

Accelerated Cassava Breeding to Meet Farmers' Needs

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Cassava Breeder

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Nov 04, 2021

Alliance



Cassava, Manihot esculenta



Root crop

Clonal propagation using stems



Staple crop

2nd largest crop for starch production



Diploid, $2n = 36$

Cross-pollination

Self-compatible



Key Elements of Plant Breeding

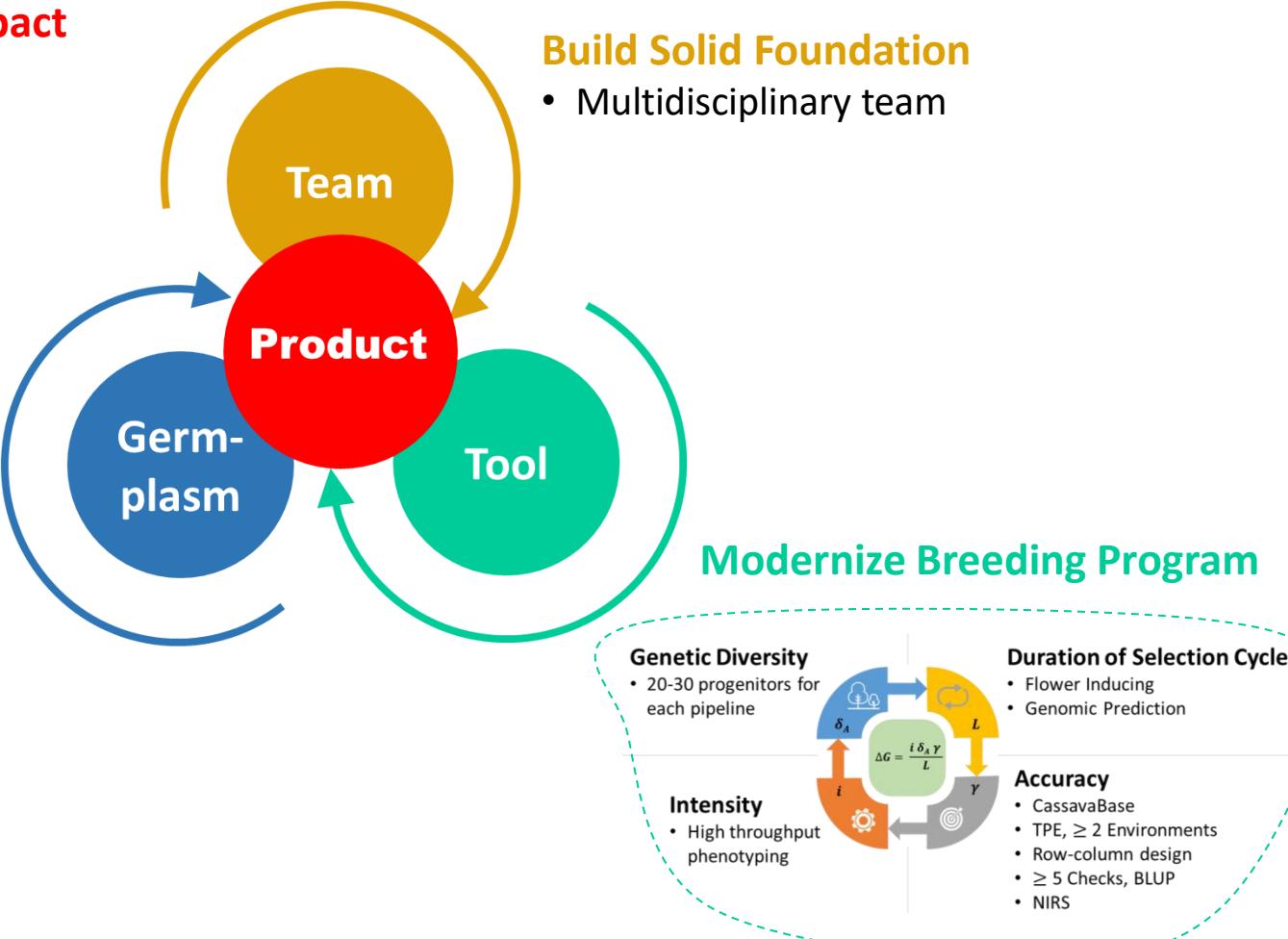


Create New Opportunities

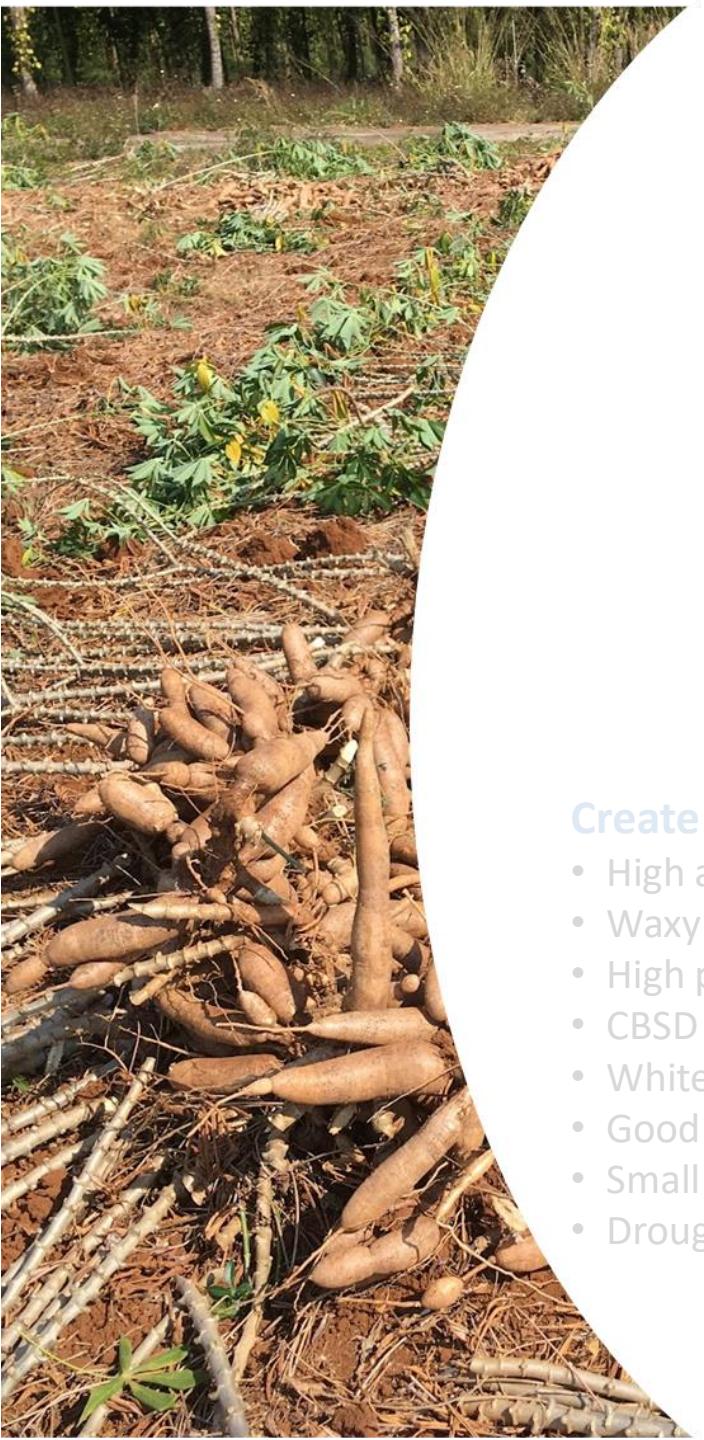
- High and stable dry matter
- Waxy starch
- High pro-vitamin A
- CBSD resistance
- Whitefly resistance
- Good cooking quality
- Small granule
- Drought and heat tolerance

Enhance Global Impact

- Market segments
- Product profiles
- Breeding pipelines



Key Elements of Plant Breeding

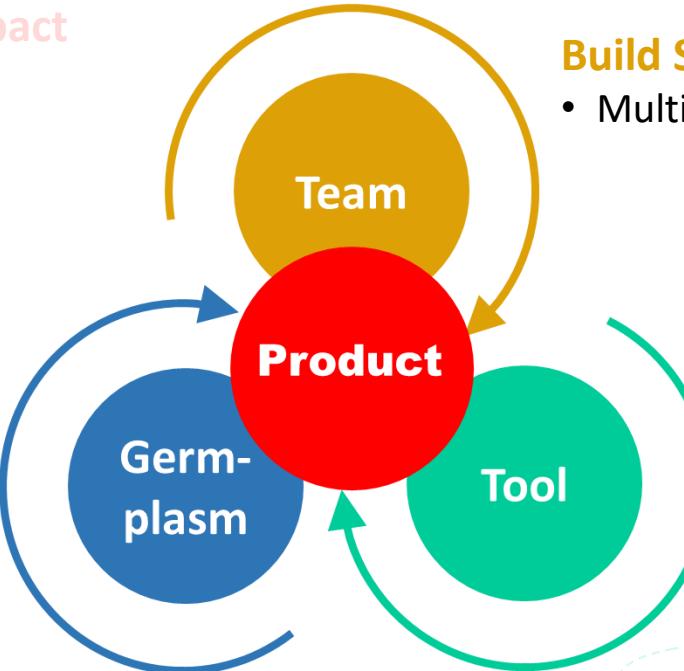


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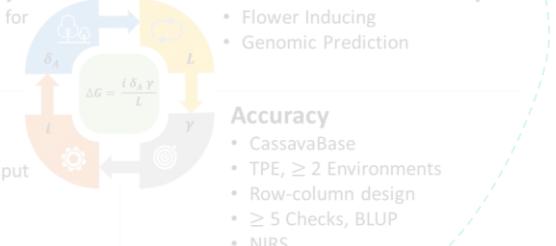
Build Solid Foundation

