Establishing sustainable solutions to cassava diseases in mainland Southeast Asia

-- Objective 2 Breeding and selection

Dr. Xiaofei Zhang

Cassava Breeder

xiaofei.zhang@cgiar.org

Project Mid-term Review

23th February 2022

Objective 2: Enhance the **capacity** and **collaboration** between breeding programs in mainland Southeast Asia to develop new product profiles for commercially viable cassava varieties by **identifying** and **incorporating** known and novel sources of resistance to Cassava Mosaic Disease (CMD) and Cassava Witches Broom Disease (CWBD) into **national breeding programs**

Introduce CMD-resistant Germplasm to Southeast Asia

- 4,246 seeds to Laos
- 4,964 seeds to Vietnam
- 3,765 seeds to Thailand

5 CMD resistant clones

- 102 CMD resistant candidates
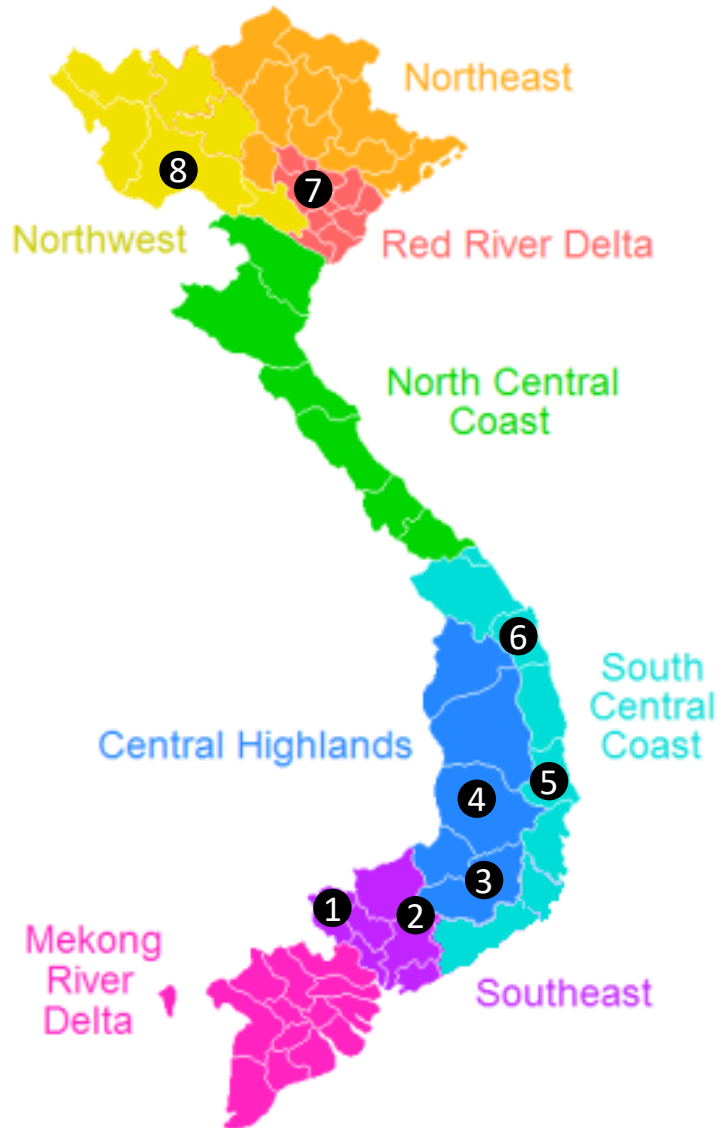- C33, C39
- DM x CMD population

Hawaii

CIAT

IITA
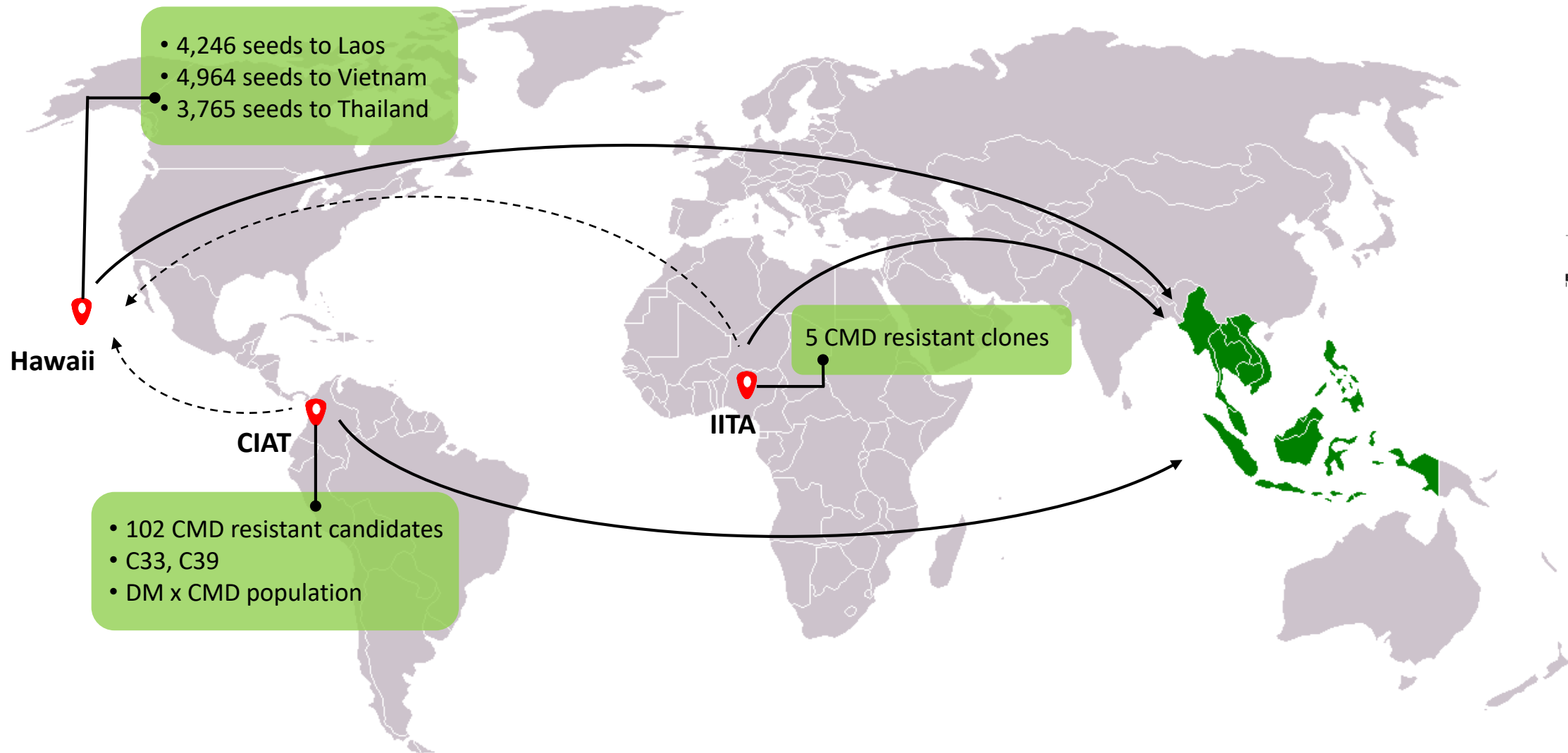
*DM, high Dry Matter cassava; **CMD**, Cassava Mosaic Disease*

