



# Data analysis Andean region

## Biofortified population

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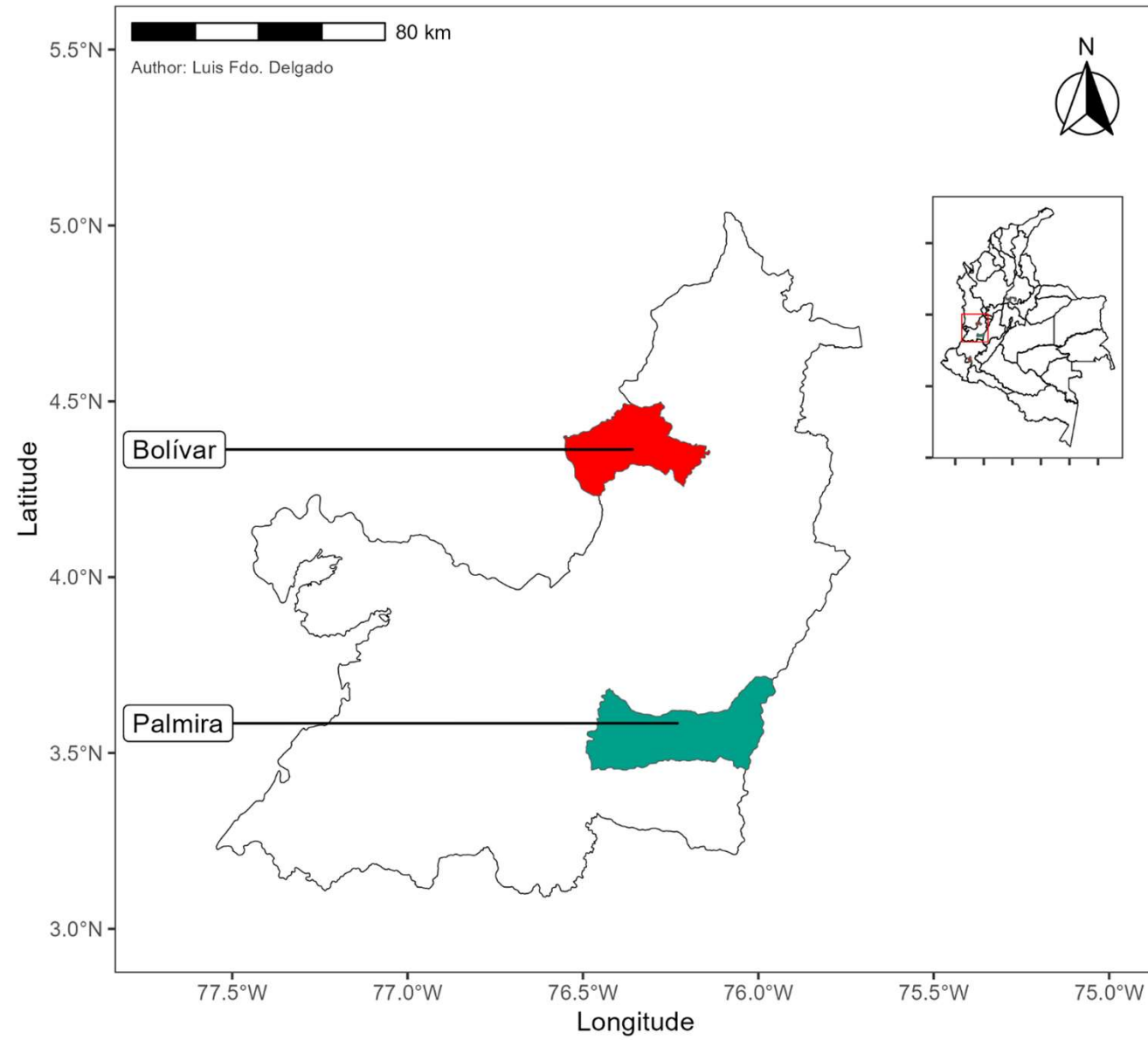
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The Alliance of Bioversity International and the International Center for Tropical Agriculture (CIAT) is part of CGIAR, a global research partnership for a food-secure future

