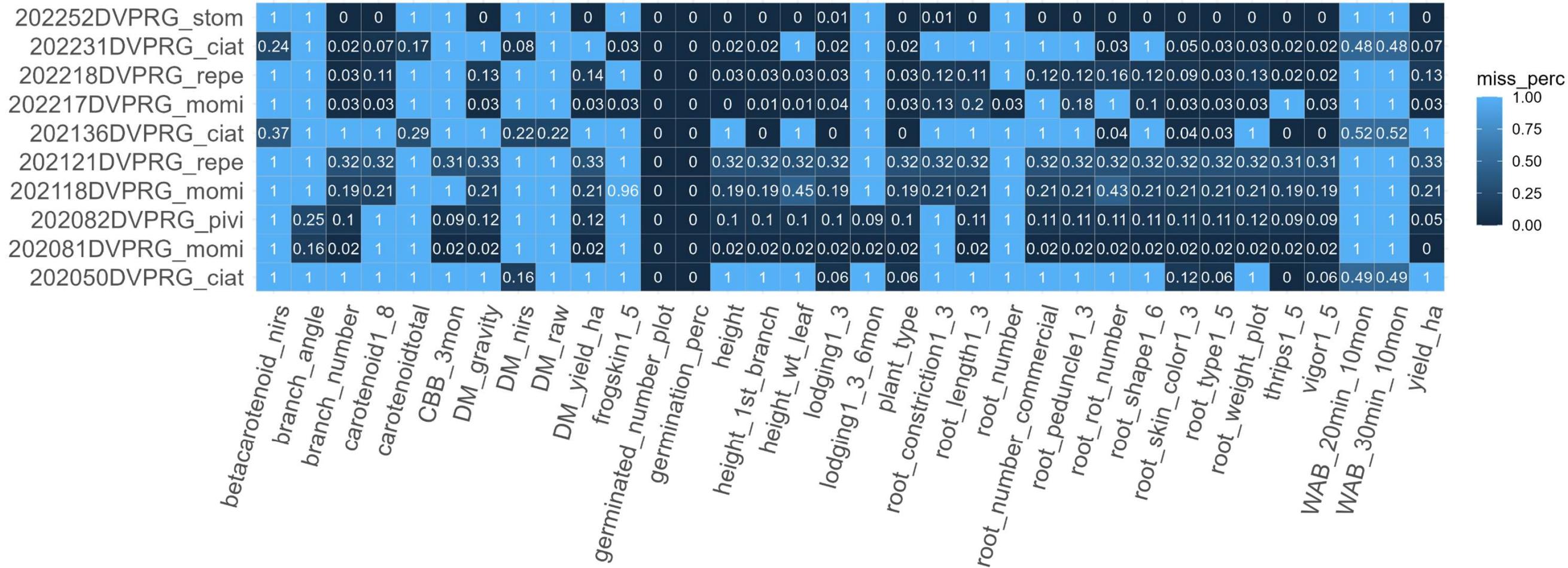
- 202050DVPRG_ciat
- 202081DVPRG_momi
- 202082DVPRG_pivi
- 202121DVPRG_repe
- 202118DVPRG_momi
- 202136DVPRG_ciat

Group 2:

- 202217DVPRG_momi
- 202218DVPRG_repe
- 202252DVPRG_stom
- 202231DVPRG_ciat

Missing values

Percentage of missing values (exp/trait)



**The shared clones were used as
a bridge to put the two groups
together to calculate the final
BLUP during GxE analysis**

Multiple corr trait (phenotypic value)

All trials



Statistical data analysis

Single heritability

Moderate to high heritability showing the good trial management at 7 locations.