- Multidisciplinary team

Modernize Breeding Program

Genetic Diversity

- 20-30 progenitors for each pipeline



Intensity

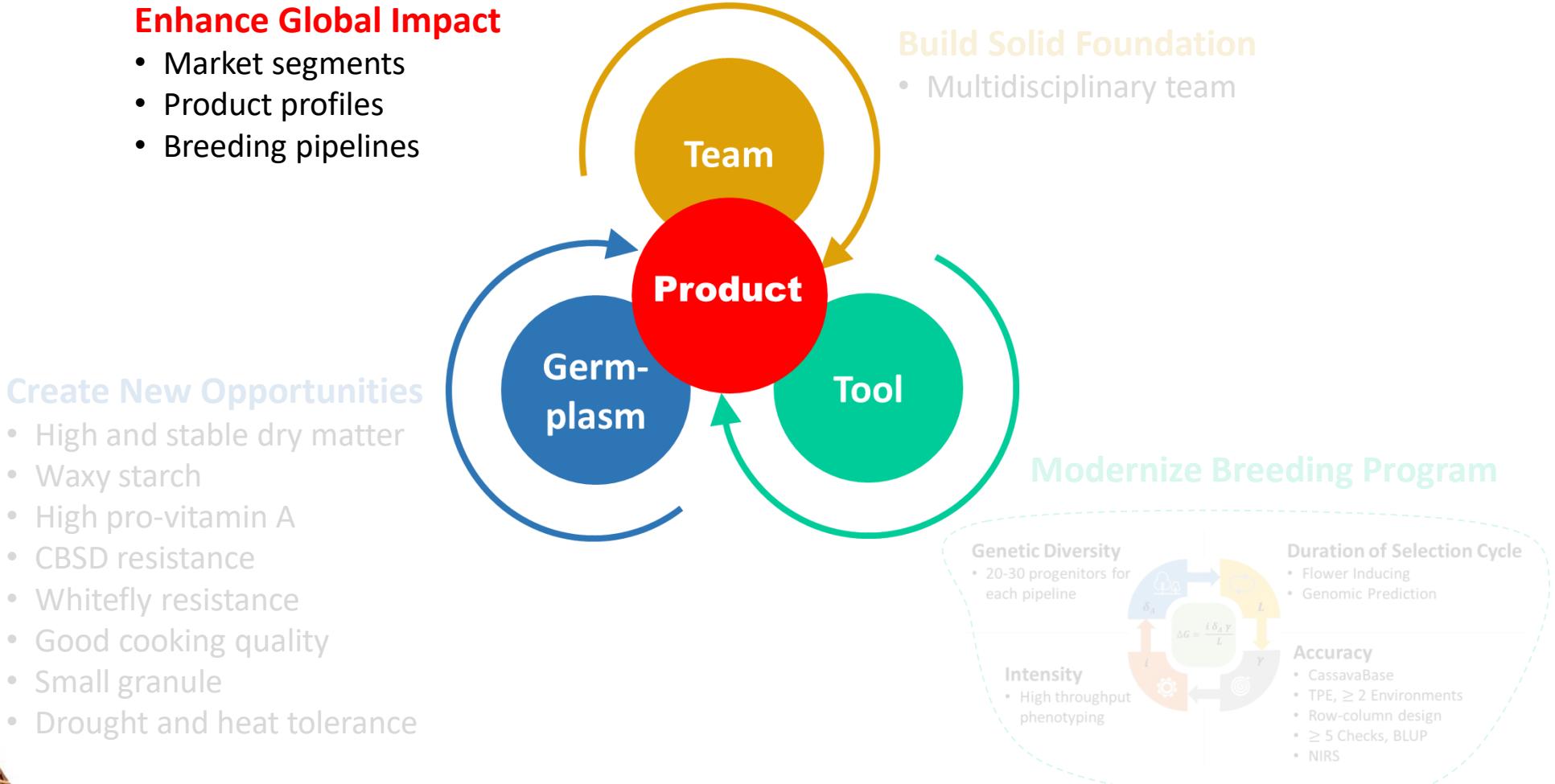
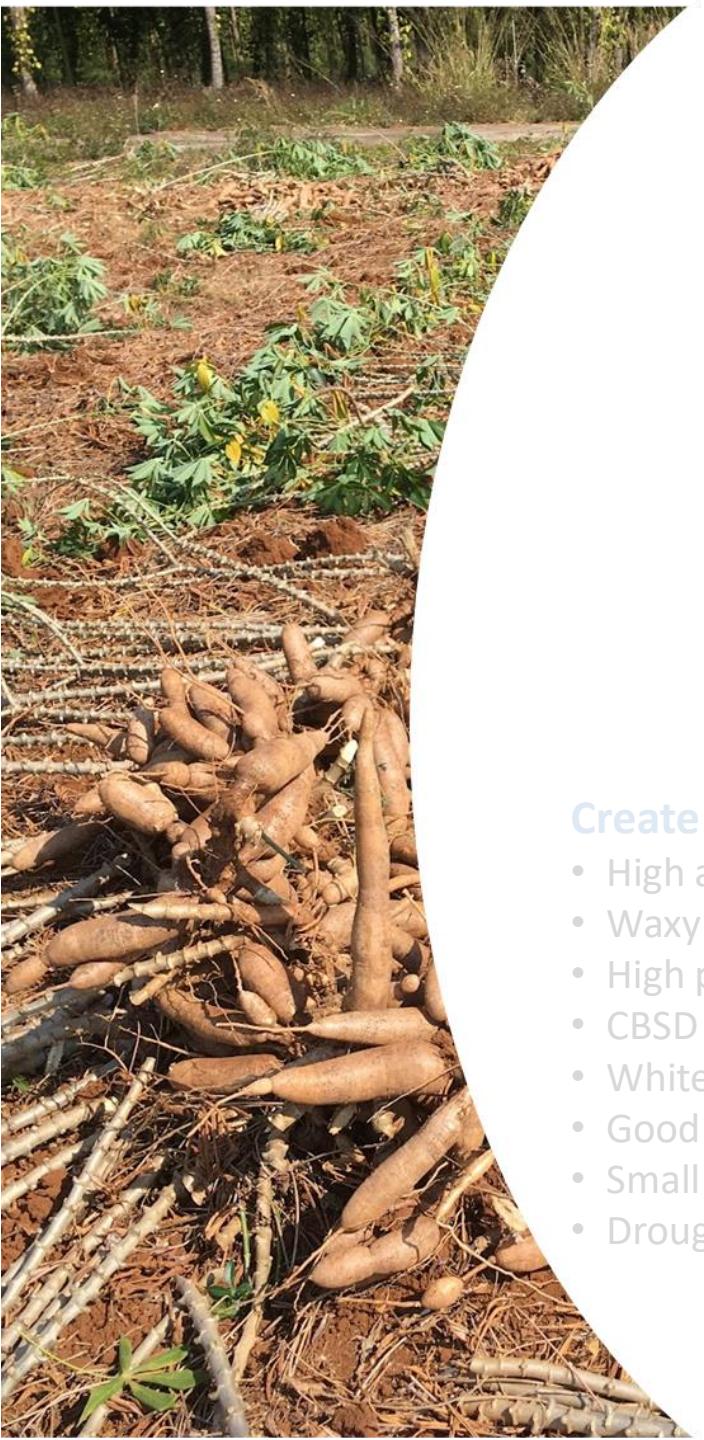
- High throughput phenotyping

Accuracy

- CassavaBase
- TPE, ≥ 2 Environments
- Row-column design
- ≥ 5 Checks, BLUP
- NIRS



Key Elements of Plant Breeding





Cassava Products



Biofortified cassava for human consumption



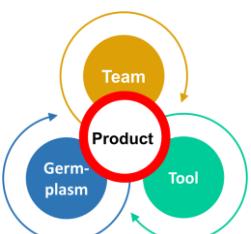
Fresh and Dried roots for human consumption



Industrial Cassava – starch and animal feed

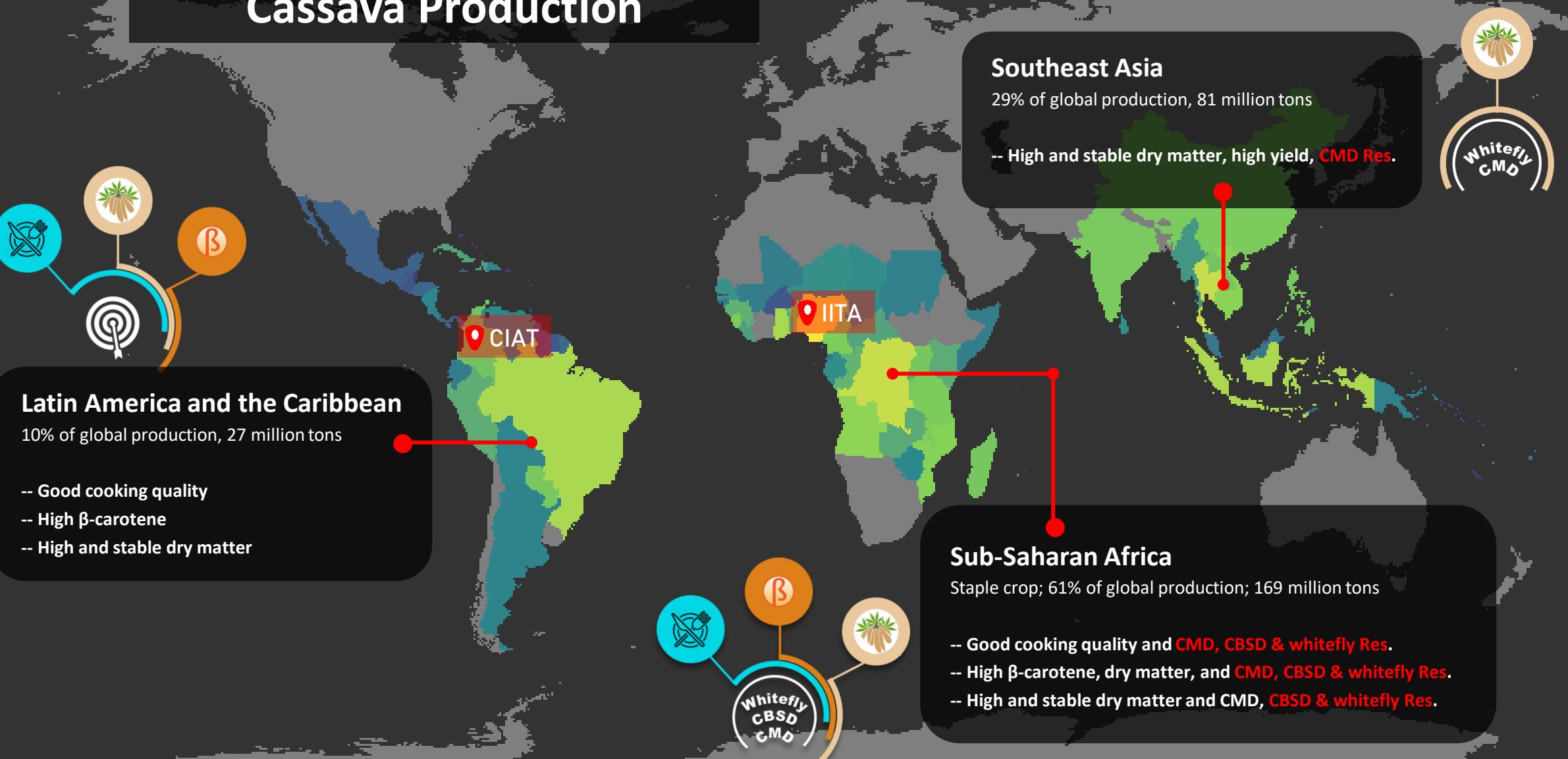


Cassava specialty starch



** Processing- granulated and Paste for human consumption*

Cassava Production



Breeding Pipelines



2019 – 

2007 – 

2019 – 

1980 – 

2019 – 

1980 – 

2008 – 

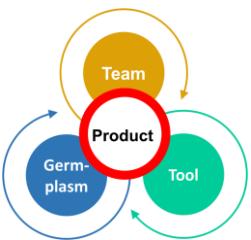
| Market Segment | Product Profile | | | Stage 1.1 | Stage 1.2 | Stage 2 | Stage 3 | Stage 4 | Stage 5 | Stage 6 | Existing Products | |
|----------------|----------------------|-------------------------|--------|-----------|-----------|--|---------|---------|---------|---------|-------------------|--|
| | high pro-Vitamin A | + CMD + CBSD + whitefly | 6,000 | 480 | 180 | 3,000 seeds of improved populations for Africa | | | | | | |
| 1.1 | | -- | 4,000 | 320 | 120 | 50 | 15 | 8 | 2 | 0 | | |
| 1.2 | good cooking quality | + CMD + CBSD + whitefly | 6,000 | 480 | 180 | 3,000 seeds of improved populations for Africa | | | | | | |
| 2.1 | | -- | 4,000 | 320 | 120 | 50 | 15 | 8 | 2 | 2 | | |
| 2.2 | stable dry matter | + CMD + CBSD + whitefly | 6,000 | 480 | 180 | 3,000 seeds of improved populations for Africa | | | | | | |
| 3.1 | | -- | 4,000 | 320 | 120 | 50 | 15 | 8 | 2 | 3 | | |
| 3.2 | special starch | + CMD + CBSD + whitefly | 6,000 | 480 | 180 | 3,000 seeds of improved populations for Africa | | | | | | |
| 4 | | -- | 10,000 | 480 | 180 | 70 | 20 | 10 | 3 | 1 | | |

40,000 2,880 1,080 220 65 34 9





Product Profile



| | | | | | | | | |
|------------------------------|----------------------|-------------------|------------|--|-----|-----|-----|-----|
| | | | | Market segment 1, beta-carotene + CMD | | | | |
| Crop | | | | Cassava | | | | |
| Geographical Region | | | | subhumid lowland and semi-arid lowland tropics | | | | |
| Biological Region/Eco System | | | | | | | | |
| | Trait | Unit | target | yes | yes | | | no |
| | CMD | MAS | yes | yes | | | | no |
| | CBSD | MAS | TBD | | | | | |
| CO_334:0000175 | CBB | | <=2 | 1 | 2 | 3 | 4 | 5 |
| CO_334:0002084 | thrips | | <=2 | 1 | 2 | 3 | 4 | 5 |
| | green mite | | <=2 | 1 | 2 | 3 | 4 | 5 |
| CO_334:0000218 | red spider mite | | <=2 | 1 | 2 | 3 | 4 | 5 |
| | mealybug | | TBD | | | | | |
| | whitefly | | TBD | | | | | |
| | frogskin | | TBD | | | | | |
| | super elongation | | TBD | | | | | |
| | witches' broom | | TBD | | | | | |
| population/variety | | | | | | | | |
| end use | | | | | | | | |
| Production System | | | | human consuption | | | | |
| | Trait | Unit | Target | | | | | |
| | beta-carotene | ug/g fr.wt | >=10 | 3 | 5 | 10 | 15 | 20 |
| | cooking time | min | <=30 | 10 | 20 | 30 | 40 | 50 |
| | water absorption | % | >=10 | 5 | 10 | 15 | 20 | 25 |
| | mealiness | | TBD | | | | | |
| | sweetness | | TBD | | | | | |
| | HCN | ug/g fr.wt | <100 | 50 | 100 | 150 | 200 | 250 |
| CO_334:0000160 | dry matter | % | >27 | 22 | 25 | 27 | 30 | 35 |
| | dry matter stability | | TBD | | | | | |
| | flesh color | | 3 | 1 | | 2 | | 3 |
| CO_334:0000161 | flesh color | 1, white, 8, pink | >5, yellow | 1 | 3 | 5 | 7 | 8 |