# Trial Locations





# Biofortified cassava population



# Clones & traits evaluated within cooking quality pop

Biofortified clones
GM3594-70
GM3650-51
P13
SM3677-74

<b>Traits evaluated</b>
branch_number
carotenoid1_8
DM_gravity
DM_yield_ha
germination_perc
height
height_1st_branch
height_wt_leaf
lodging1_3
plant_type
root_constriction1_3
root_length1_3
root_number
root_number_commercial
root_peduncle1_3
root_shape1_6
root_skin_color1_3
root_type1_5
thrips1_5
vigor1_5
yield_ha



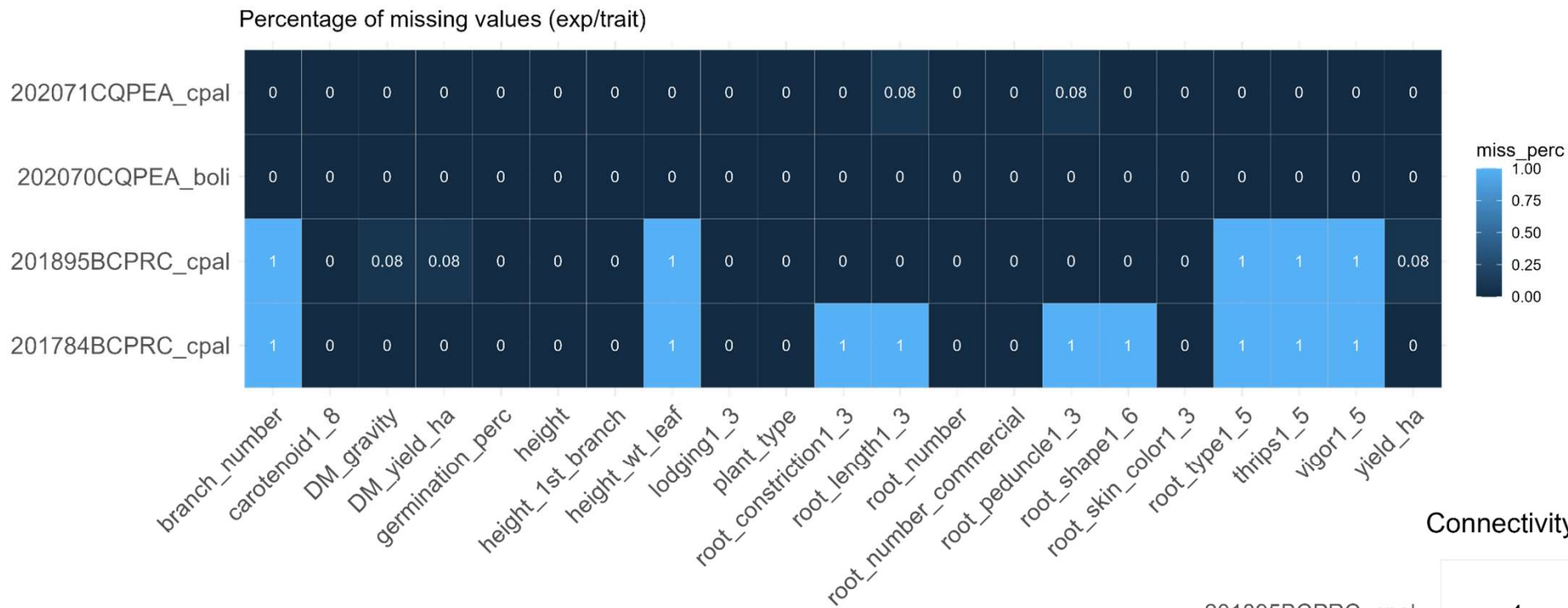
# Exploratory data analysis



# Trait variation across locations.







# Missing values

## Shared genotypes

Connectivity Matrix

201895BCPRC_cpal	4	4	4	4
201784BCPRC_cpal	4	4	4	4
202070CQPEA_boli	4	4	4	4
202071CQPEA_cpal	4	4	4	4

202071CQPEA\_cpal  
202070CQPEA\_boli  
201784BCPRC\_cpal  
201895BCPRC\_cpal



# Statistical data analysis



# Experimental design

1. A resolvable row col design was carried out. The following model was used:

$$y = \textit{accession}_{name} + \textit{trial}_{name} + \textit{accession}_{name} * \textit{trial}_{name} + \textit{rep}_{number} + \textit{rep}_{number} * \textit{row}_{fct} + \textit{rep}_{number} * \textit{col}_{fct} + \textit{error}$$

Where y means Traits evaluated (see slide 4)

