ACIAR project “Developing Sustainable Solutions to Cassava Disease in Mainland Southeast Asia”

ZMI93, a SLCMV resistant variety

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1. ZMI93, a CMD resistant variety produced from Shuttle Breeding
2. The Character of ZMI93 to resist SLCMV in Cambodia
3. The schedule for the next research work

1. ZMI93, a CMD resistant variety produced from Shuttle Breeding

Shuttle Breeding

SC8

Shuttle Breeding

Using SC8 as female, to produce Natural Hybrid group

China –Aided Congo (Brazzaville) Agricultural Demonstration Center

Release a CMD resistant variety, ZMI93

Shuttle Breeding

National Cassava Germplasm Bank in CATAS, Danzhou

ZMI93 virus-free seedling and propagation

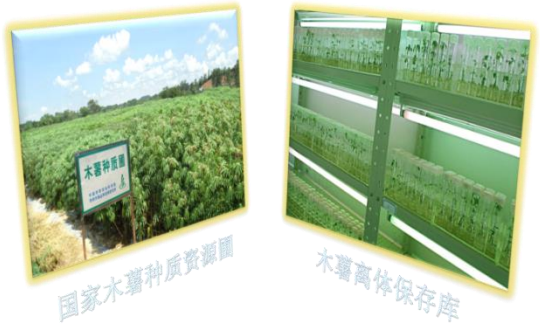
SLCMV resistant experiments

CHHUN HONG RUBBER BETTER CO., LTD, Guangdong Agricultural Reclamation

ZMI93 has an immune ability to SLCMV

National Cassava Germplasm Bank

National Cassava Germplasm Bank



Cassava Genetic Resources Bank

National Cross Cassava Base

Cassava varieties with high yield, high β-carotene and PPD tolerance

Rapid propagation of cassava seedlings

National Cassava Germplasm Bank

华南8号

SC8, a variety with high yield and high starch content

China –Aided Congo (Brazzaville) Agricultural Demonstration Center

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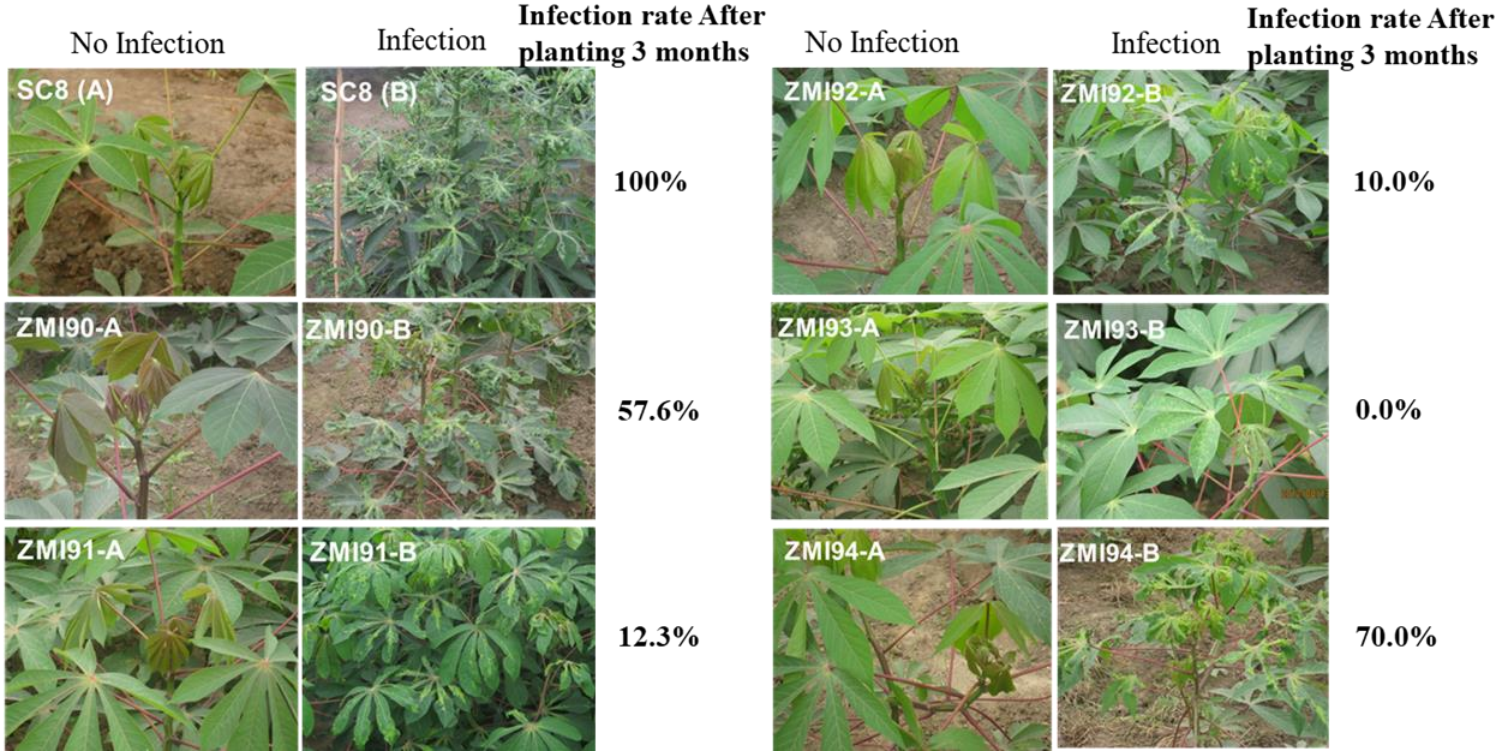
Cassava SC8 nature hybrid population