trial	branch_angle	branch_number	carotenoid1_8	CBB_3mon	DM_gravity	DM_yield_ha	frogskin1_5	germinated_number_plot	germination_percent	height_branch	height_1st_leaf	height_weight	lodging1_3mon	plant_type	root_constriction1_3	root_length	root_number	root_number_commercial	root_number_cle1_3	root_number_peduncular	root_number_root	root_number_sha1_6	root_skin_color1_3	root_type1_5	root_weight	thrips1_5	vigor1_5	yieldha	
202081DVPR	0.5	0.89		0.22	0.95	0.88		0.87	0.87	0.89	0.84	0.64	0.85	0.73	0.88		0.5		0.82	0.72	0.23	0.58	0.97	0.78	0.85	0.86	0.72	0.86	
202082DVPR	0.49	0.88		0.45	0.94	0.87		0.9	0.90	0.88	0.89	0.8	0.79	0.28	0.86		0.71		0.82	0.74	0.52	0.74	0.96	0.86	0.63	0.82	0.71	0.87	
202118DVPR		0.84	0.96		0.96	0.86		0.96	0.96	0.77	0.88	0.53	0.73		0.8	0.3	0.39		0.82	0.64	0.19	0.48	0.96	0.79	0.83	0.62	0.74	0.83	
202121DVPR		0.92	0.94	0.01	0.91	0.84		0.92	0.92	0.88	0.88	0.7	0.71		0.83	0.34	0.67		0.8	0.51	0.01	0.52	0.98	0.78	0.83	0.81	0.67	0.83	
202217DVPR		0.88	0.92		0.81	0.6	0.58		0.74	0.74	0.5	0.89	0.58	0.75		0.87	0.6	0.49	0.62		0.66		0.49	0.98	0.61	0.61		0.57	0.61
202218DVPR		0.85	0.76		0.65	0.53		0.33	0.33	0.74	0.89	0.65	0.54		0.76	0.39	0.34		0.28	0.46	0	0.21	0.94	0.64	0.51	0.94	0.42	0.51	
202252DVPR		0.89	0.9		0.84	0.83		0.68	0.68	0.81	0.92	0.51	0.42		0.66	0.67	0.31		0.72	0.85	0.24	0.48	0.98	0.79	0.8	0.78	0.42	0.8	

Heritability gxe all trials

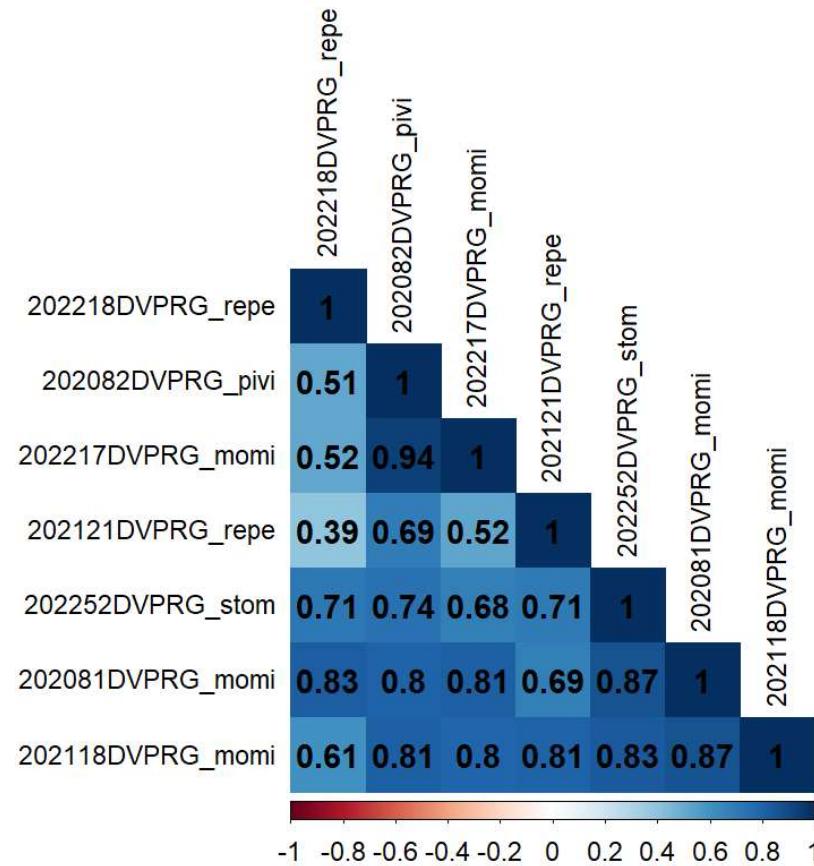
trait	h2
root_skin_color1_3	0.98
carotenoid1_8	0.95
branch_number	0.92
thrips1_5	0.91
height_1st_branch	0.9
DM_gravity	0.89
plant_type	0.88
root_type1_5	0.83
height	0.83
DM_yield_ha	0.82
root_number_commercial	0.8
root_peduncle1_3	0.8
lodging1_3	0.79
yield_ha	0.79
root_weight_plot	0.76
germinated_number_plot	0.74
germination_perc	0.74
height_wt_leaf	0.7
vigor1_5	0.58
root_length1_3	0.58
branch_angle	0.56
root_constriction1_3	0.43
CBB_3mon	0.4
root_shape1_6	0.32
lodging1_3_6mon	0.01