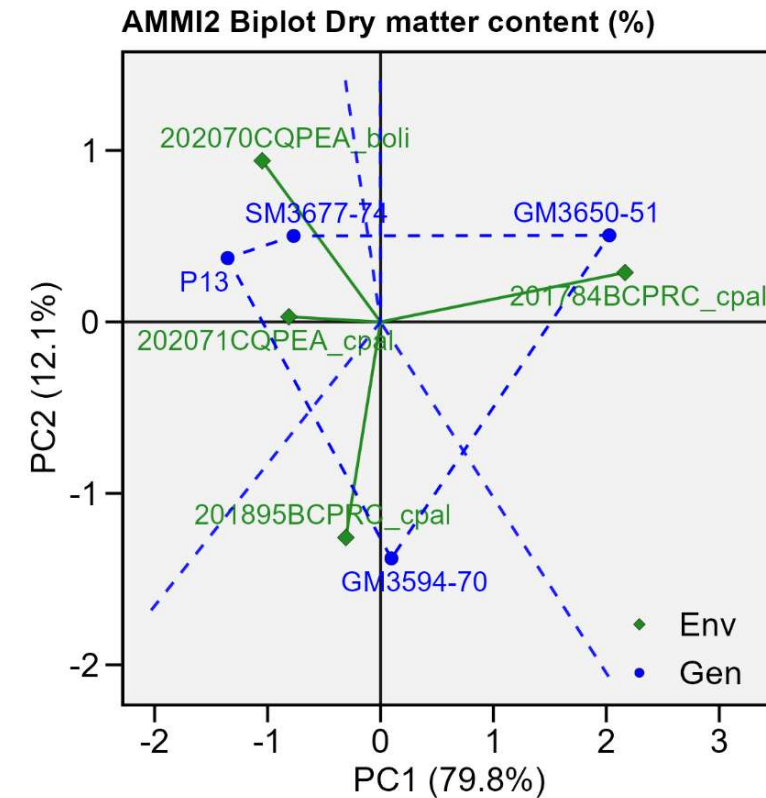
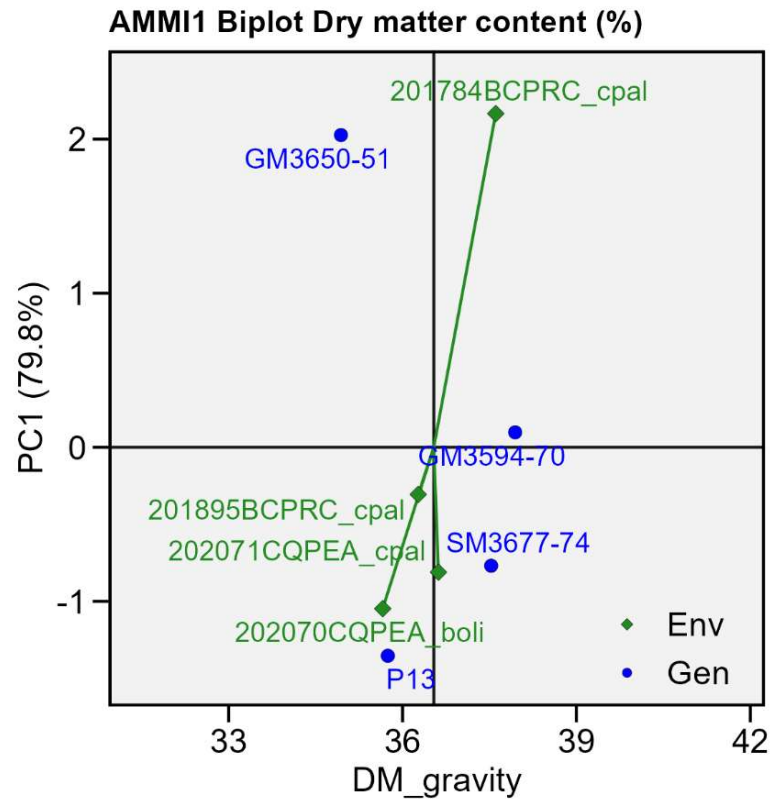
2. Tukey post-hoc test was performed.
3. R Core Team software with the Agricolae library was used for data processing and statistical analysis.