Breeding Trial Testing Network in Vietnam

❶ Tay Ninh

❷ Dong Nai (**HLARC**)

❸ Lam Dong

❹ Dak Lak

❺ Phu Yen

❻ Quang Ngai

❼ Ha Noi (**AGI**)

❽ Son La

HLARC, Hung Loc Agricultural Research Center
AGI, Agricultural Genetics Institute

Introduce and Evaluate CMD–resistant Germplasm in Vietnam

Introduction 2018-2019 CIAT and IITA	Evaluation 2019-2020 (1 loc)	AYT 2020-2021 (2 loc)	RYT 2021-2022 (6 loc)	Demonstrate & Release 2022-2023
AGI Ha Noi	Tay Ninh	*Multiplication	Tay Ninh Son La	Tay Ninh Dong Nai Quang Ngai Gia Lai Thanh Hoa Quang Tri Son La
HLARC Tay Ninh *Evaluated 142 collections from farmers' field	Tay Ninh *Evaluated collections from farmers' field	Dong Nai Tay Ninh *Imported seeds from Hawaii	Tay Ninh Dong Nai Dak Lak Phu Yen Quang Ngai	Tay Ninh Dong Nai Dak Lak Phu Yen Quang Ngai

Share CMD-resistant Germplasm in Southeast Asia

Introduction	Evaluation	AYT	RYT	Demonstrate & Release
2018-2019 CIAT and IITA	2019-2020 (1 loc)	2020-2021 (2 loc)	2021-2022 (6 loc)	2022-2023
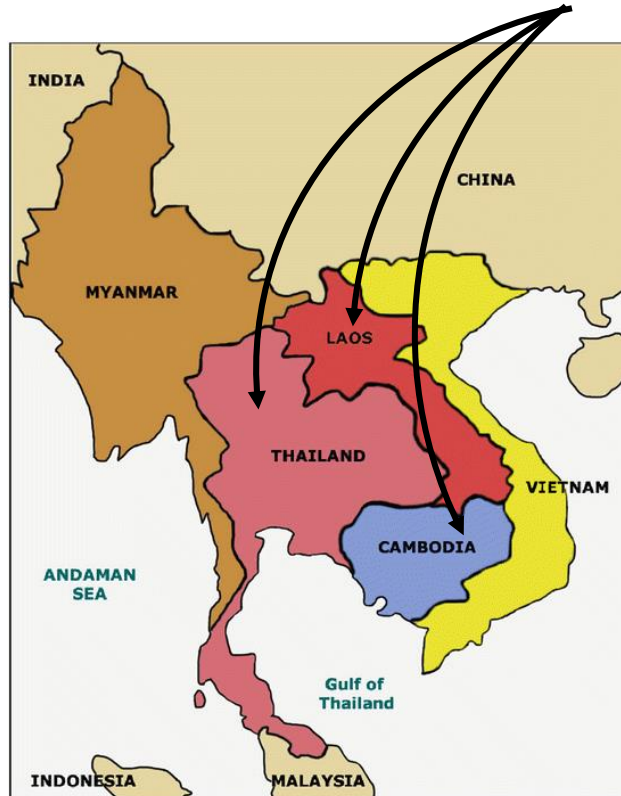
- The CMD-resistant clones with the best agronomic performance from CIAT and IITA were shared with **Thailand, Laos and Cambodia**.

- The tissue culture plantlets were sent from **AGI or CIAT**

Develop CMD-resistant Varieties in Vietnam

Introduction
2018-2019
CIAT and IITA

Evaluation
2019-2020
(1 loc)

AYT
2020-2021
(2 loc)

RYT
2021-2022
(6 loc)

Demonstrate & Release
2022-2023

2020-2021 **Crossing Nursery**

2021-2022 **Seedling Trial**
3,000 seeds; 2 loc
CMD2 markers

2022-2023 **Single Row trial**
200 clones; 2 loc

2023-2024 **Preliminary Yield Trial**

Photoperiod extension induces early flowering
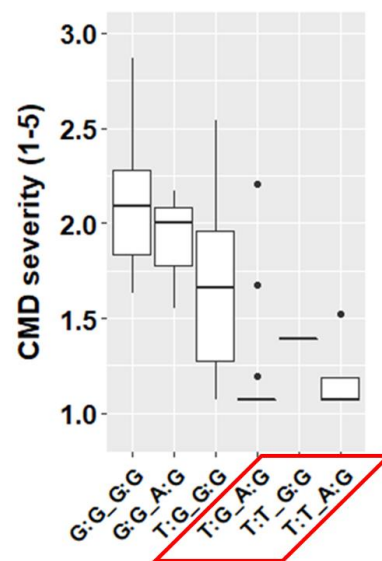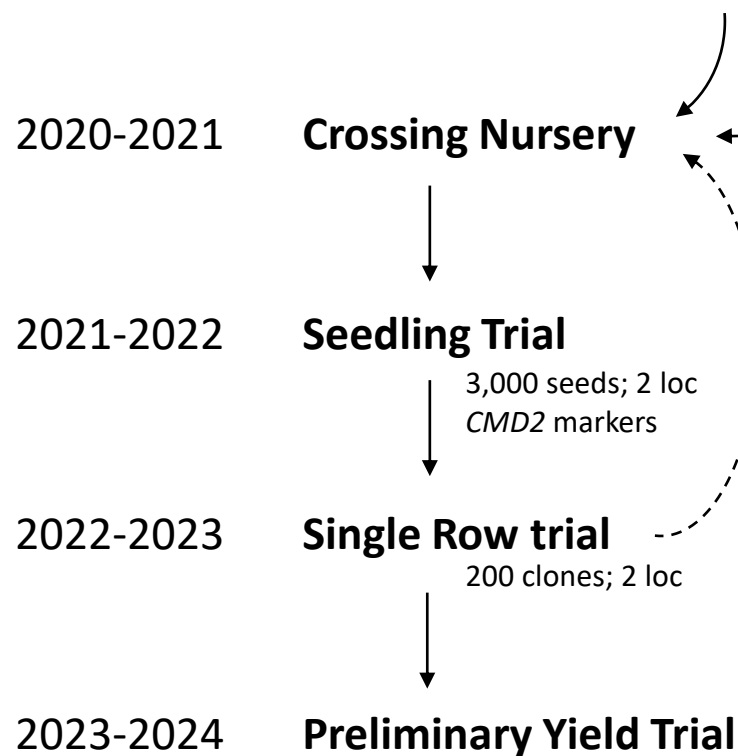
Validated and Implemented *CMD2* markers
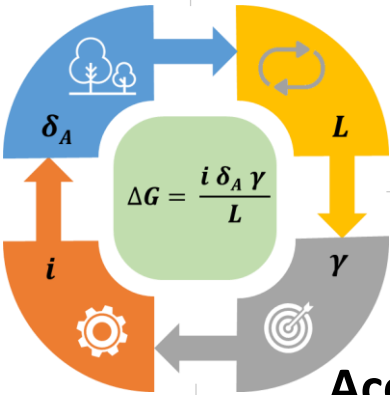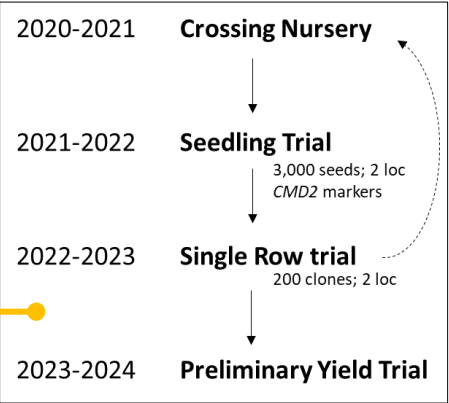
Breeding Program Improvement

