

RTB (Root, Tuber & Bananas) Project reporting for 2017 and planning 2018 and beyond [Cluster SW 2.6 (2 = varieties, breeding, and seed dissemination; 6 = sweetpotato), 2017)

Wolfgang Grüneberg

Cluster SW 2.6 a code for "User preferred sweetpotato varieties and seed technologies (SW2.6)"

## **Overview of RTB reporting / CRP 3.4**

#### PRODUCT PORTFOLIO REPORTING 2014 - Themes 1-7 (SITUATION 03.April 2015)

Blue colored milestones are UNFUNDED (as mentioned in the PP updating for 2014 - and obvisously were unfunded throughout 2014 as not reported)

Theme/ Commodity	RED	YELLOW	GREEN	BLUE	Total
1.1	2	5	5	0	1
1.2	5	28	8	0	4
1.3	7	12	3	3	2
1.4	0	6	2	5	1
1.5	1	3	0	6	1
1.6	7	12	2	2	2
1.7	1	0	0	9	1
2.1	4	18	0	7	2
2.2	9	27	5	5	4
2.3	14	70	9	7	10
2.4	7	37	4	0	4
2.5	0	37	2	0	3
2.6	3	16	8	1	2
2.7	2	6	2	0	1
	62	277	50	45	43

Commodity	RED	Total products	
1: Crosscutting	75	209	36%
2: Banana	45	216	21%
3: Cassava	60	248	24%
4: Potato	30	141	21%
5: Sweetpotato	21	90	23%
6: Yam	40	99	40%
7: Other RTB	13	30	43%
	284	1033	27%

Commodity	BLUE	Total products	26
1: Crosscutting	23	209	11%
2: Banana	10	216	5%
3: Cassava	20	248	8%
4: Potato	23	141	16%
5: Sweetpotato	19	90	21%
6: Yam	11	99	11%
7: Other RTB	9	30	30%
	115	1033	11%

Theme/ Commodity	RED	YELLOW	GREEN	BLUE	Total
3.1	0	10	1	0	٣
3.2	12	24	23	0	٣
3.3	2	20	5	2	
3.4	3	14	14	0	**
3.5	0	6	0	5	٣
3.6	2	2	0	4	
3.7	0	0	0	0	
4.1	0	3	0	5	
4.2	2	2	6	3	٣
4.3	8	10	5	4	
4.4	1	10	0	6	*
4.5	5	0	0	0	
4.6	13	0	0	2	4
7.1	47	38	- 4	0	8
	95	139	58	36	30

Commodity	Yellow	Total products	75
1: Crosscutting	100	209	48%
2: Banana	115	216	53%
3: Cassava	137	248	55%
4: Potato	68	141	48%
5: Sweetpotato	48	90	53%
6: Yam	38	99	38%
7: Other RTB	6	30	20%
	512	1033	50%

- red = nothing reported at all
- yellow = reported but information incomplete or misleading,
- green = completely reported, no comments,
- blue = unfunded throughout 2014

Commodity	RED	YELLOW	GREEN	BLUE
5.1	3	14	0	4
5.2	0	31	4	1
5.3	13	22	5	1
5.4	4	0	0	12
5.5	2	0	0	8
5.6	2	7	0	1
5.7	4	0	0	0
6.1	19	1.2	1	2
6.2	17	3	0	1
6.3	16	3	- 4	3
6.4	15	1	0	0
6.5	13	2	0	0
6.6	13	1	0	1
6.7	6	0	0	0
	127	96	14	34

Commodity	Green	Total producta	2
1: Crosscutting	11	209	5%
2: Banana	46	216	21%
3: Cassava	31	248	13%
4: Potato	20	141	14%
5: Sweetpotato	2	90	2%
6: Yam	10	99	10%
7: Other RTB	2	30	7%
	122	1033	12%

#### Commodities:

- x.1 cross cutting across all RTB crops
- x.2 Bananas
- x.3 Cassava
- x.4 Potato
- x.5 Sweetpotato
- x.6 Yam
- x.7 Others

## **RTB** is structured in Flagships

- Flagship 1 Enhanced genetic resources / Develops & applies leading-edge science toward building advanced tools, methods, models & systems to improve accuracy & scale of breeding. It also adds value to genebanks through enhanced conservation research, linking of genes or traits to genebank accessions & the increased characterization of diversity,
- Flagship 2 Adapted productive varieties and quality seed / Make available goodquality planting materials of a diverse set of high-yielding RTB varieties that are adapted to the needs and preferences of different stakeholders in the value chain.
- Flagship 3 Resilient crops / Close yield gaps arising from biotic and abiotic threats & to develop more resilient production systems, thereby strengthening food security & improving natural resource quality.
- Flagship 4 Nutritious food and added value / Harnesses the changing demand of consumers & other users as drivers of change to positively transform production, utilization of RTB crops & increase their contributions to nutritious, profitable, and environmentally sustainable food systems.
- Flagship 5 Improved livelihoods at scale / Improve livelihoods by scaling RTB solutions in agri-food systems, builds on RTB crop improvement and production (FP1–FP3) and post-harvest technologies (FP4) and facilitates understanding and enhance impact of RTB crops in livelihoods.