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

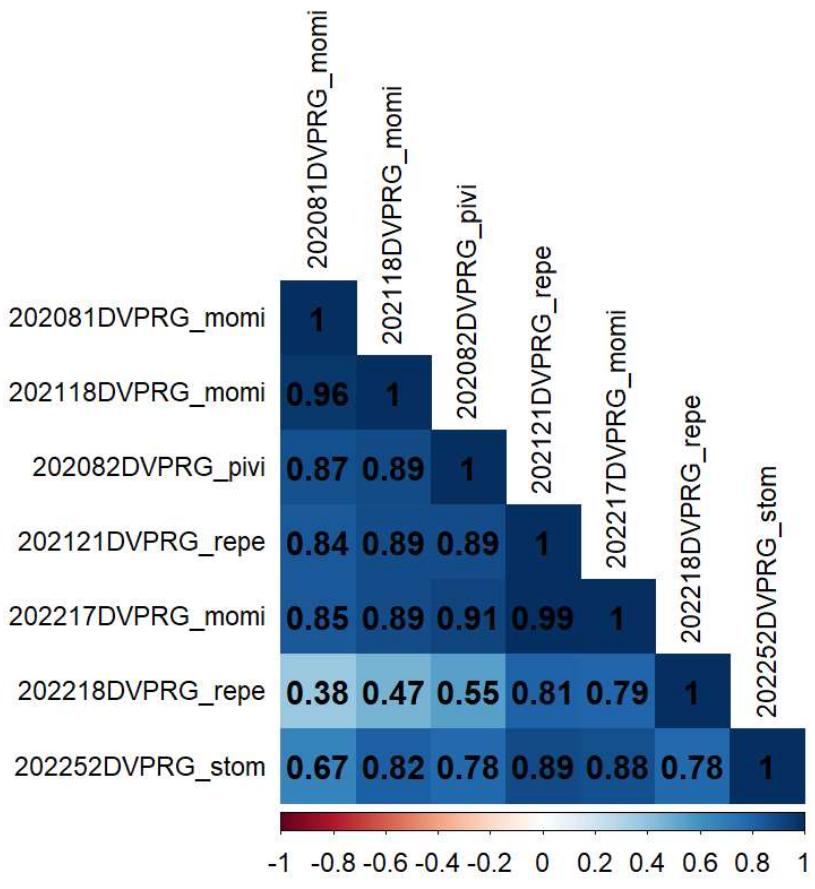
- root_constriction1_3 = 0.43
- CBB_3mon = 0.4
- root_shape1_6 = 0.32
- lodging1_3_6mon = 0.01