# AMMI analysis

1. AMMI model was performed to yield and DM\_gravity
- 2.
3. R Core Team software with **metan** library was used for perform both AMMI models

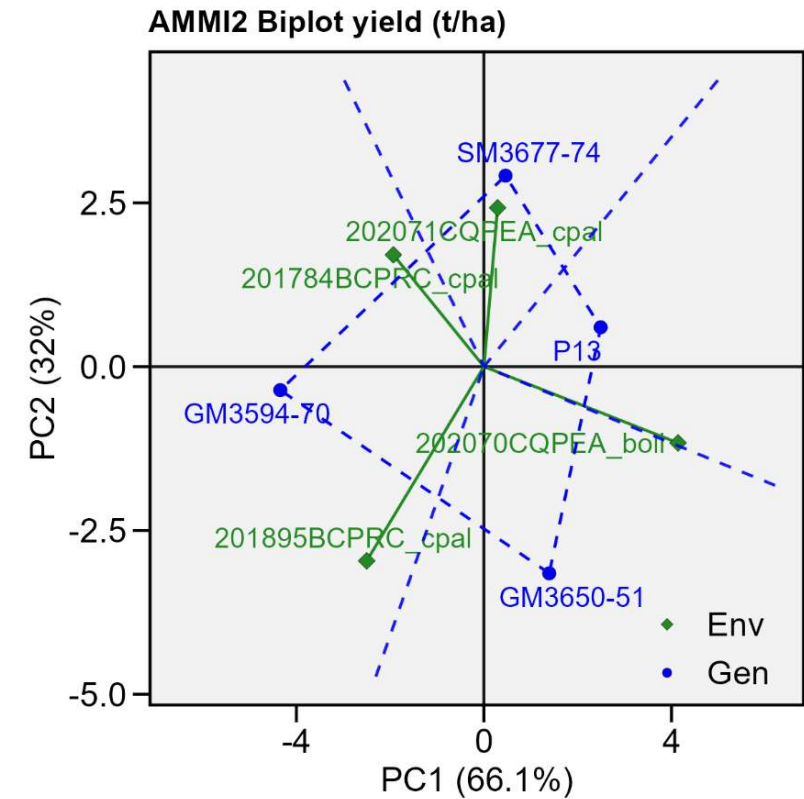
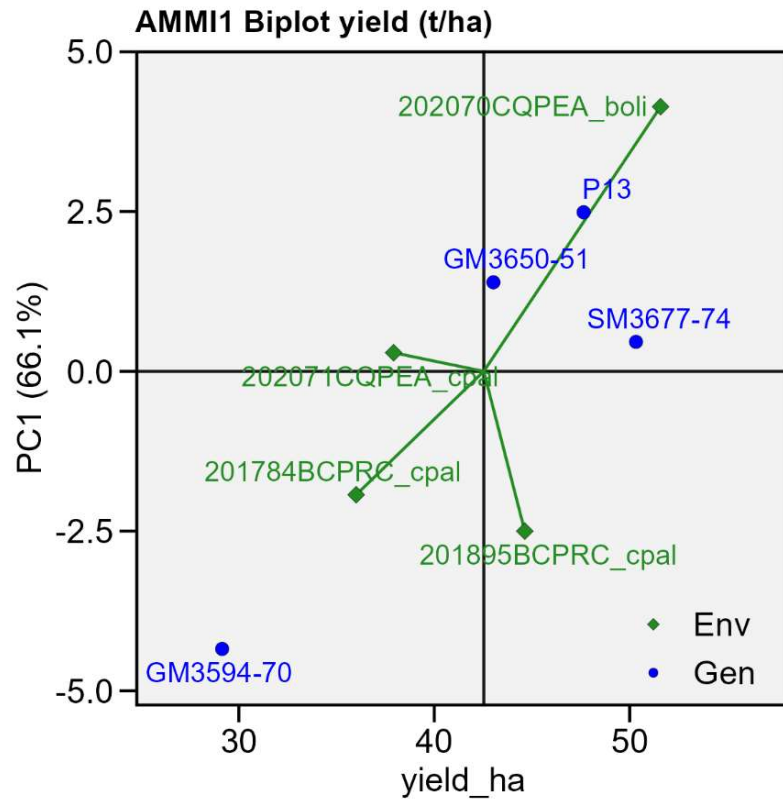


# AMMI DM\_gravity



Genotypes close to origin tend to be more stable than others  
(**SM3677-74 & GM3594-70**).

# AMMI yield\_ha



Genotypes close to origin tend to be more stable than others  
(**SM3677-74 & GM3650-51**).