Genetic Diversity
- CMD Resistant Germplasm
- Flower Inducing Technology
  - Elite x Elite

Duration of Selection Cycle
- Rapid Cycling – 3 years/cycle

2020-2021	**Crossing Nursery**
2021-2022	**Seedling Trial**
	3,000 seeds; 2 loc
	CMD2 markers
2022-2023	**Single Row trial**
	200 clones; 2 loc
2023-2024	**Preliminary Yield Trial**

$$\Delta G = \frac{i\ \delta_A\ \gamma}{L}$$

Intensity
MAS for Year1 Selections

Accuracy
- CassavaBase
- Multiple Environments
- ≥ 4 Checks, BLUP
- Row-column design

Excellence in Breeding Platform

CGIAR
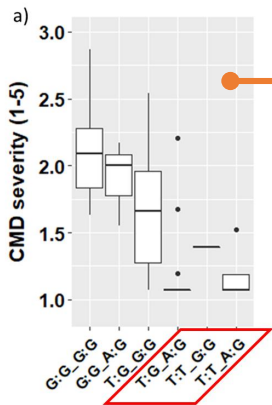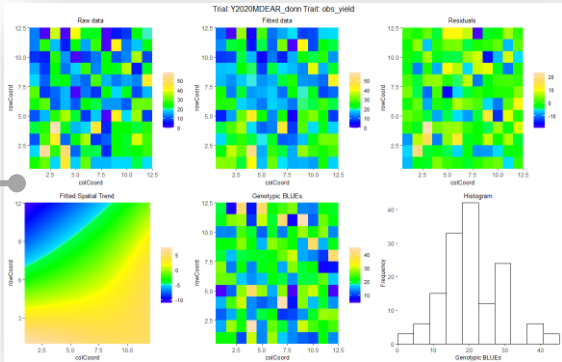
Photoperiod Extension Induced Early Flowering
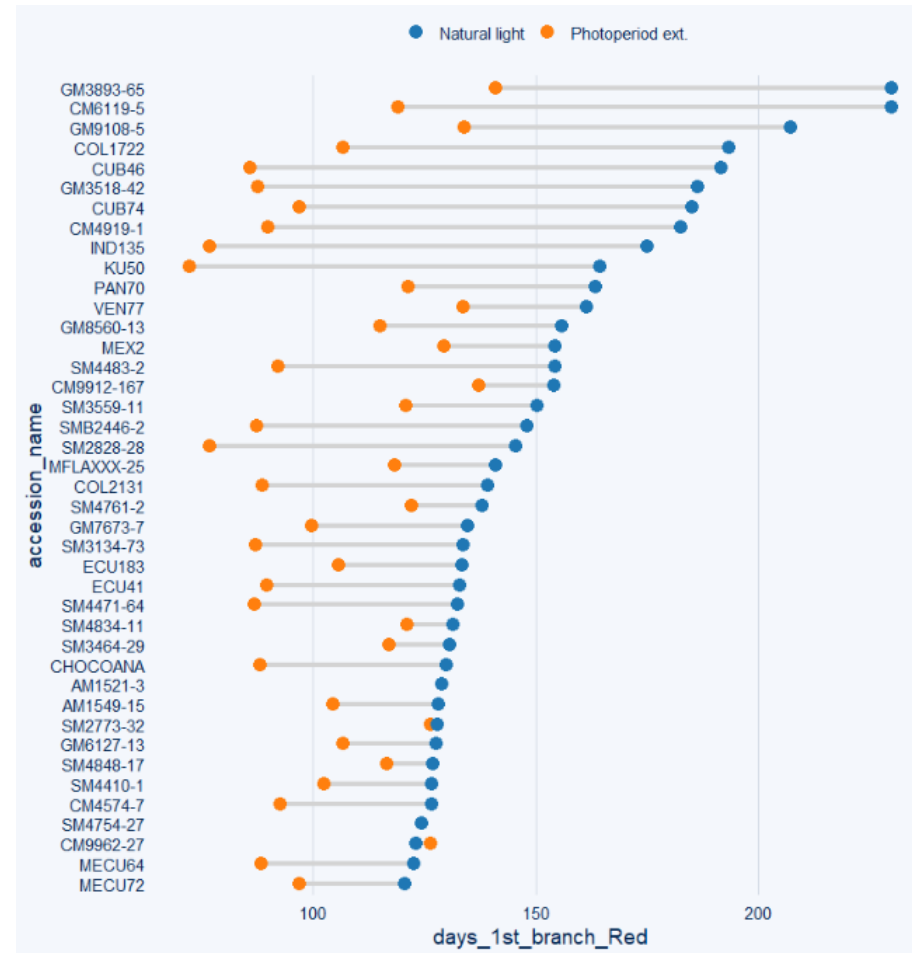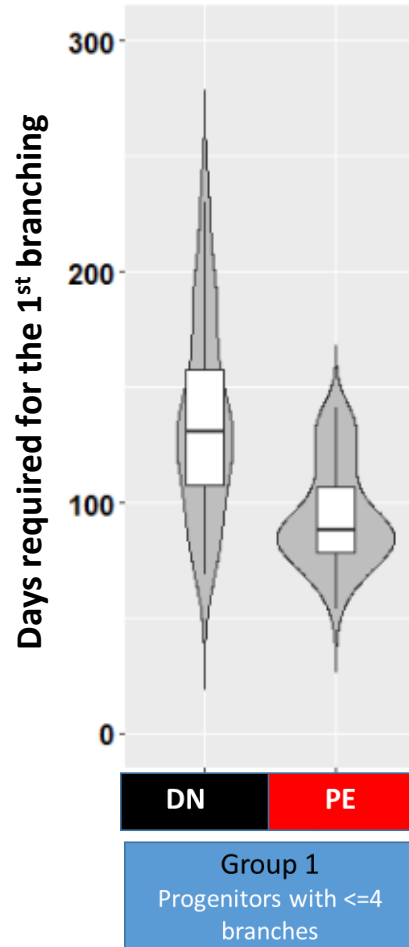
Days required for the 1st branching