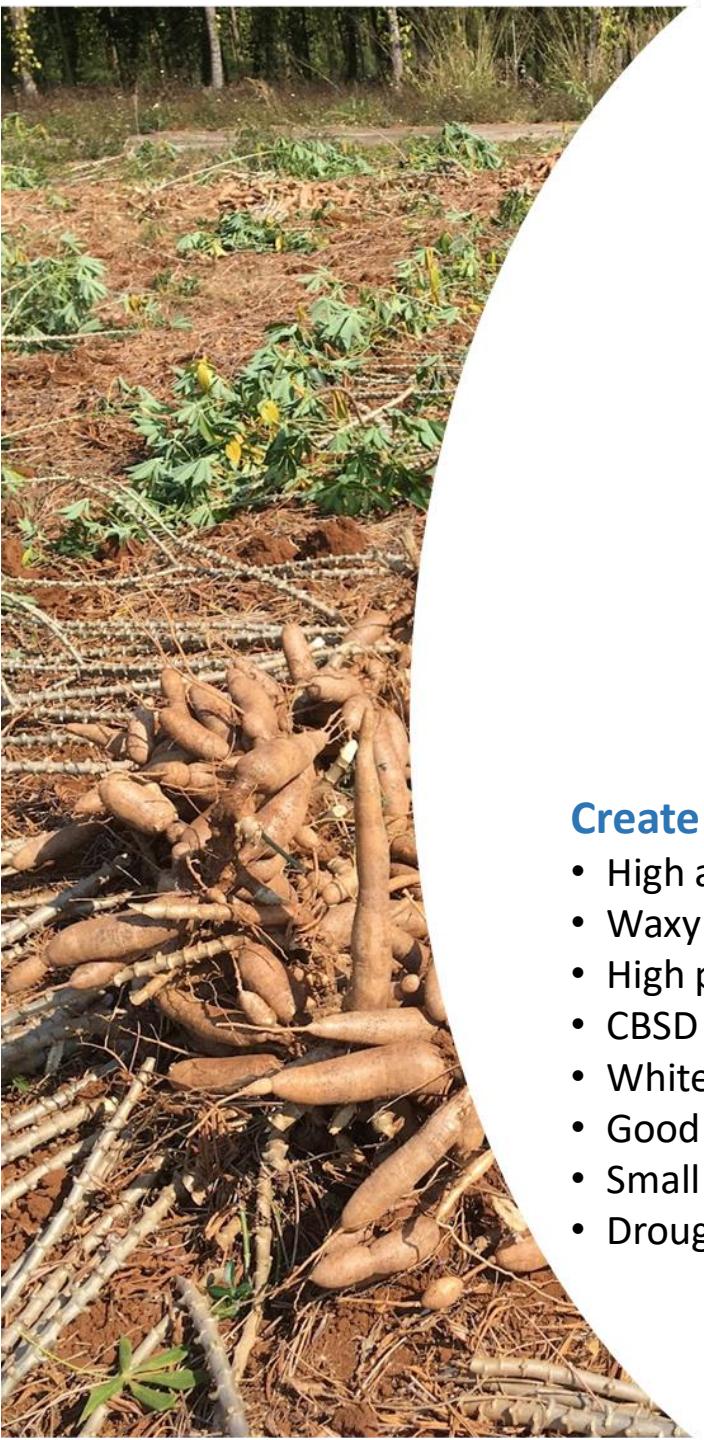


Product Profile



| | | | | | | | | |
|----------------------------------|-------------------------|-----------|---------|-----|-----|-----|-----|-----|
| Input level | | | | low | | | | |
| Maturity | | | | -- | | | | |
| Biofortification | | | | yes | | | | |
| Production/Multiplication Traits | | | | | | | | |
| | Trait | Unit | Target | | | | | |
| CO_334:0000138 | germination | % | >80 | 70 | 80 | 85 | 90 | 100 |
| CO_334:0000220 | vigor | | >=3 | 1 | 2 | 3 | 4 | 5 |
| CO_334:0000301 | lodging | | <=2 | 1 | | 2 | | 3 |
| CO_334:0000099 | plant type | | <=3 | 1 | 2 | 3 | 4 | 5 |
| CO_334:0000079 | branch number | | <=3 | 1 | 2 | 3 | 4 | 5 |
| CO_334:0000018 | height | cm | 200-300 | 150 | 200 | 250 | 300 | 350 |
| CO_334:0000106 | height_1st_branch | cm | >150 | 50 | 100 | 150 | 200 | 250 |
| CO_334:0002082 | angle_1st_branch | | TBD | | | | | |
| CO_334:0000123 | stem length with leaves | cm | >30cm | 20 | 30 | 40 | 50 | 60 |
| CO_334:0000300 | number_sticks_available | | >=8 | 6 | 7 | 8 | 9 | 10 |
| not in CassavaBase | easy harvest | | <=2 | 1 | | 2 | | 3 |
| | peduncle length_visual | | 2 | 1 | | 2 | | 3 |
| CO_334:0000221 | skin color | | 3 | 1 | | 2 | | 3 |
| CO_334:0000228 | root type | | <=3 | 1 | 2 | 3 | 4 | 5 |
| CO_334:0000109 | constriction | | 1 | 1 | | 2 | | 3 |
| CO_334:0000020 | root shape | | 2-3 | 1 | 2 | 3 | 4 | |
| CO_334:0000226 | root length_visual | | 2 | 1 | | 2 | | 3 |
| | easy peel | | TBD | 1 | | 2 | | 3 |
| CO_334:0000011 | root number | per plant | >=5 | 3 | 5 | 7 | 9 | 12 |
| CO_334:0000169 | commercial root num. | per plant | >=4 | 2 | 4 | 6 | 8 | 10 |
| CO_334:0000458 | rotted root | % | <=10 | 0 | 5 | 10 | 15 | 20 |
| yield of aboveground | | | | | | | | |
| CO_334:0000013 | yield | ton/ha | >20 | 15 | 20 | 25 | 30 | 35 |
| | yield_check | % check | >=105% | 90 | 100 | 105 | 110 | 115 |
| CO_334:0000131 | commercial yield | ton/ha | >18 | 15 | 18 | 21 | 24 | 27 |

Key Elements of Plant Breeding

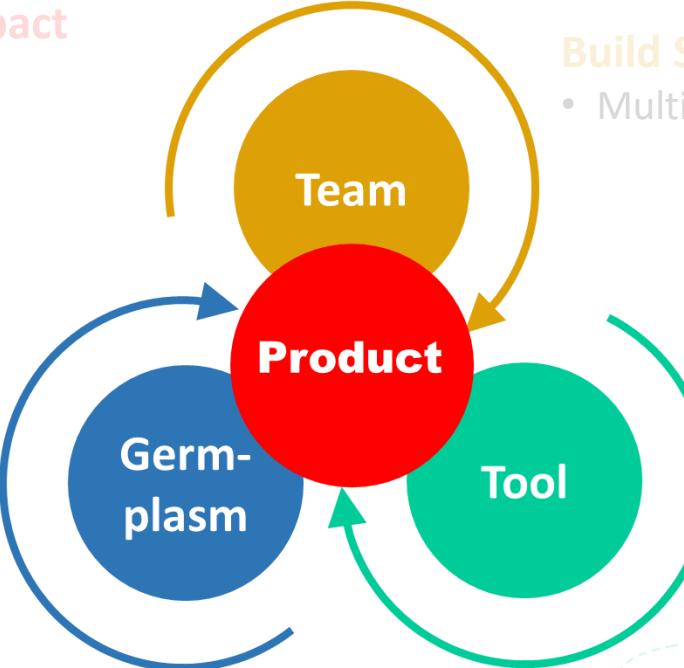


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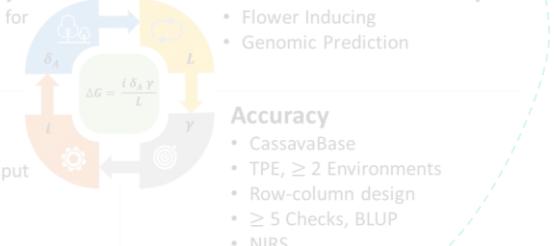
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Intensity

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Duration of Selection Cycle

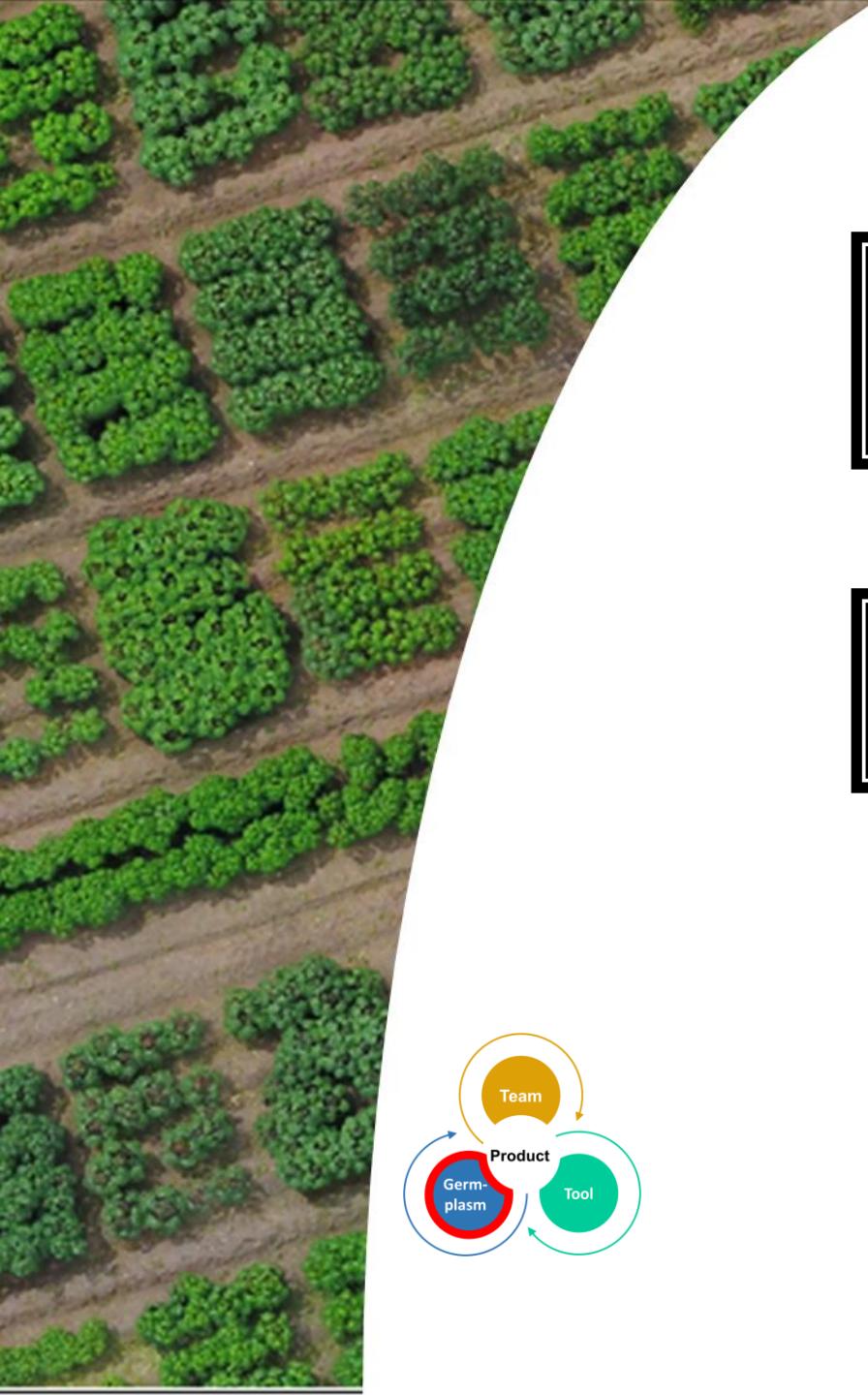
- Flower Inducing
- Genomic Prediction

Accuracy

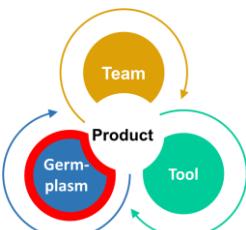
- CassavaBase
- TPE, ≥ 2 Environments
- Row-column design
- ≥ 5 Checks, BLUP
- NIRS



*Standard approvals (SMTA, Export and import permits etc) are given by the authorized institutions.