# Multiple correlation (Pearson coef.) CQ population

# Multiple correlation (Pearson coef.) CQ population

DM_gravity	-0.26 ns																			
height_1st_branch	-0.34 ns	0.14 ns																		
yield_ha	-0.24 ns	0.01 ns	0.22 ns																	
vigor1_5	0.11 ns	0.17 ns	0.42 ns	-0.04 ns																
lodging1_3	0.13 ns	0.02 ns	0.05 ns	-0.34 ns	-0.17 ns															
root_number_commercial	-0.14 ns	0.11 ns	0.06 ns	0.75 ***	-0.01 ns	-0.26 ns														
plant_type	0.13 ns	-0.18 ns	-0.64 ***	-0.07 ns	-0.37 ns	0.01 ns	-0.02 ns													
height	0.3 ns	0.15 ns	0.48 ns	0.01 ns	0.78 **	0.01 ns	-0.03 ns	-0.53 *												
height_wt_leaf	0.1 ns	0.2 ns	-0.04 ns	-0.38 ns	-0.31 ns	0.48 ns	-0.29 ns	-0.06 ns	0 ns											
root_skin_color1_3	-0.25 ns	0.32 ns	0.02 ns	-0.1 ns	-0.28 ns	-0.04 ns	-0.2 ns	0.1 ns	-0.16 ns	0.36 ns										
root_constriction1_3		-0.06 ns	0.27 ns	0.14 ns		-0.03 ns	0.01 ns	-0.25 ns	0.07 ns		0.27 ns									
root_type1_5	0.3 ns	-0.09 ns	-0.16 ns	-0.58 ns	0.32 ns	0.14 ns	-0.25 ns	-0.17 ns	0.37 ns	-0.05 ns	-0.47 ns									
root_length1_3	-0.02 ns	-0.2 ns	0.15 ns	0.25 ns	0.38 ns	-0.1 ns	0.18 ns	-0.07 ns	0.22 ns	-0.55 ns	-0.39 ns	-0.02 ns	0.23 ns							
root_number	-0.48 ns	0.18 ns	0.22 ns	0.76 ***	-0.21 ns	-0.19 ns	0.64 ***	-0.05 ns	-0.07 ns	-0.29 ns	-0.04 ns	0.11 ns	-0.43 ns	0.23 ns						
root_peduncle1_3	0.12 ns	-0.21 ns	0.08 ns	0.04 ns	0.11 ns	-0.01 ns	0.12 ns	-0.29 ns	0.22 ns	0.09 ns	-0.35 ns	-0.35 ns	-0.02 ns	0.26 ns	-0.11 ns					
root_shape1_6	-0.36 ns	0.19 ns	0.11 ns	0.07 ns	-0.11 ns	0.12 ns	0.13 ns	0.07 ns	-0.12 ns	-0.25 ns	-0.07 ns	0.05 ns	0.12 ns	0.29 ns	0.45 ns	-0.09 ns				
thrips1_5	-0.13 ns	-0.01 ns	-0.37 ns	-0.11 ns	-0.33 ns	-0.24 ns	-0.28 ns	0.29 ns	-0.44 ns	-0.23 ns	0.19 ns		0.08 ns	0.05 ns	0.13 ns	-0.39 ns	0.4 ns			
carotenoid1_8	0.29 ns	-0.13 ns	0.4 ns	0.01 ns	0.73 *	-0.03 ns	-0.05 ns	-0.4 ns	0.62 ***	-0.03 ns	-0.61 ***	-0.16 ns	0.34 ns	0.26 ns	-0.16 ns	0.6 *	-0.2 ns	-0.52 ns		
germination_perc	-0.06 ns	-0.04 ns	0.05 ns	0.32 ns	-0.03 ns	0.12 ns	0.33 ns	-0.07 ns	0 ns	-0.64 ns	-0.2 ns	0.06 ns	0.09 ns	0.34 ns	0.34 ns	-0.08 ns	0.32 ns	0.05 ns	-0.22 ns	
DM_yield_ha	-0.29 ns	0.23 ns	0.25 ns	0.97 ***	-0.04 ns	-0.32 ns	0.76 ***	-0.1 ns	0.04 ns	-0.34 ns	-0.02 ns	0.12 ns	-0.58 ns	0.21 ns	0.8 ***	-0.01 ns	0.13 ns	-0.11 ns	-0.02 ns	0.32 ns
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**Thank you!**