Variation of CMD severity in VNM142 and CIAT102 populations

Population	Trial	Trait	Mean	Median	Rang	V_g	V_e	H^2
VNM142	201801MDEAR	CMD_1.5MAP	1.56	1.43	1.00-4.00	0.10	0.21	0.50
		CMD_3MAP	1.87	1.75	1.00-4.00	0.18	0.22	0.63
		CMD_6MAP	2.23	2.20	1.00-4.00	0.27	0.19	0.75
		CMD_10MAP	2.82	2.86	1.19-4.00	0.40	0.19	0.82
	201901MDEAR*	CMD_10MAP	2.65	2.33	1.00-4.12	1.30	0.04	0.99
	201902MDEAR[#]	CMD_10MAP	2.83	2.63	1.70-4.10	0.62	0.11	0.94
CIAT102	201903MDEAR	CMD_3MAP	1.73	1.64	1.00-3.77	0.42	0.12	0.91

V_g, total genetic variance among unique clones; V_e, the variance of residue. The calculation of genetic variance was performed by using the mixed models by fitting replications and clones as random effects.
*the trials with 3 clones from VNM142 and four checks, HLS11, KM419, KU50 and C33. MDEAR, cassava mosaic disease advanced yield trial.
[#]the trials with 9 clones from VNM142 and three checks, HLS11, KM419 and KU50.

CMD2 Markers Works in Segregation Populations
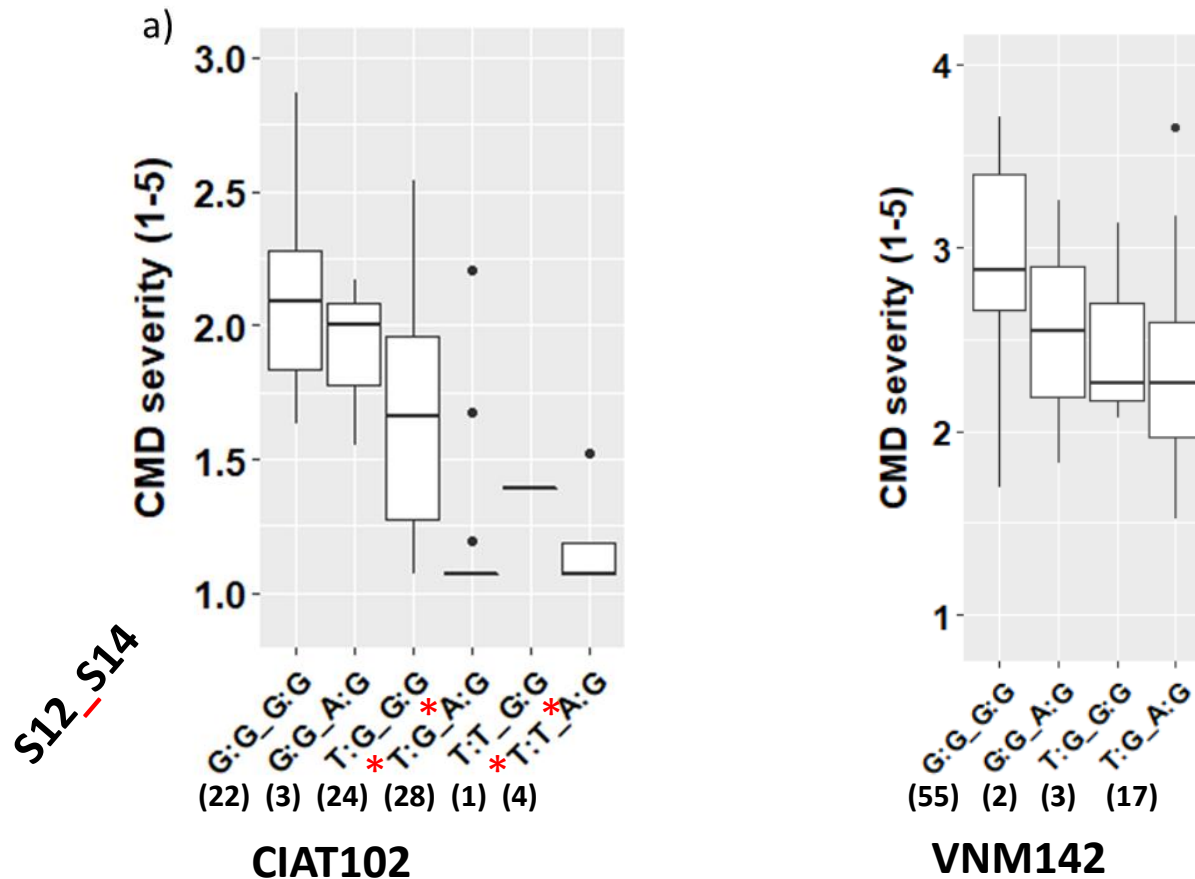
S12_7926132 and S14_4626854

For marker S12, *T is the resistant allele; For marker S14, *A is the resistant allele

S12_7926132 and S14_4626854 worked well for **segregation populat**ions (e.g., CIAT102), but not for **diversity populations** (e.g., VNM142)

New CMD Resistance to SLCMV Identified from VNM142

Genotype/group	Clone	2018-2019	2019-2020	S12_7926132	S14_4626854
UNK-CI-2	VN19-442	1.5	2.3	T:G	A:G
CR63_PER262_TAI9	VN19-1432, VN19-1556	1.6	1.9	T:G	A:G
KM57_VNM8_Xanh Vinh Phu	VN19-1039, VN19-1050	1.6	1.9	T:G	A:G
UNQ-115	VN19-773	1.7	2.1	T:G	A:G
UNK-F	VN19-1184, VN19-1194	2.0	2.6	T:G	A:G
UNQ-44	VN19-320	1.7	1.8	G:G	G:G
UNK-AF-2	VN19-1805	1.8	NA	G:G	A:G
UNK-CH	VN19-390	1.9	2.2	G:G	G:G
KU50_KM94_TAI16	11 clone samples (e.g., VN19-1739	2.6	3.5	G:G	G:G
KM140	4 clone samples (e.g., VN19-2659)	3.6	NA	G:G	G:G
KM419	2 clone samples (e.g., VN19-2202)	3.0	4.0	G:G	G:G
C33	C33	NA	1.1	T:G	A:G