New Germplasm Opens up New Opportunities



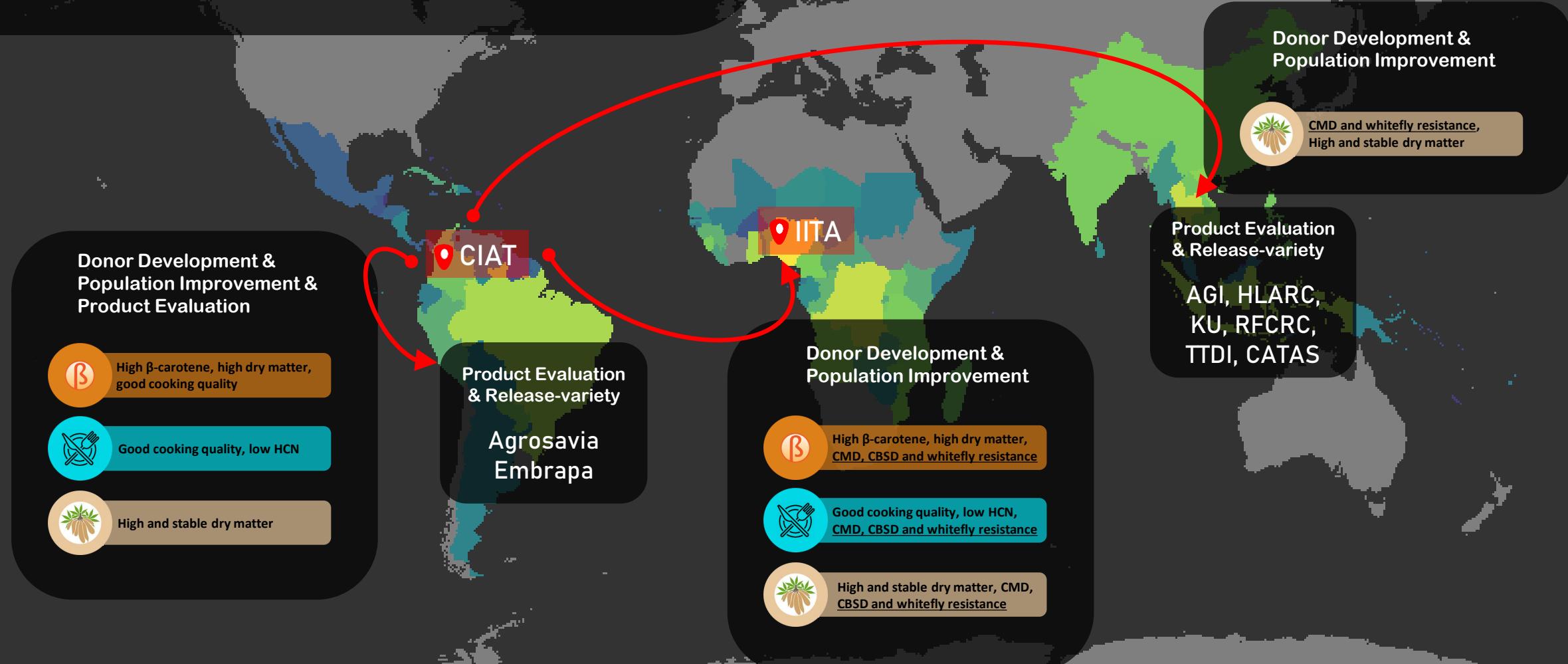
CMD, CBSD and whitefly resistance
High pro-vitamin A
Good cooking quality
Low hydrogen cyanide (HCN)
Low Postharvest physiological deterioration (PPD)

High and stable dry matter
Waxy starch
Small granule

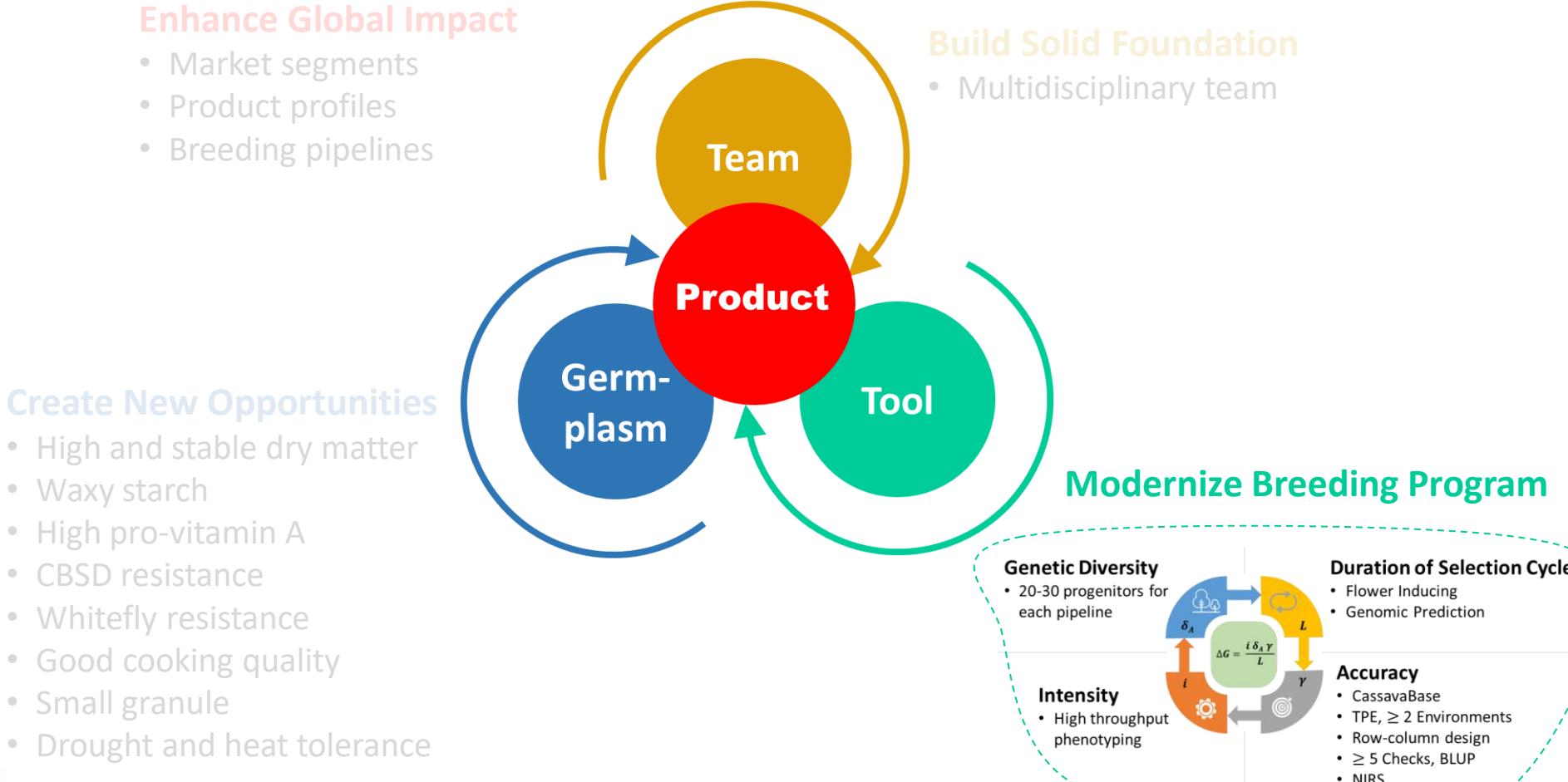
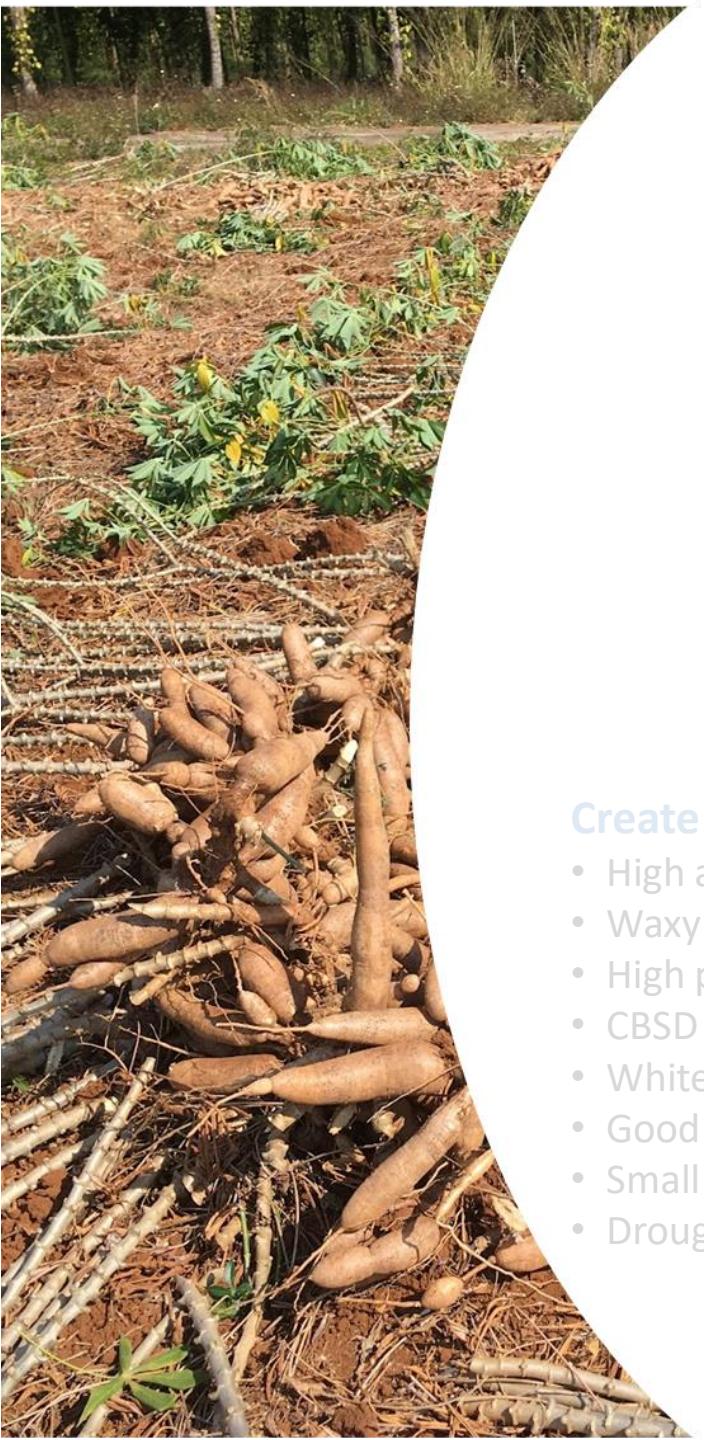
Drought tolerance
Heat tolerance
Haploid inducing
High amylose
Herbicide resistance
Early maturity
High density tolerance

~~Some changing~~

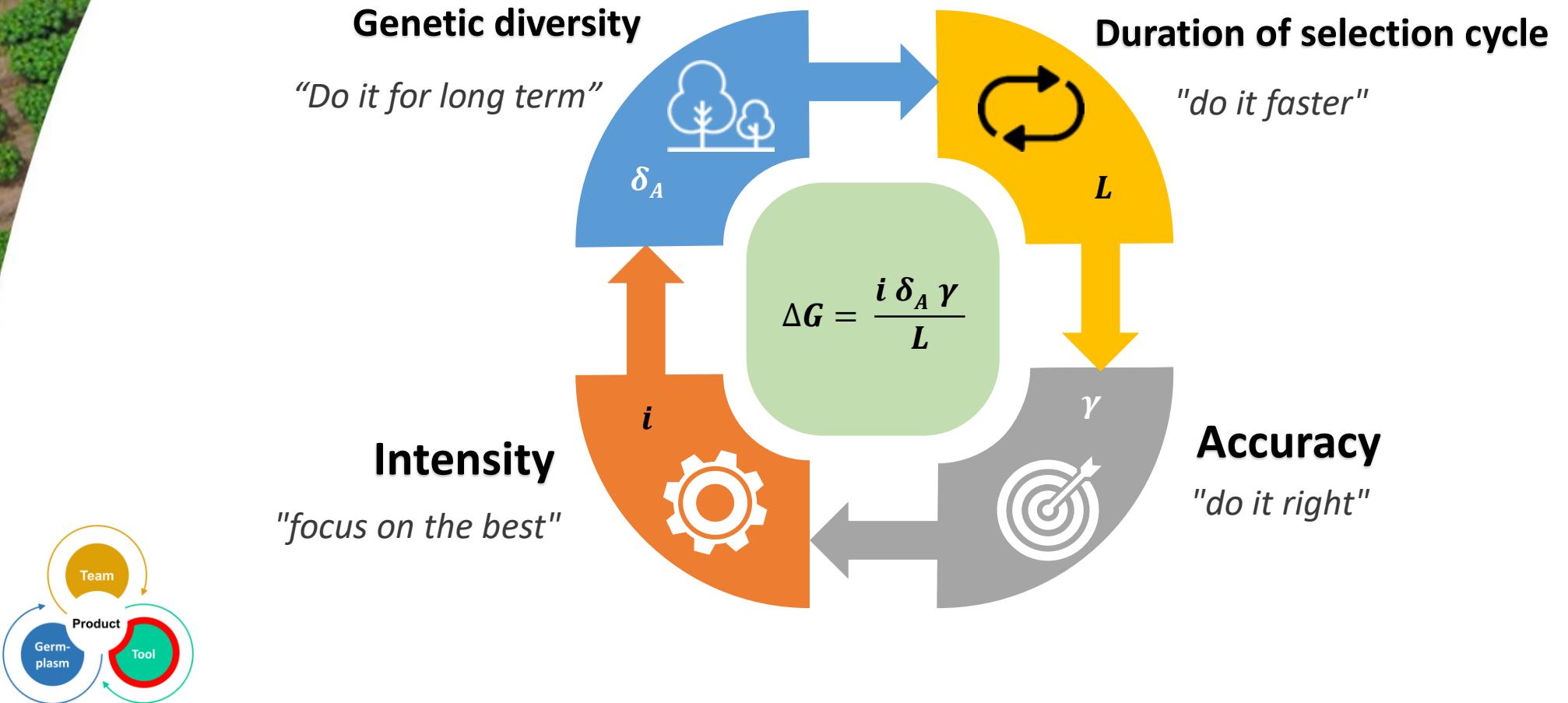
Provide both trait donors and improved breeding populations with CMD, CBSD, and whitefly resistance to IITA and NARS.