China –Aided Congo (Brazzaville) Agricultural Demonstration Center



China –Aided Congo (Brazzaville) Agricultural Demonstration Center

The root yield of different cassava varieties

2. The Character of ZMI93 to resist SLCMV in Cambodia

CHHUN HONG RUBBER BETTER CO., LTD, Guangdong Agricultural Reclamation

The base of cassava intercropping with Rubber in CHHUN HONG RUBBER BETTER CO., LTD

SLCMV Resistant Experiments

Levels	SLCMV incidence grading standards （In the whole plant ）
0	No infection
1	Mosaic leaves are one third in the whole plant. Leaves are mosaic but not deformed, or the infected plant is not significantly dwarfed.
2	Mosaic leaves are one second in the whole plant. The main vein of leaf or 1/2 lobes are deformed, or the infected plant is dwarfed, and equal to two third of the normal plant height.
3	Mosaic leaves are two third in the whole plant or mosaic leaves in the whole plant. The leaves are seriously deformed, or the infected plant is dwarfed, and equal to one second of the normal plant height.

The incidence=(Number of infected plants/total plants investigated)*100%

SLCMV Resistant Experiments

M19-0 level M19-1 level M19-2 level M19-3 level

ZMK265-0 level ZMK265-1 level ZMK265-3 level

P19-1 level P19-2 level P19-3 level

ZMK93 ZM93-0 level

SLCMV resistant experiments with 4 varieties in the base of CHHUN HONG RUBBER BETTER CO., LTD

SLCMV Resistant Experiments

Varieties	Planting for 3 months							Planting for 6 months						
	Plants investigated	Number of infected plants	incidence (%)	Levels of infected leaves				Plants investigated	Number of infected plants	incidence (%)	Levels of infected leaves			
				0	1	2	3				0	1	2	3
M19	100	44	44.0	680	180	66	74	100	50	50.0	679	186	60	75
P19	100	72	72.0	220	400	360	20	100	80	80.0	209	413	361	19
ZMK265	90	2	2.2	880	4	0	16	90	4	4.4	875	5	0	20
ZMI93	100	0	0.0	1000	0	0	0	100	0	0.0	1000	0	0	0

The Root Yield of Cassava Varieties

NO.	Varieties	Root distribution	Tuberization condition	Root number/Plant	Yield (t/hm^2)	Starch content （%）	Fresh biomass (kg/Plant)	Harvest index
1	M19	Horizontal elongation	decentralization	6±1.23c	23.55 ± 1.00b	**26.01±0.13a**	2.64±0.14b	0.57±0.02b
2	P19	Horizontal elongation	centralization	8± 2.55b	16.80 ± 1.10c	23.85±0.11d	2.16±0.19c	0.51±0.02bc
3	ZMK265	Irregularity	decentralization	6±1.55 c	**42.60±1.30 a**	**26.01±0.25a**	4.25±0.11a	0.65±0.03a
4	ZMI93	Irregularity	decentralization	9±2.23a	**42.30 ± 1.50a**	**25.88±0.47ab**	4.20±0.12a	0.67±0.02a



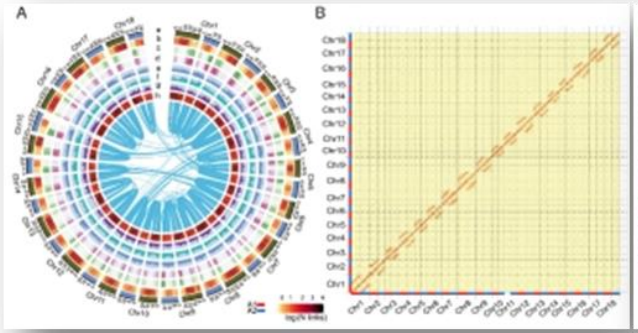

ZMI93 Root Yield

3. The schedule for the next research work

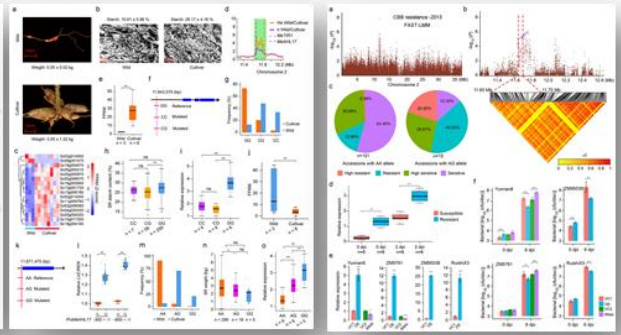
The Next Research Work

- Perform the whole Genome of cassava SC8 and ZMI93;
- Indicate the molecular mechanisms of cassava ZMI93 immunization to SLCMV;
- Find a way to breed cassava varieties to resist SLCMV.

Hu, et al. Molecular Plant, 2021



Hu et al. Genome Biology, 2021



Acknowledgments

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