BLUP of the CMD score at 10 month after planting was provided here for each unique clone (or group)

Five Yield Trials Harvested
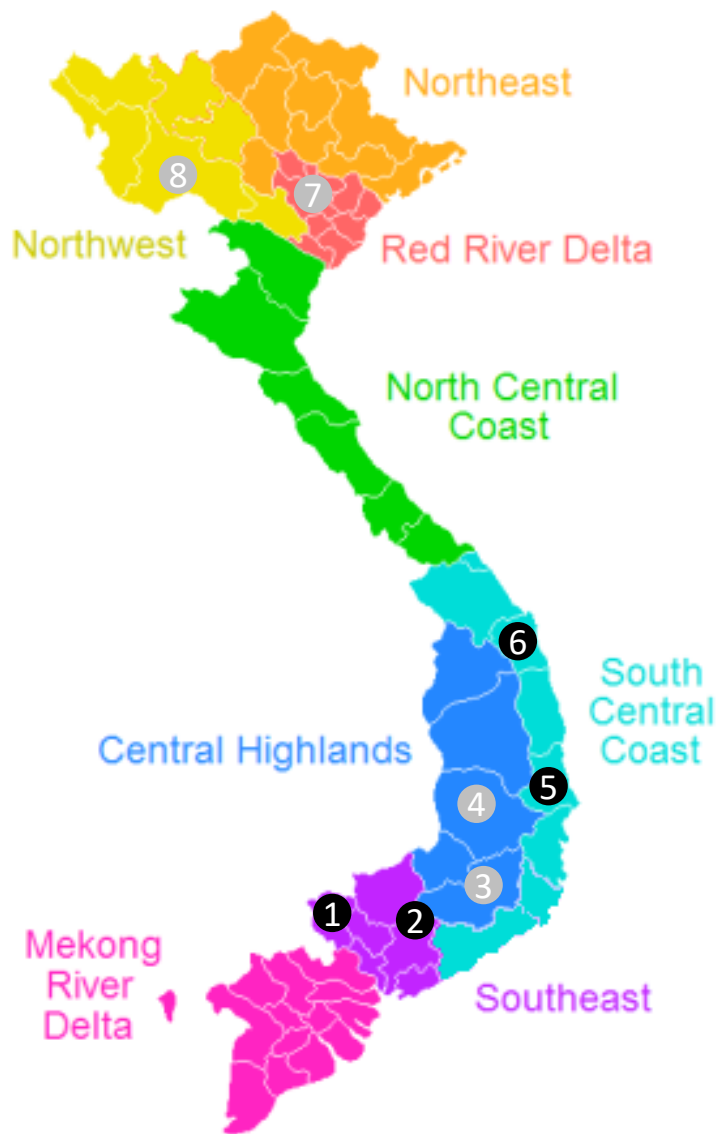
❶ Tay Ninh (2020, 2021)
❷ Dong Nai (2020)
③ Lam Dong
④ Dak Lak
❺ Phu Yen (2021)
❻ Quang Ngai (2021)
⑦ Ha Noi (**AGI**)
⑧ Son La

Good Yield Trial Quality – Moderate to High Heritability

| trial	CMD_1mon	CMD_3mon	CMD_6mon	CMD_10mon	height	height_1st_branch	branch_number	starch	yield_v2	starch_yield	harvest_index
Y2020MDEAR_donn	0.99	0.98	0.99	0.96	0.49	0.93	0.92	0.75	0.67	0.49	NA
Y2020MDEAR_tayn	0.98	1	0.99	0.96	0.7	0.85	0.87	0.49	0.82	0.76	NA
Y2021MDEAR_phuy	0.9	0.94	NA	0.98	0.87	0.8	0.94	0.95	0.61	0.5	0.91
Y2021MDEAR_quan	1	1	NA	0.99	0.53	0.72	0.89	0.92	0.77	0.76	0.95
Y2021MDEAR_tayn	0.91	0.98	0.98	0.96	0.88	0.81	0.97	0.88	0.54	0.4	0.78