Key Elements of Plant Breeding



Breeder's Equation



Realized Genetic Gain

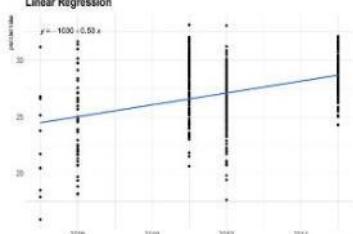
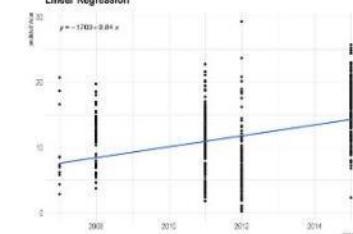
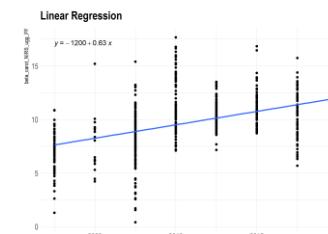
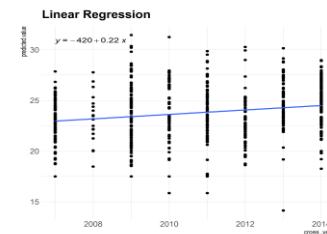
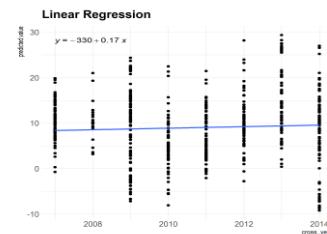


Biofortified cassava for human consumption



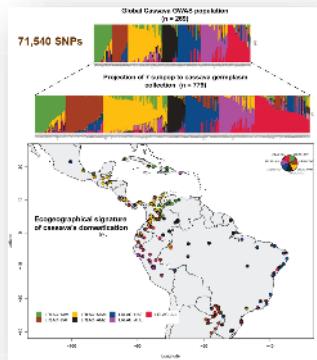
Cassava specialty starch

| | Yield (ton/ha) | Dry matter (%) | Beta-carotene content (ug/g fresh weight) | Yield (ton/ha) | Dry matter (%) |
|-----------------------------|----------------|----------------|---|----------------|----------------|
| Gain per year | 2.03% | 0.96% | 8.19% | 12.2% | 1.94% |
| Num. of trials [#] | 53 | 68 | 7 | 13 | 16 |
| Year | 2013-2019 | 2013-2019 | 2013-2019 | 2011-2020 | 2011-2020 |
| Num. of loc* | 13 | 20 | 1 (station) | 9 | 10 |
| Common checks | 4 | 4 | NA | 4 | 4 |
| Origin years | 2007-2014 | 2007-2014 | 2007-2014 | 2008-2015 | 2008-2015 |



*Location TPE, sub-humid and semi-arid lowland tropics & farmer's field

#All data were stored in CassavaBase

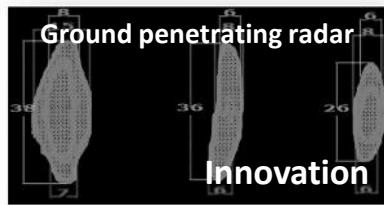


Genetic Diversity

- New traits, e.g., CBSD res., CMD res., good cooking quality et al.
- Sequencing of progenitors (2020-)
 - **Hybrid breeding** (2018-)

Intensity

- High throughput phenotyping



Above ground biomass and plant type

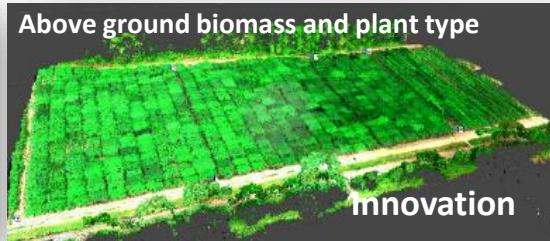
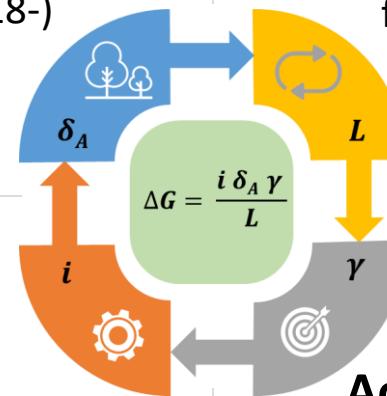
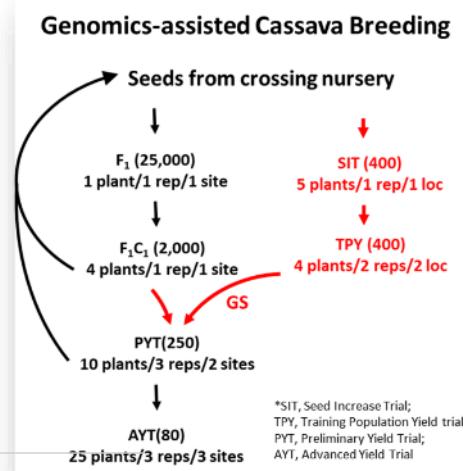


Image analysis for whitefly resistance



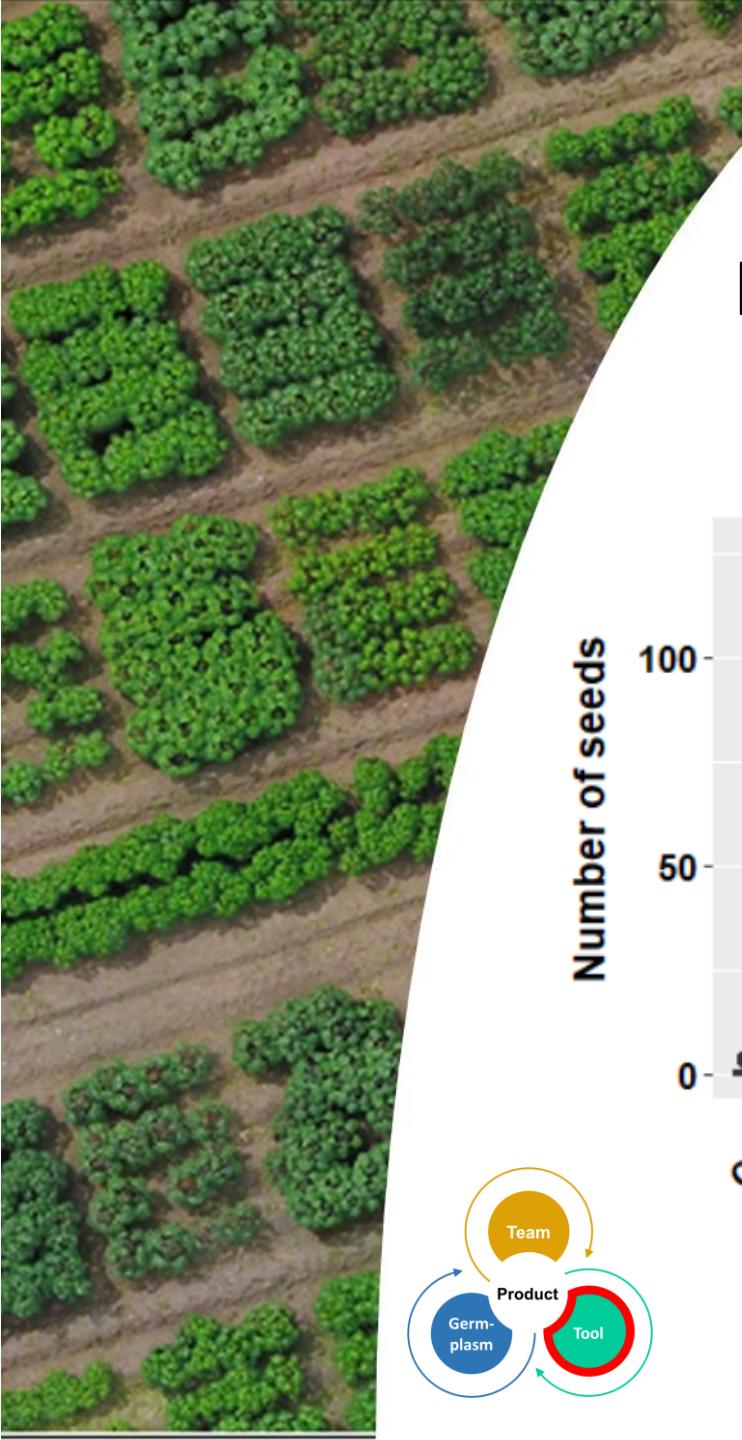
Duration of Selection Cycle

- Flower Inducing (2016-)
- Genomic Selection (2019-)
- Rapid Recycling Progenitors from 5 to 3 years (2019-)

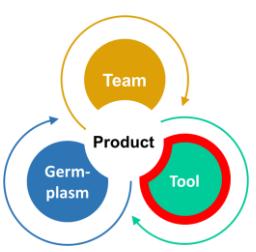
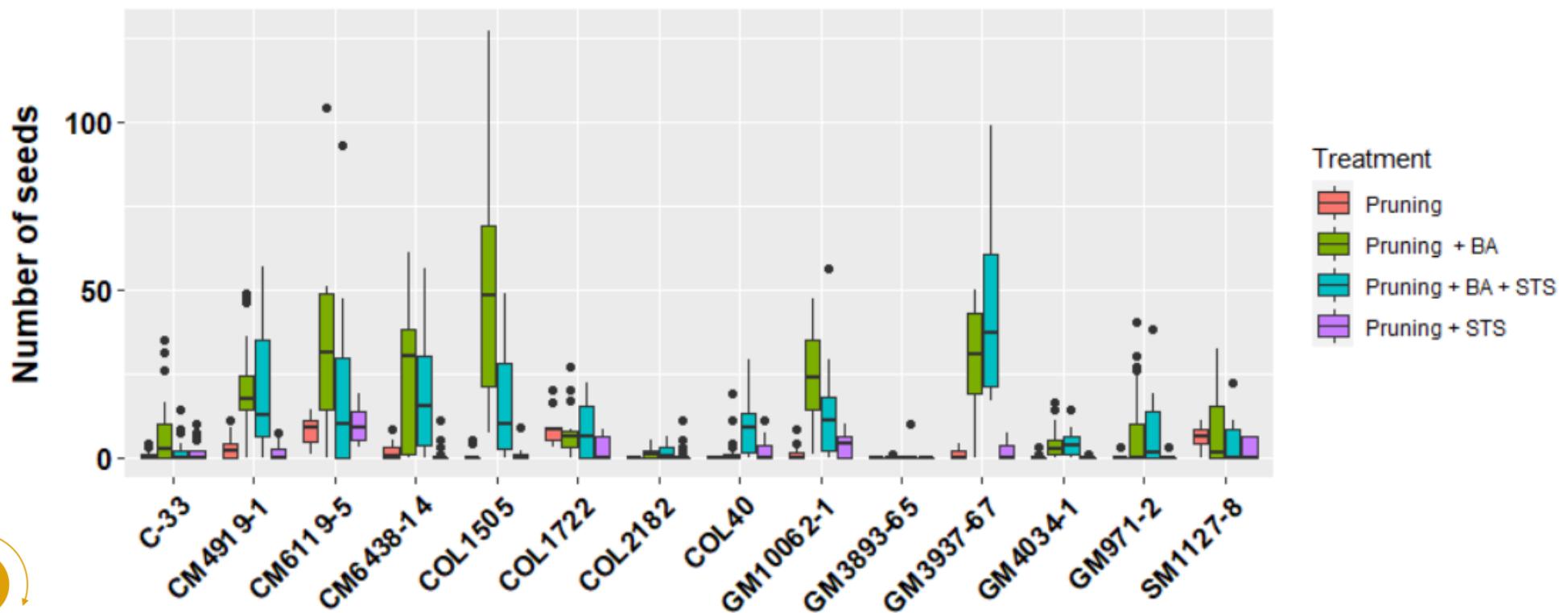