Genotypic Correlation: Locations

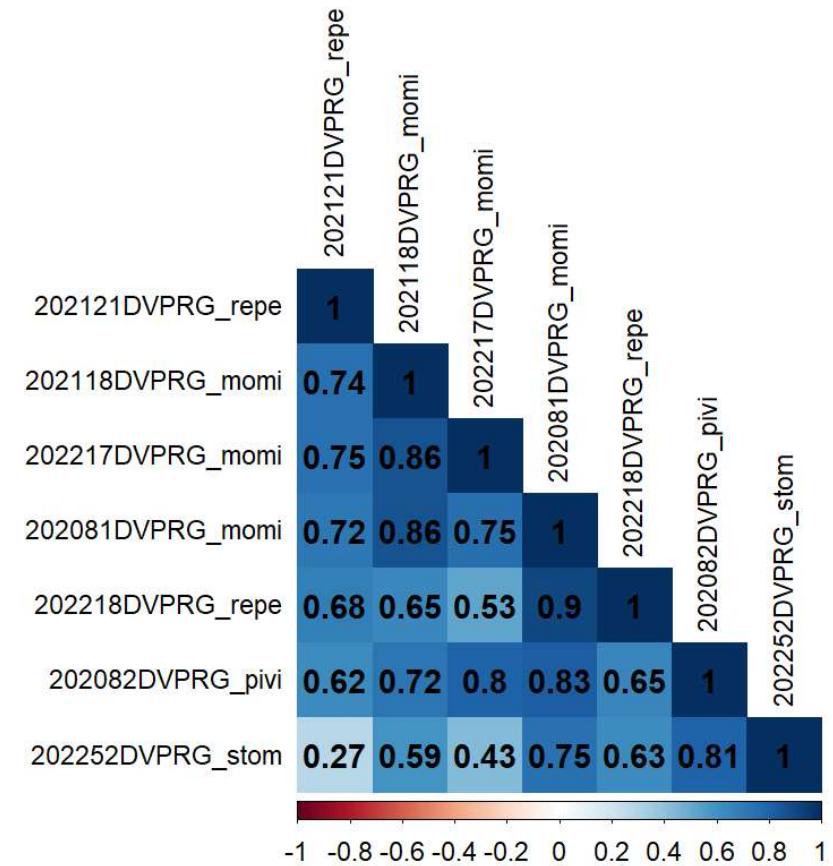
Yield



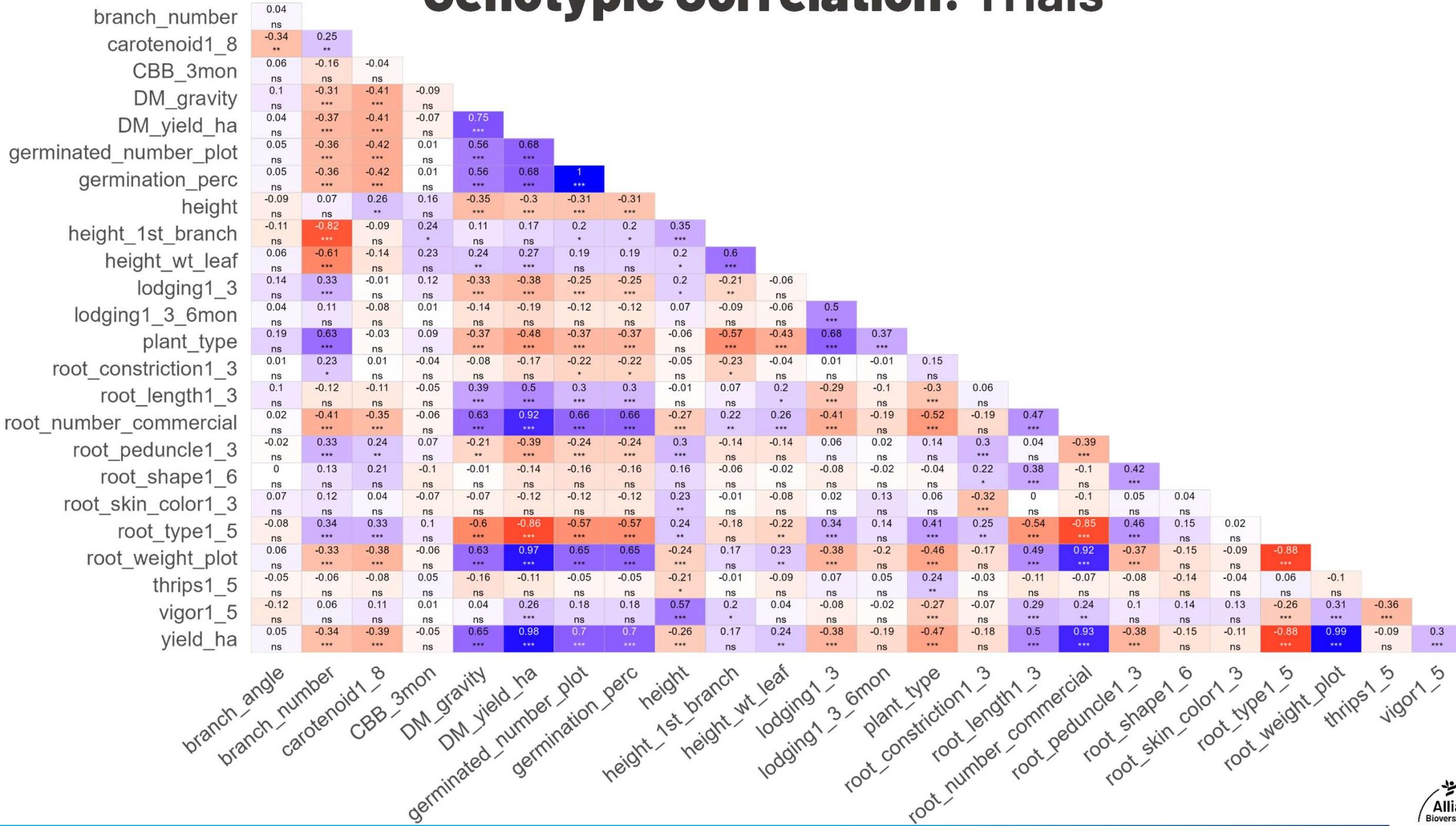
Dry Matter



Plant type