Good	Bad

Different CMD Pressure
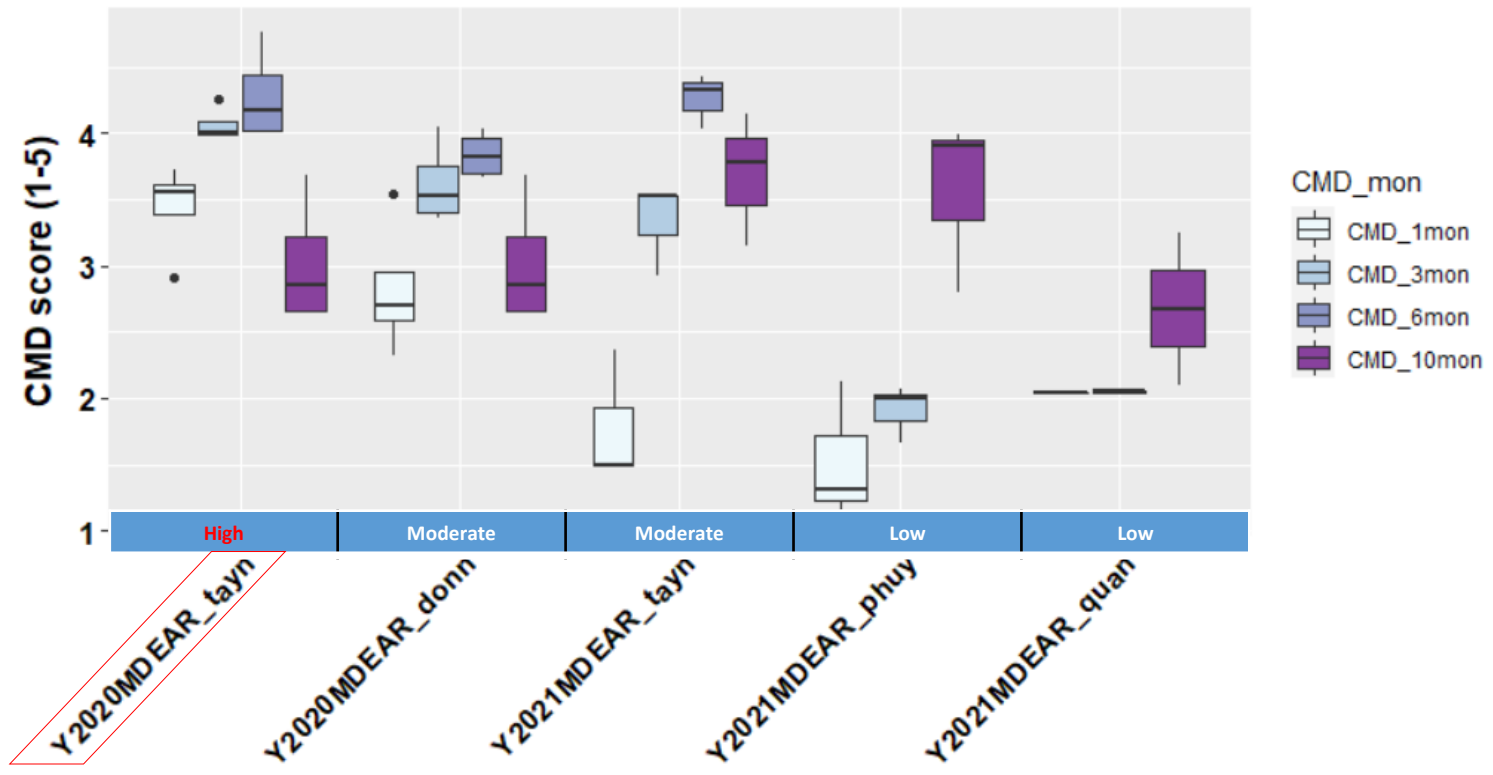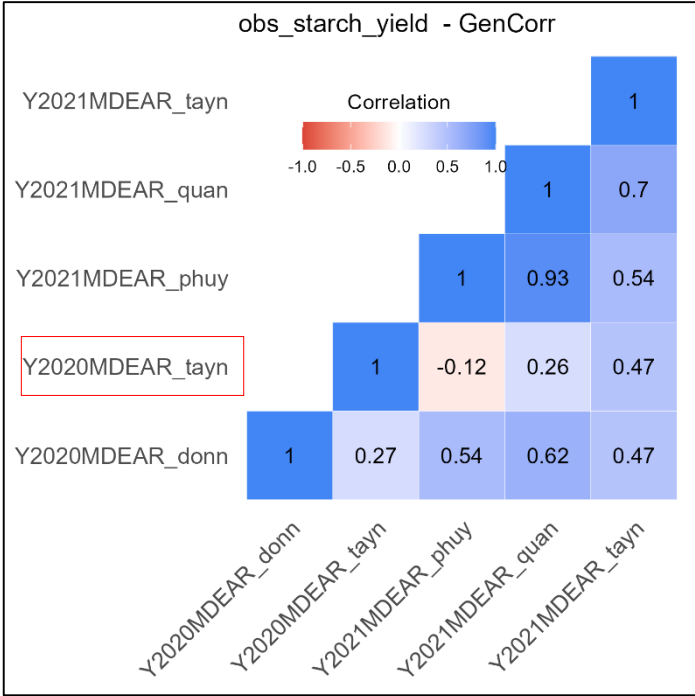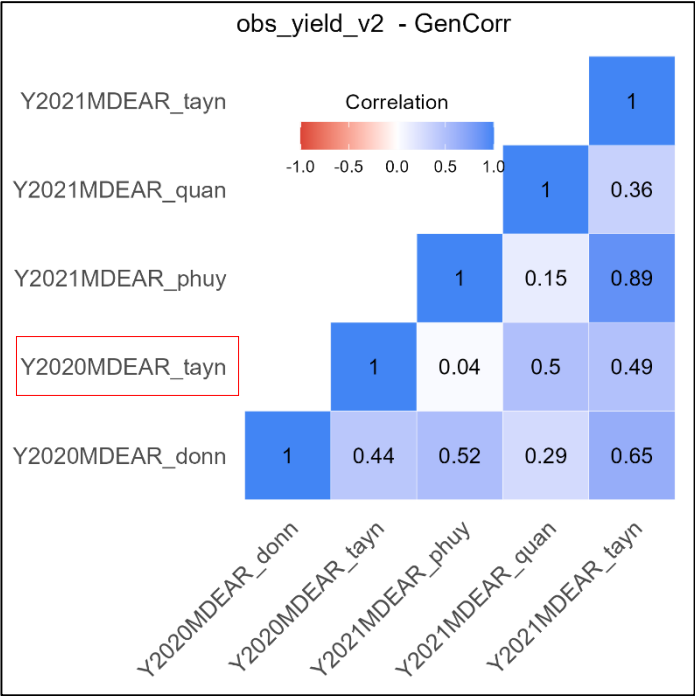
Genetic Correlation among Environments