Accuracy

- **CassavaBase**, Fieldbook & Barcode (2018-)
- TPE, ≥ 2 Environments (2020-)
- ≥ 5 Checks, BLUP and GBLUP (2020-)
- Selection Index (2012-)
- NIRS & Image Analysis (2012-)
- Stage&Gate System (2020-)
- Operational Excellence (2019-)

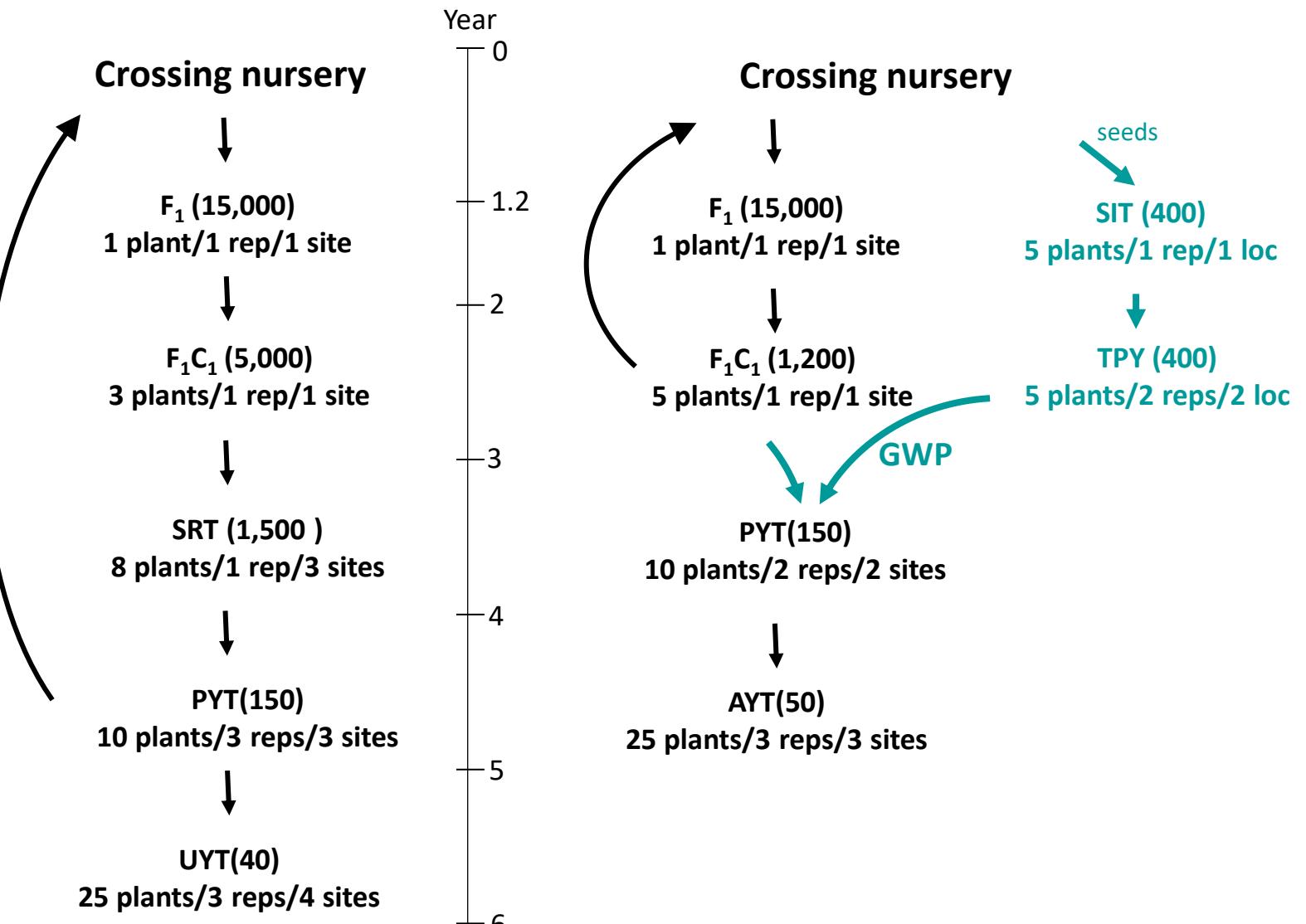
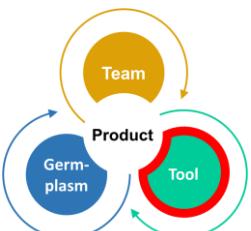


Flower Inducing Technology



BA, 6-Benzylaminopurine; STS, silver thiosulfate

Genome Wide Prediction-based Recurrent Selection





Diploid
Cross-pollinated
Self-compatible
Inbreeding depression

Heterosis

Clonal propagation

– no seed production system

Pollination is labor-intensive



Cell

 **CellPress**

Article

Genome design of hybrid potato

Chunzhi Zhang,¹ Zhongmin Yang,¹ Dié Tang,¹ Yanhui Zhu,¹ Pei Wang,¹ Dawei Li,¹ Guangtao Zhu,² Xingyao Xiong,¹ Yi Shang,² Canhui Li,² and Sanwen Huang^{1,3,*}

¹Shenzhen Branch, Guangdong Laboratory of Lingnan Modern Agriculture, Genome Analysis Laboratory of the Ministry of Agriculture and Rural Area, Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences, Shenzhen, Guangdong 518120, China

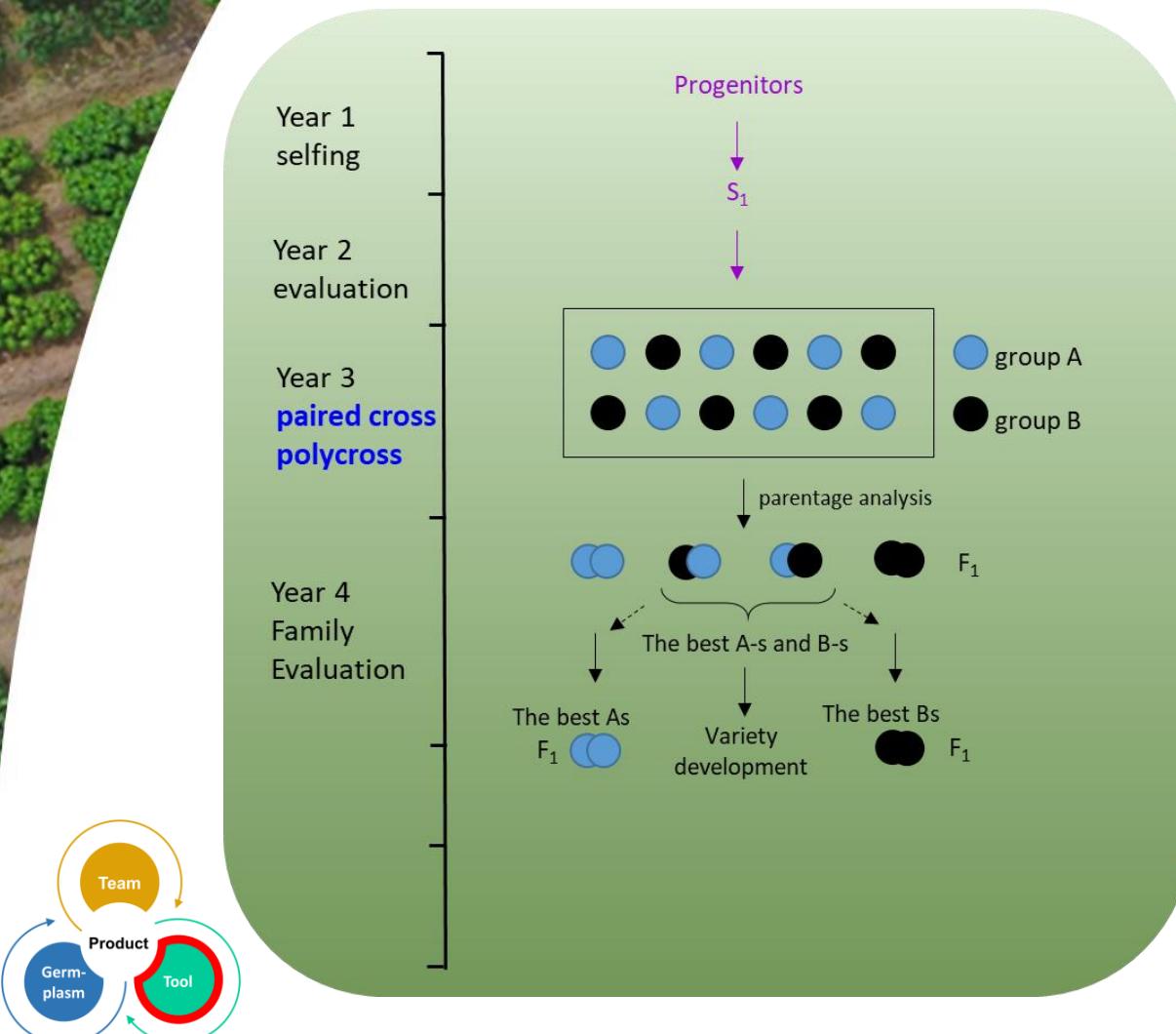
²The AGISCAAS-YNNU Joint Academy of Potato Sciences, Yunnan Normal University, Kunming, Yunnan 650500, China

³Lead contact

*Correspondence: huangsawen@caas.cn

<https://doi.org/10.1016/j.cell.2021.06.006>

Initiate Hybrid Breeding



Select progenitors:

- 1) Different progenitors of breeding pops
- 2) Historical progenitors from the genebank
- 3) Breeding progenitors from Brazil

Data collection:

- 1) Genotypic and phenotypic data
- 2) Family effect, GCA, SCA, heterosis

Aim to:

- Understand the **heterosis** level and **inbreeding depression**;
- Identify **heterotic patterns**



Fully Use CassavaBase, FieldBook and Barcode

CASSAVABASE Search Manage Analyze Maps About

Search Wizard

Don't see your data? Refresh Lists Update Wizard

Breeding Programs

Search

Select All 1/24 Clear

+ 5CP
+ BTI
+ CARI
+ CH
+ CNRA
X CIAT

Years

Search

Select All 1/40 Clear

+ 2016
+ 2017
+ 2018
+ 2019
+ 2020
X 2021

Trials

Search

Select All 69/69 Clear

X 202151GSF1C_ciat
X 202152MDEPR_momi
X 202153BCEAR_repe
X 202155DVGXE_ciat
X 202156DVGXE_repe

Plots

Search

Select All 18018/18018 Clear

X 202034BCPRC_cere_rep1(CG
X 202034BCPRC_cere_rep1(CM
X 202034BCPRC_cere_rep1(CO
X 202034BCPRC_cere_rep1(GM
X 202034BCPRC_cere_rep1(GM

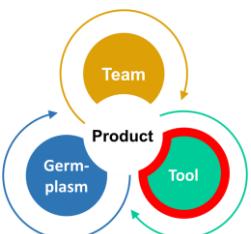




Markers for Quality Control and MAS



Excellence in Breeding Platform



KASP low density genotyping Platform

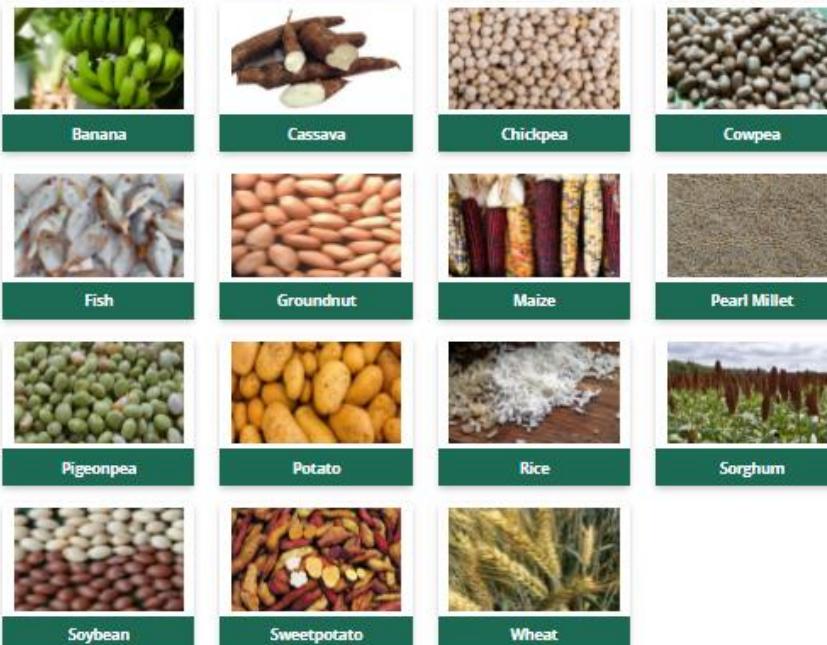
Tools

Genotyping / sequencing tools and services

A DNA-based molecular marker is a genomic DNA (gDNA) fragment located within a genome at a specific position that may or may not be linked to a specific trait of agricultural interest. Trait linked DNA based markers allow us to easily screen breeding materials for favorable alleles associated with traits of interest.