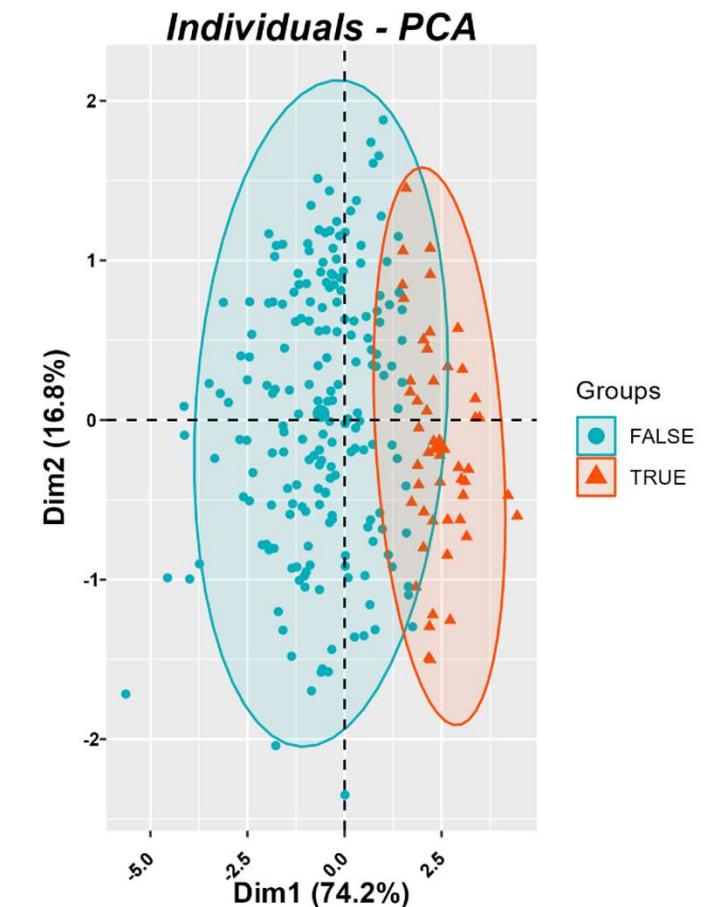
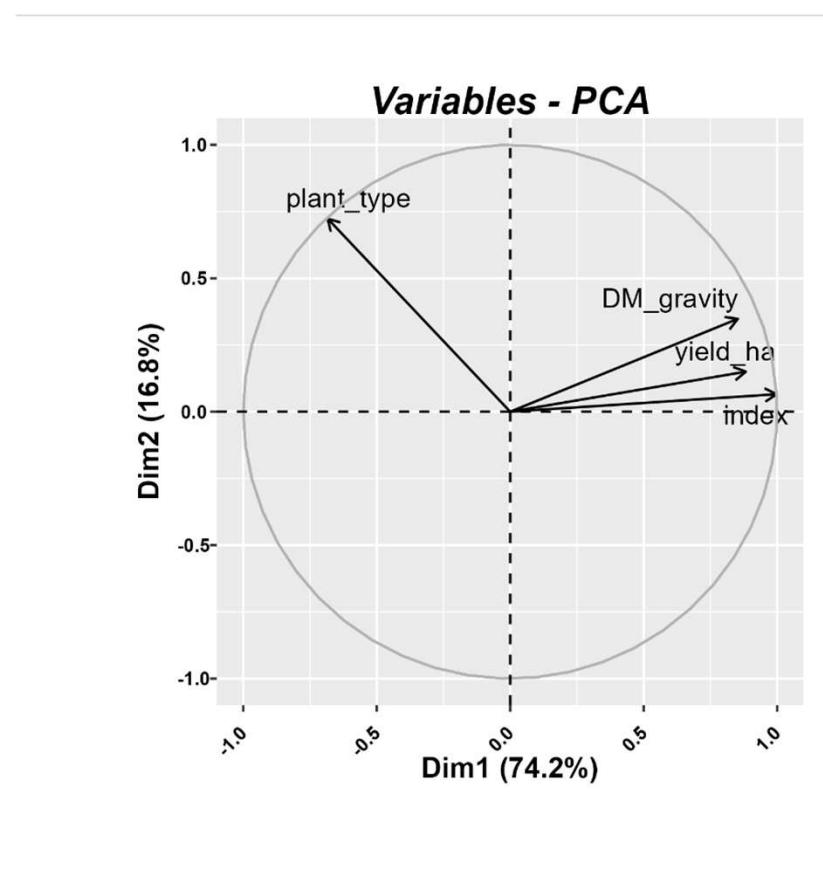


Genotypic Correlation: Trials



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%**





Thank you!