– CMD and Plant Type
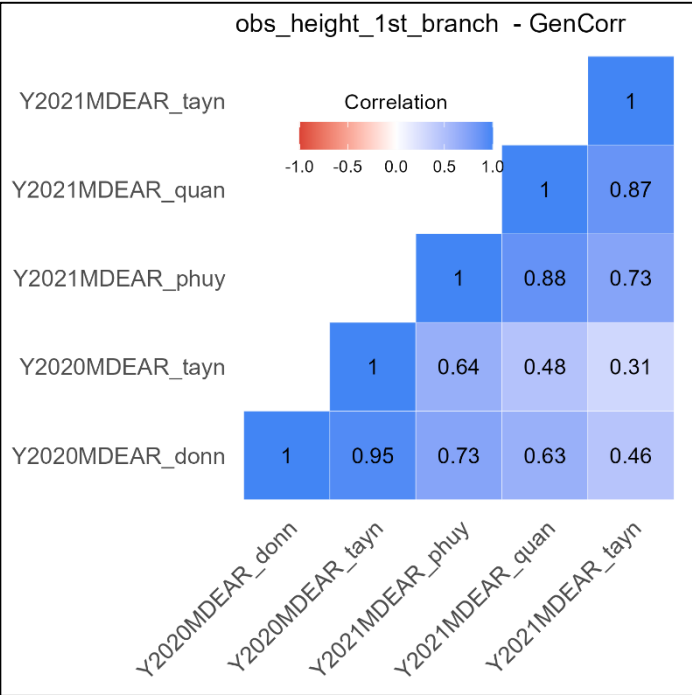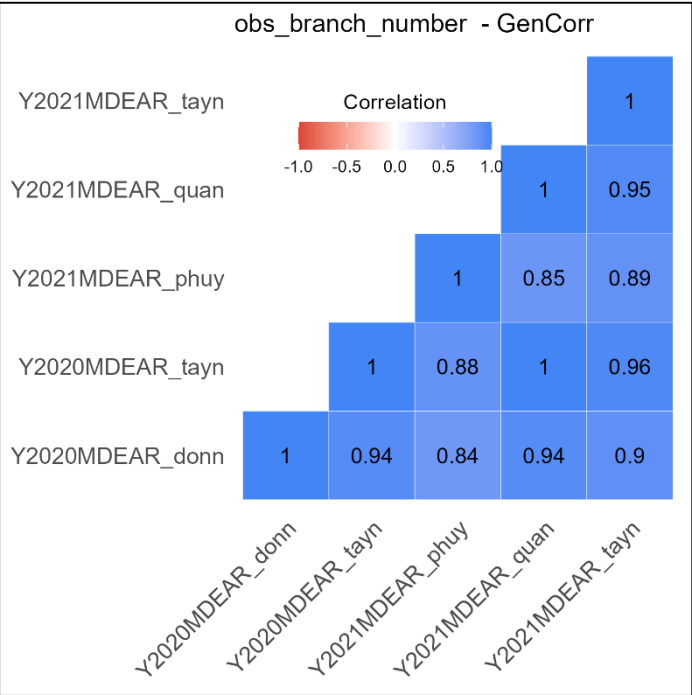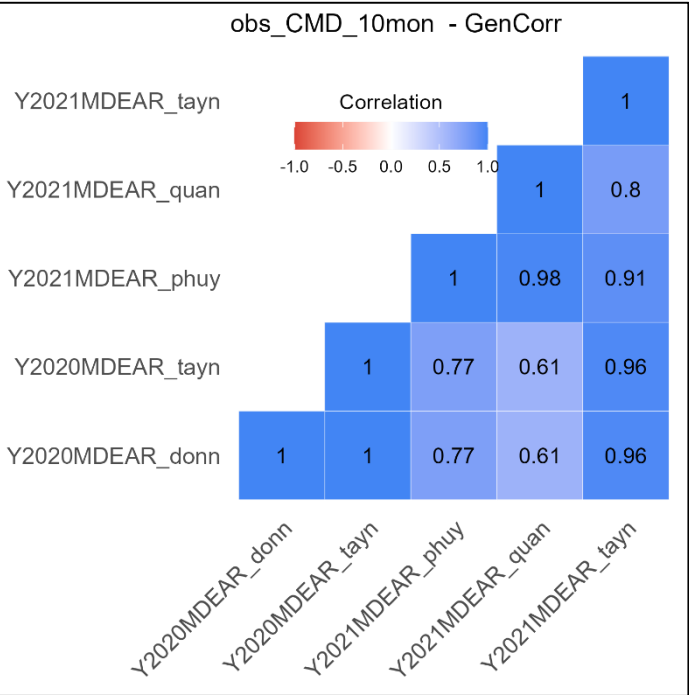
Genetic Correlation among Environments

– Starch Yield
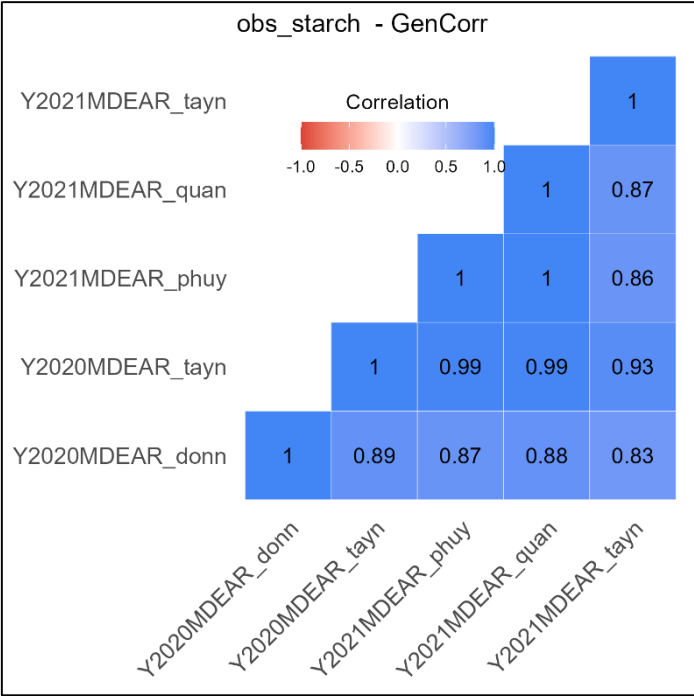
Multi-environment BLUP
-- Summary of the best clones and checks

clone	CMD_10mon	height_1st_branch	branch_number	starch (%)	yield (ton/ha)	starch_yield (ton/ha)
KU50	3.0	200	0.4	27.1	28.0	8.0
TMEB419	1.1	212	0.7	24.3	30.5	7.9
CR24-16	1.0	249	0.0	26.0	25.5	7.6
CR13-8	1.0	190	2.5	24.5	26.8	7.2
CR24-3	1.0	110	2.9	22.3	28.7	7.1
CR52A-2	1.0	136	3.2	24.2	26.7	7.1
AR9-48	1.0	204	2.4	25.4	27.5	6.7
CR52A-4	0.9	89	3.3	27.1	24.7	6.7
IBA980581	1.0	159	0.7	20.5	29.1	6.1
IBA972205	1.0	98	2.8	18.5	29.1	5.9
IBA920057	1.0	251	1.3	22.8	23.7	5.8
IBA980505	1.0	114	2.2	18.9	23.3	5.2
HL-S11	3.7	225	0.0	28.3	19.2	5.8
KM140	3.5	191	0.2	21.4	22.9	5.8
KM419	3.5	147	0.9	24.7	19.8	5.7
KM505	2.6	215	0.6	25.8	19.9	5.3

The clones were sorted based on **starch yield**.