The EiB low-density genotyping service is based on KASP markers. Kompetitive Allele Specific PCR (KASP) is a simplified fluorescence-based methodology to genotype specific polymorphisms or INDELs. This approach is cost effective and offers rapid turnaround for low-density marker applications (between 1 and 200 markers), with applications including specific trait screening, quality control and marker assisted selection (MAS).

The markers available for use in low-density genotyping can be consulted below. This list is continuously updated and improved: kindly remember to revise the list of markers and [consult with EiB genotyping services](#) when planning for genotyping, especially new users.



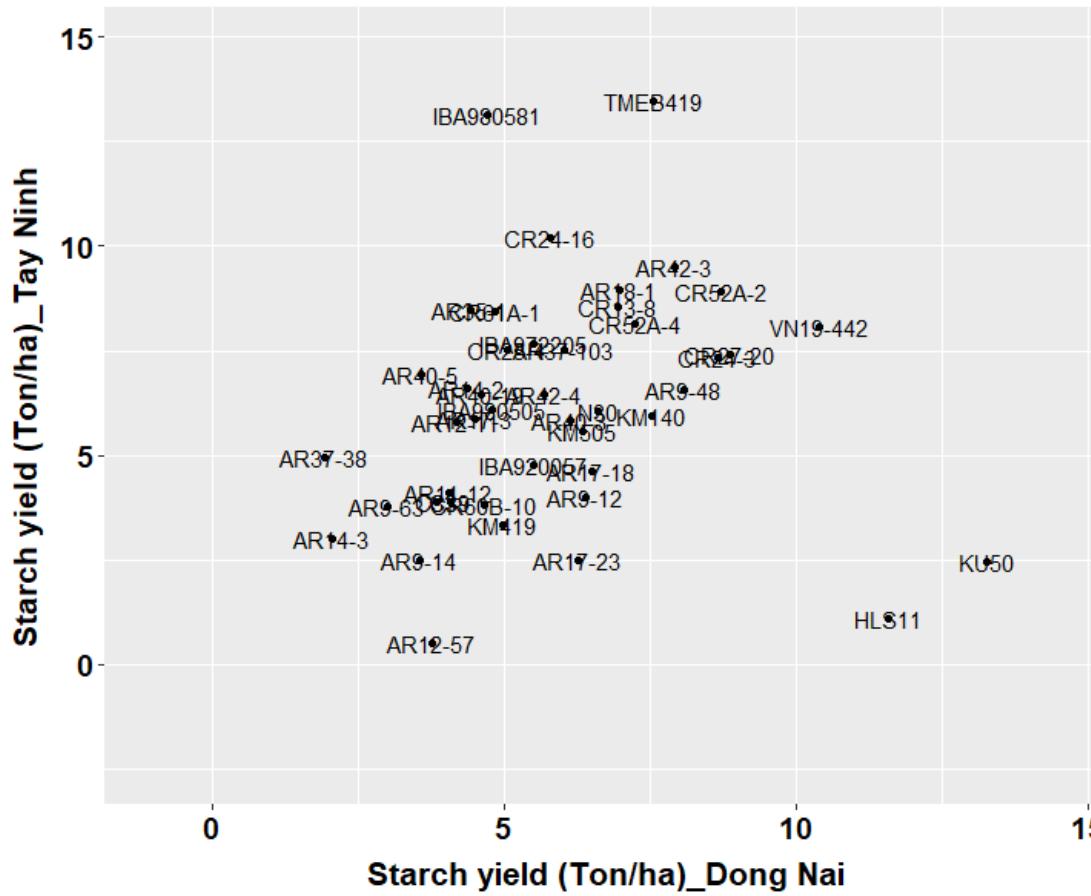


Major Sources of CMD Resistance In South-East Asia

- 1) 5 IITA clones, all showing high resistance in Tay Nihn;
- 2) C33, C39, TME3 and other clones from CIAT and IITA
- 3) 10 resistant varieties from the clones collected in Vietnam
- 4) 102 CIAT clones containing CMD2 genes according to SSR markers
- 5) introduced seeds from Hawaii (progenitors from CIAT and IITA)
- 6) 474 seeds for genomic selection derived from CMD donors at CIAT

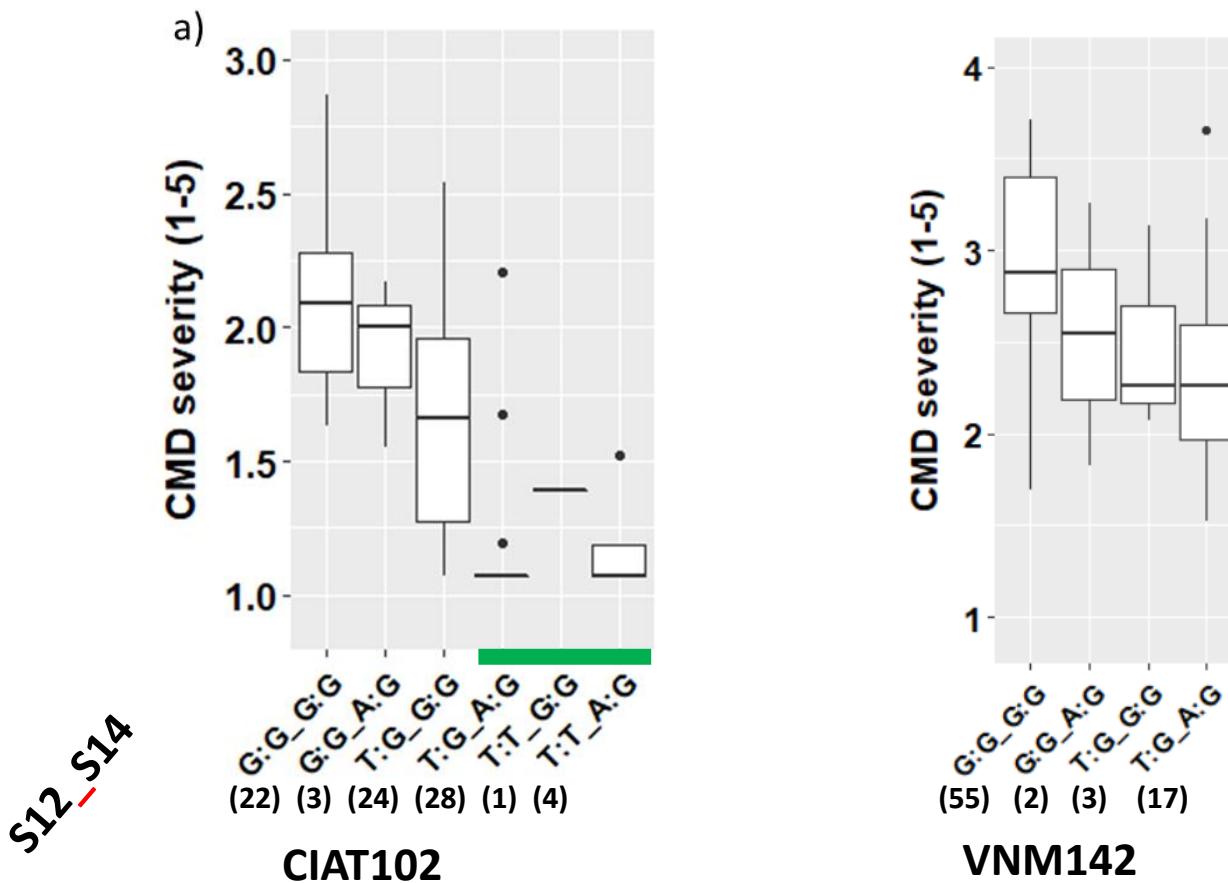


Stability of Starch Yield





Validation of *CMD2* markers in CIAT102 and VNM142



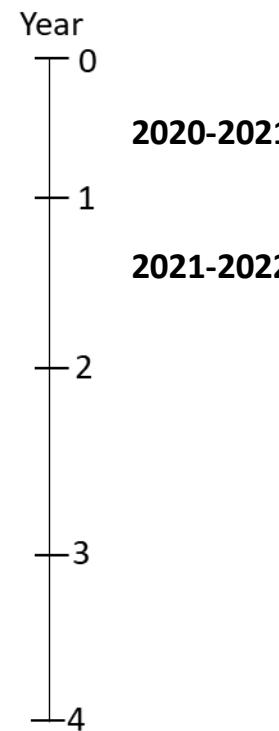
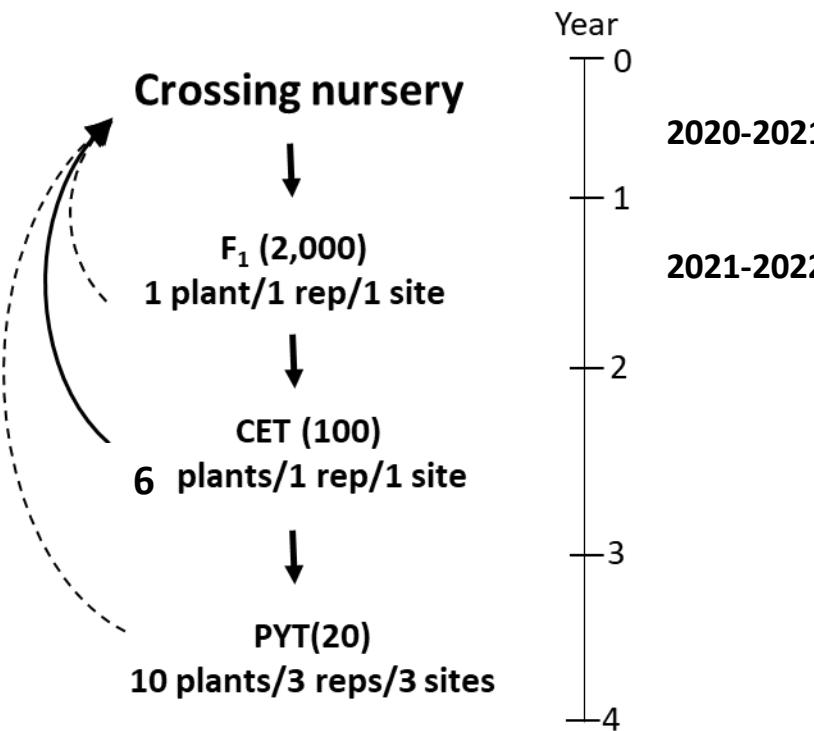
S12_7926132 and S14_4626854

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 populations, but not for diversity populations



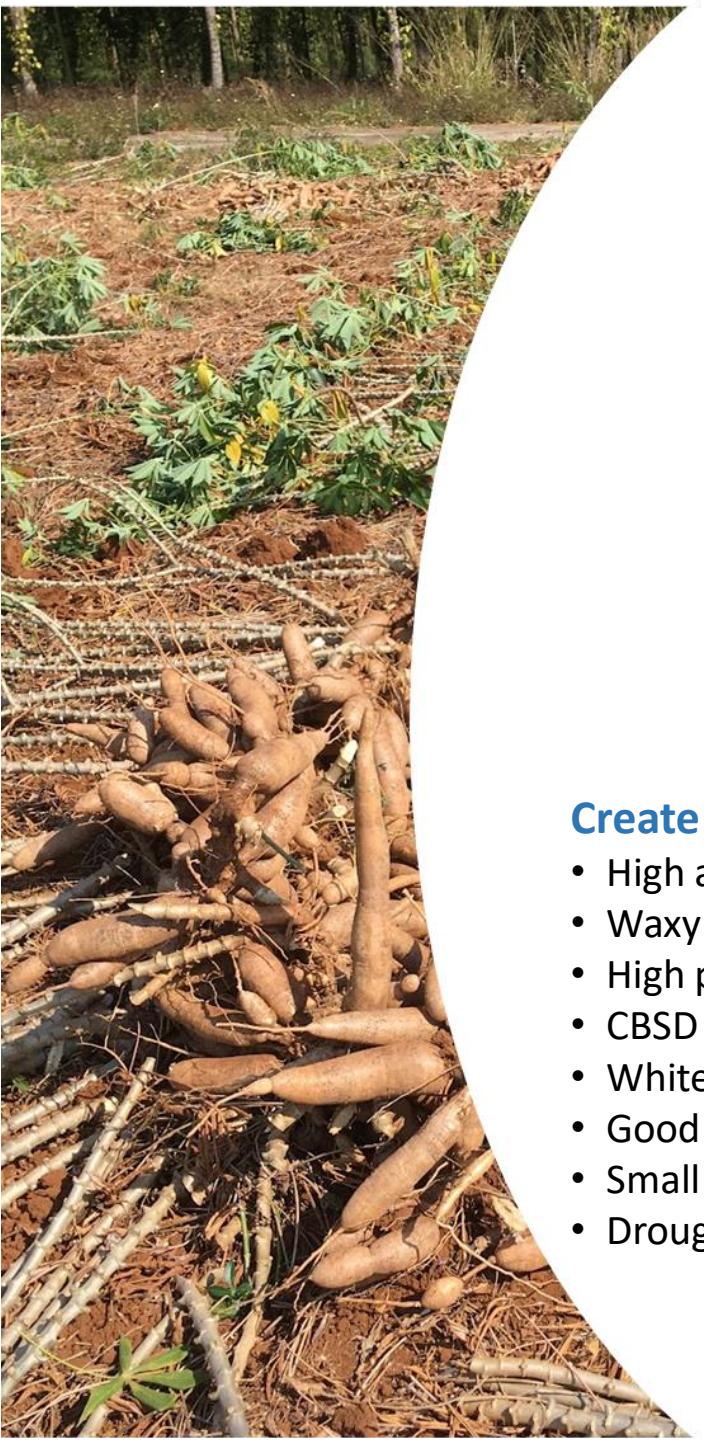
Recurrent Selection for Improving the Breeding Population



Two cycles of quick recurrent selection to introgress CMD resistance to elite variety to provide improved breeding populations to NARS.

MAS for *CMD2* locus increased the selection efficiency.

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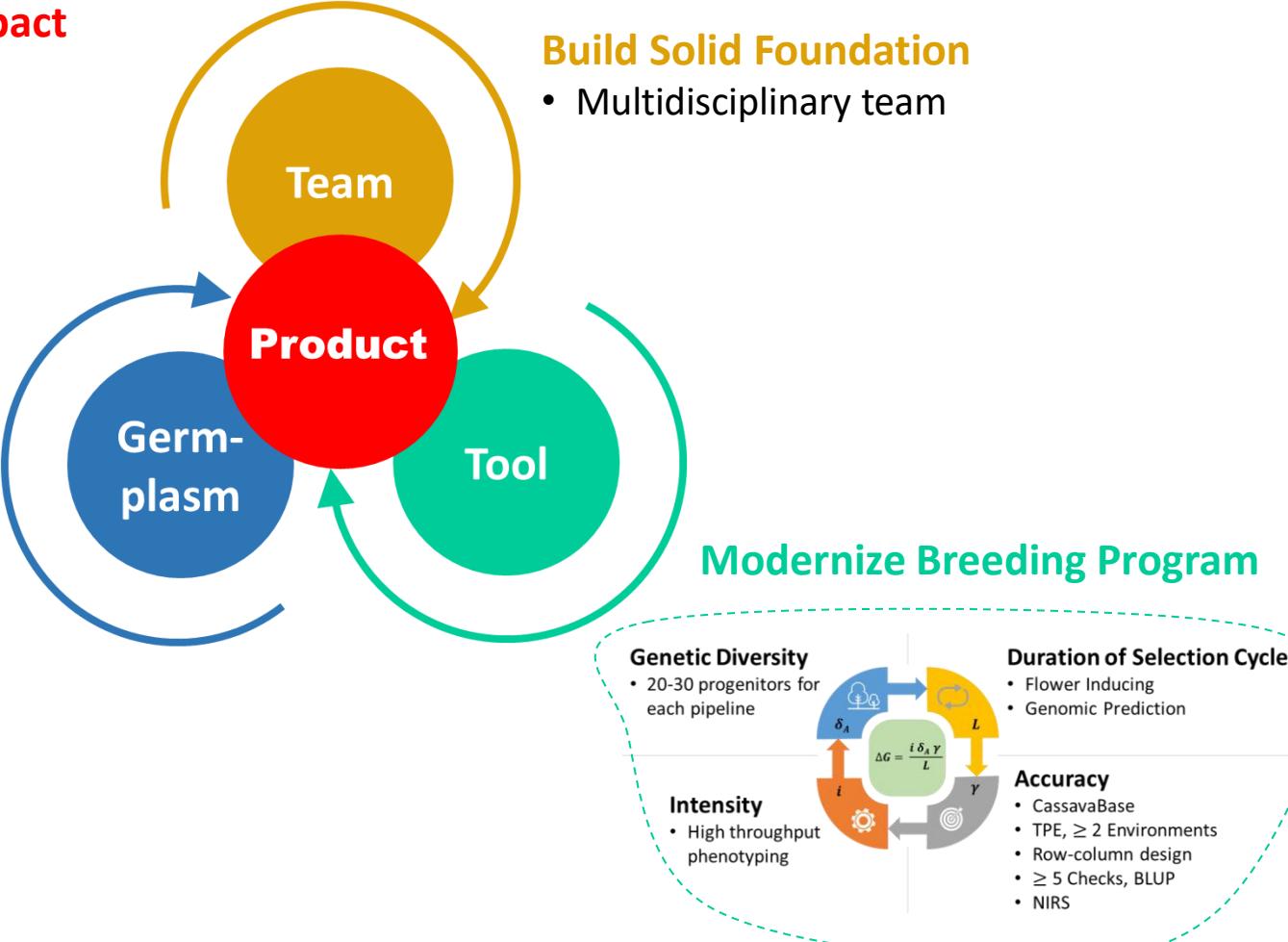


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- Waxy starch
- High pro-vitamin A
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- Whitefly resistance
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- Small granule
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Enhance Global Impact

- Market segments
- Product profiles
- Breeding pipelines





Theoretical and Applied Genetics (2021) 134:2335–2353
<https://doi.org/10.1007/s00122-021-03852-9>

REVIEW



Fifty years of a public cassava breeding program: evolution of breeding objectives, methods, and decision-making processes

Hernán Ceballos^{1,2}  · Clair Hershey³ · Carlos Iglesias⁴ · Xiaofei Zhang^{1,2} 

Received: 19 February 2021 / Accepted: 3 May 2021 / Published online: 4 June 2021
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Abstract

This paper reviews and analyzes key features from cassava breeding at the International Center for Tropical Agriculture (CIAT) over 50 years and draws lessons for public breeding efforts broadly. The breeding team, jointly with national program partners and the private processing sector, defined breeding objectives and guiding business plans. These have evolved through the decades and currently focus on four global product profiles. The recurrent selection method also evolved and included innovations such as estimation of phenotypic breeding values, increasing the number of locations in the first stage of agronomic evaluations, gradual reduction of the duration of breeding cycles (including rapid cycling for high-heritability traits), the development of protocols for the induction of flowering, and the introduction of genome-wide predictions. The impact of cassava breeding depends significantly on the type of target markets. When roots are used for large processing facilities for starch, animal feeding or ethanol production (such as in SE Asia), the adoption of improved varieties is nearly universal and productivity at the regional scale increases significantly. When markets and relevant infrastructure are weak or considerable proportion of the production goes for local artisanal processing and on-farm consumption, the impact has been lower. The potential of novel breeding tools needs to be properly assessed for the most effective allocation of resources. Finally, a brief summary of challenges and opportunities for the future of cassava breeding is presented. The paper describes multiple ways that public and private sector breeding programs can learn from each other to optimize success.



RTB foods

Australian Government
Australian Centre for
International Agricultural Research

Ingredion

华大生命科学研究院
BGI • research

AGROSAVA

CGIAR

Excellence in
Breeding
Platform



MAKERERE UNIVERSITY

USDA ARS
United States Department of Agriculture
Agricultural Research Service

NaCRRI
NATIONAL CROPS RESOURCES RESEARCH INSTITUTE

Embrapa

BTI
BOYCE THOMPSON INSTITUTE

UNIVERSITY OF HAWAII
MĀLĀMĀLA
UA MAU KE EA O KA 'ĀINA I KA PONO
1907

Foreign, Commonwealth
& Development Office

BILL & MELINDA
GATES foundation



Cornell University

DSMZ

CGIAR

RESEARCH
PROGRAM ON
Roots, Tubers
and Bananas

WACCI
WEST AFRICA
CENTRE FOR
CROP
IMPROVEMENT

IITA
Transforming African Agriculture

CIAT

NATIONAL ROOT CROPS
RESEARCH INSTITUTE

TARI
Transforming Agriculture



Centro Universitario de
Investigaciones Agropecuarias

H.Usma



Cassava Hybrid Breeding

- 1) Explore **germplasm pools** to understand the genetic distance and heterosis among pools;
- 2) Determine **heterotic patterns**
- 3) Use genomics technology to understand **inbreeding depression** and identify favorable alleles to select for and major deleterious mutations to select against;
- 4) Develop technologies to **shorten crossing cycle** for inbreed development and trait introgression;
- 5) Implement **two-part strategy** to enhance population improvement and variety development.

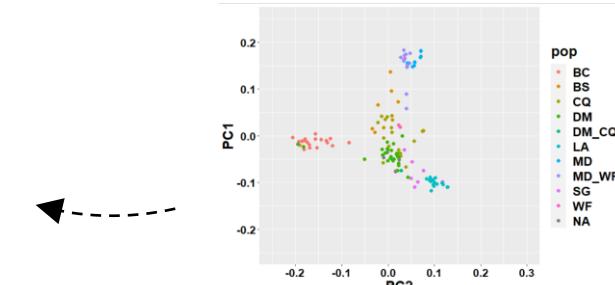


Table 2. Inbreeding depression (ID, as a percentage of the performance from the S_0 generation) measured in eight S_1 cassava (*Manihot esculenta* Crantz) families.

| Family | Plant height | Root yield | Foliation yield | Harvest index | DMC [†] | | | | | |
|--------|--------------|------------|-----------------|---------------|------------------|------|------|-------|------|-----|
| | S_0 ID | S_1 ID | S_0 ID | S_1 ID | S_0 ID | | | | | |
| AM320 | 203 | 15.8 | 4.48 | 77.8 | 2.51 | 56.5 | 0.62 | 38.5 | 30.0 | 8.7 |
| AM331 | 246 | 6.9 | 0.20 | 65.6 | 2.94 | 27.0 | 0.76 | 25.2 | 29.7 | 6.9 |
| AM334 | 224 | 0.7 | 4.92 | 56.9 | 2.57 | 31.9 | 0.65 | 18.0 | 26.1 | 1.5 |
| AM335 | 217 | 10.8 | 4.50 | 64.0 | 1.80 | 42.8 | 0.71 | 16.6 | 35.3 | 8.7 |
| AM336 | 208 | 9.6 | 1.03 | 61.7 | 1.96 | 33.1 | 0.33 | 43.0 | 29.7 | 0.3 |
| AM337 | 175 | 6.0 | 1.29 | 50.6 | 1.93 | 16.4 | 0.63 | 25.2 | 32.1 | 2.9 |
| AM338 | 208 | 7.6 | 4.23 | 65.6 | 2.70 | 50.4 | 0.61 | 20.2 | 31.8 | 4.5 |
| AM339 | 239 | 24.9 | 4.52 | 68.8 | 1.86 | 44.5 | 0.65 | 25.31 | 35.6 | 7.0 |
| Avg. | 215 | 10.1 | 4.4 | 63.9 | 2.3 | 37.9 | 0.62 | 26.5 | 31.3 | 5.3 |

[†]DMC, dry matter content.

$ID = [(S_0 \text{ mean} - S_1 \text{ mean})/S_0 \text{ mean}] \times 100$.