Good

Bad

Multi-environment BLUP

-- Summary of the best clones and checks

		BLUE – single environment mean					BLUP	BLUE – single environment mean					BLUP
		2020_donn	2020_tayn	2021_tayn	2021phuy	2021_quan	CMD_10mon	2020_donn	2020_tayn	2021_tayn	2021phuy	2021_quan	starch_yield (ton/ha)
	KU50	4.0	4.0	3.4	2.3	1.0	**3.0**	13.3	2.4	11.0	6.4	7.8	**8.0**
	TMEB419	1.0	1.0	1.4	1.3	1.0	**1.1**	7.6	13.5	10.1	4.4	9.0	**7.9**
	CR24-16	1.0	1.0	1.1	1.1	1.0	**1.0**	5.8	10.2	11.7	3.3	8.0	**7.6**
	CR13-8	1.0	1.0	1.0	1.0	1.0	**1.0**	7.0	8.5	9.4	4.4	6.1	**7.2**
CIAT & IITA	CR24-3	1.0	1.0	1.0	NA	NA	**1.0**	8.7	7.3	12.7	NA	NA	**7.1**
	CR52A-2	1.0	1.0	NA	NA	NA	**1.0**	8.7	8.9	NA	NA	NA	**7.1**
	AR9-48	1.0	1.0	1.1	1.1	1.0	**1.0**	8.1	6.6	9.6	4.5	8.6	**6.7**
	CR52A-4	0.9	0.9	0.9	NA	1.0	**0.9**	7.2	8.1	9.2	NA	6.5	**6.7**
	IBA980581	1.1	1.1	1.0	0.9	1.0	**1.0**	4.7	13.1	8.1	2.6	5.9	**6.1**
	IBA972205	1.0	1.0	0.9	1.1	1.0	**1.0**	5.5	7.7	11.6	3.8	3.1	**5.9**
	IBA920057	1.1	1.1	1.1	0.9	NA	**1.0**	5.5	4.8	10.6	4.1	NA	**5.8**
	IBA980505	1.0	1.0	NA	1.0	NA	**1.0**	4.8	6.1	NA	2.1	NA	**5.2**
	HL-S11	3.1	3.1	4.1	4.0	NA	**3.7**	11.6	1.1	7.0	3.4	NA	**5.8**
	KM140	2.7	2.7	3.1	3.9	NA	**3.5**	7.5	6.0	6.4	3.2	NA	**5.8**
	KM419	3.7	3.7	3.8	2.8	3.3	**3.5**	5.0	3.4	6.5	3.2	5.9	**5.7**
	KM505	2.6	2.6	NA	NA	2.1	**2.6**	6.4	5.6	NA	NA	6.2	**5.3**

The clones were sorted based on **starch yield**.

Multi-environment BLUP

-- Summary of the best clones and checks

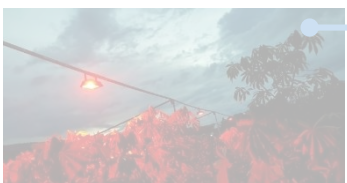|		BLUE – single environment mean					**BLUP**	BLUE – single environment mean					**BLUP**
		2020_donn	2020_tayn	2021_tayn	2021phuy	2021_quan	starch_yield (ton/ha)	2020_donn	2020_tayn	2021_tayn	2021phuy	2021_quan	starch (%)
	KU50	13.3	2.4	11.0	6.4	7.8	**8.0**	28.4	28.2	27.2	24.1	29.1	**27.1**
HN1	**TMEB419**	7.6	13.5	10.1	4.4	9.0	**7.9**	26.8	29.7	25.3	20.0	24.1	**24.3**
HN36	**CR24-16**	5.8	10.2	11.7	3.3	8.0	**7.6**	27.1	30.9	27.0	22.5	27.2	**26.0**
	CR13-8	7.0	8.5	9.4	4.4	6.1	**7.2**	25.9	29.5	25.6	20.8	25.3	**24.5**
	CR24-3	8.7	7.3	12.7	NA	NA	**7.1**	22.5	27.7	24.7	NA	NA	**22.3**
	CR52A-2	8.7	8.9	NA	NA	NA	**7.1**	23.8	30.7	NA	NA	NA	**24.2**
HN97	**AR9-48**	8.1	6.6	9.6	4.5	8.6	**6.7**	25.8	25.8	25.9	23.2	25.8	**25.4**
	CR52A-4	7.2	8.1	9.2	NA	6.5	**6.7**	26.8	29.6	29.3	NA	26.9	**27.1**
HN80	**CR27-20**	8.9	7.4	8.9	NA	4.6	**6.5**	25.9	30.4	26.5	NA	26.4	**26.3**
HN5	**IBA980581**	4.7	13.1	8.1	2.6	5.9	**6.1**	21.0	27.1	20.5	18.0	19.8	**20.5**
HN3	**IBA972205**	5.5	7.7	11.6	3.8	3.1	**5.9**	21.4	26.1	21.0	12.8	14.2	**18.5**
	IBA920057	5.5	4.8	10.6	4.1	NA	**5.8**	22.0	25.8	26.6	19.0	NA	**22.8**
	IBA980505	4.8	6.1	NA	2.1	NA	**5.2**	21.4	23.5	NA	14.8	NA	**18.9**
	HL-S11	11.6	1.1	7.0	3.4	NA	**5.8**	29.0	29.1	27.6	27.1	NA	**28.3**
	KM140	7.5	6.0	6.4	3.2	NA	**5.8**	21.3	27.1	23.3	17.9	NA	**21.4**
	KM419	5.0	3.4	6.5	3.2	5.9	**5.7**	23.8	30.7	23.8	22.5	23.0	**24.7**
	KM505	6.4	5.6	NA	NA	6.2	**5.3**	25.8	31.3	NA	NA	27.9	**25.8**

CIAT & IITA

The clones were sorted based on **starch yield**.
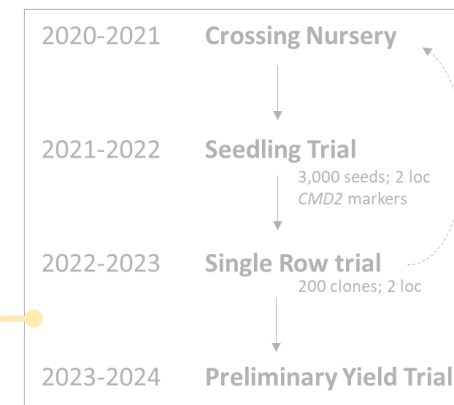
Breeding Program Improvement (cont.)

Genetic Diversity
- CMD Resistant Germplasm
- Flower Inducing Technology
  - Elite x Elite
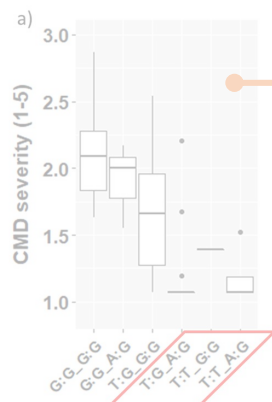- **Witches' Broom Resistance**

Duration of Selection Cycle
- Rapid Cycling – 3 years/cycle
- **Genomics-assisted Breeding**

2020-2021	Crossing Nursery
2021-2022	Seedling Trial
	3,000 seeds; 2 loc *CMD2* markers
2022-2023	Single Row trial
	200 clones; 2 loc
2023-2024	Preliminary Yield Trial

$$\Delta G = \frac{i \, \delta_A \, \gamma}{L}$$

δ_A L i γ

Intensity
- MAS for Year1 selections
- **MAS for DM and Plant Type**

Accuracy
- CassavaBase
- Multiple Environments
- $\geq$ 4 Checks, BLUP
- Row-column design

- **Fieldbook and Barcode**
- **Determine TPE**
- **Stage&gate System**
- **Quality Control**

Excellence in Breeding Platform

CGIAR