## Our 7 sister clusters in FP2 (Adapted productive varieties and quality seed)

- CC2.1: Access to quality seed/ varieties Aim: Learn from and support other clusters across all crops to improve the economic sustainability of RTB seed systems in providing quality seed of demanded varieties
- **BA2.2: User- preferred banana cultivars/hybrids** Aim: Make available high-yielding cultivars/ hybrids that better fit demands and are adapted to target environments and populations
- CA2.3: Added- value cassava varieties Aim: Produce cassava varieties and production packages to meet the needs of regionally diverse markets and production constraints in Africa, Asia, and Latin America
- **PO2.4: Seed Potato for Africa** Aim: Establish functional seed system to improve health status of planting material and to disseminate advanced newly developed varieties and existing market demanded varieties
- **PO2.5: Agile potato for Asia** Aim: Provide alternatives for sustainably intensifying, diversifying, and increasing productivity and quality value of potato food systems, many of which are cereal based
- SW2.6: User- preferred sweetpotato varieties Aim: Investigate, develop, and disseminate better sweetpotato varieties and ensure that they meet farmer and consumer preferences
- YA 2.7: Quality seed yam Aim: Develop and deploy improved varieties with enhanced pest and disease resistance, adapted to competitive cropping systems, with viable seed and ware yam value chains

# Custer SW2.6: User-preferred sweetpotato varieties – was structured as follows:

Breeding and seed systems for sweetpotato is divided in 5 product lines:

- 1. Trait capture & gene discovery (including range of trait expression such as min & max. temperatures)
- Breeding Methods and their implementation into applied breeding programs such as implementing the "Accelerated Breeding Scheme" in country xy
- 3. Varieties and Breeding Populations the medium and long term genetic gain is driven by Population Improvement
- 4. Seed systems / Implementation of new methods and modifications
- 5. Capacity Building

Resulting in the code SW2.6.1 to SW2.6.5

Each product line SW2.6.1 to SW2.6.5 must have several outputs (N > 3) with specification of the year to deliver the output and each output has 2 to 4 deliverables as milestones to check progress towards the output



Fig. Illustration of the general strategy of variety development and population improvement in linkage with genetic resources (from Gallais 2003)

## **Our Output list** – Product lines 1 & 2

SW2.6.1.1 Promising dry & starchy OFSP clones identified for East African environments with high SPVD pressure [2019]

SW2.6.1.2 Promising OFSP & PFSP clones for drought prone regions (mainly Southern Africa) [2019]

SW2.6.1.3 Promising OFSP & NSSP clones for West Africa [2019]

SW2.6.1.4 Promising early & widely adapted OFSP clones for the Americas, South Asia, South East Asia & the Pacific [2022]

SW2.6.1.5 Summary documentation of OFSP varieties available by world regions [2018]

SW2.6.1.6 Genotypes and gene(s) for early bulking (the <100 day sweetpotato) identified (2018) SW2.6.1.7Genotypes and gene(s) for non-sweetpotato identified [2018]

SW2.6.1.8 Genotypes and gene(s) for purple fleshed sweetpotato (PFSP) identified [2017]

SW2.6.2.1 Accelerated breeding schemes implemented in South & South East Asia [2018] SW2.6.2.2 Genetic gain (GG) studies for Southern Africa [2019]

SW2.6.2.3 GG studies for West Africa [2019]

SW2.6.2.4 GG studies for temperate & humid tropics of the Americas [2019]

SW2.6.2.5 Optimization & calculating (GG) for later breeding stages [2018]

SW2.6.2.6 Description & and GGs for the accelerated breeding scheme (ABS) in early breeding stages [2020]

SW2.6.2.7 MAS for SPVD resistance in applied breeding programs [2019]

RTB-SW2.6.2.8 Association mapping for novel trait capture available [2017]

## **Our Output list (is long except ...)** – Product lines 3 & 4

SW2.6.3.1 Global OFSP breeding population for wide adaptation & earliness [2019]

SW2.6.3.2 Testing of OFSP pre-breeding populations with high expression of sweetpotato virus disease (SPVD) [2019]

SW2.6.3.3 OFSP dry & starchy populations with elevated SPVD resistance for East Africa [2019]

SW2.6.3.4 OFSP & PFSP populations for drought prone regions (mainly Southern Africa [2019] SW2.6.3.5 OFSP & NSSP populations for West Africa [2019]

SW2.6.3.6 Efficiency estimates for polycross and controlled cross breeding in sweetpotato available [2017]

SW2.6.3.7 Magnitude genetic gains in experimental hybrid populations by genepool seperation and one reciprocal recurrent selection cycle [2018]

SW2.6.3.8 OFSP dry & starchy experimental hybrid population selection for East and Southern Africa - based on a small number of parents [2019]

SW2.6.3.9 OFSP dry & starchy experimental hybrid population selection for East Africa [2020]

SW2.6.4.1 At least 3 improved methods verified for assuring adequate quantity and quality of planting materials retained by farmers in SSA 3 agro-ecologies [2016]

SW2.6.4.2 Elaborate seed-related sweetpotato projects in different SSA agroecosystems [2017]

SW2.6.4.3 Strategy for community-based production of healthy planting materials developed and tested for Asian Conditions [2019]

SW2.6.4.4 Strategies for reliable and cost-effective disease detection piloted by NARS and private sector for seed production schemes [2018]

## Our Output list (is long except ...) – Product line 5

SW2.6.5.1 Annual Breeders & Seed Systems Meetings in SSA & Asia [2019]

SW2.6.5.2 Bi-annual communication & press releases of material and tools published [2016 to 2022]

SW2.6.5.3 Intensification of sweetpotato breeders network in Asia [2022]

### SW2.6.5.4 Establishing and managing the breeding data base for genetic gains in OFSP [2018]

SW2.6.5.5 Diagnostic tools for rapid and accurate detection of major sweetpotato viruses in lab and field (including capacity building for their appropriate use in quarantine and seed systems) are developed [2016]

## SW2.6.5.6 Global sweetpotato pathogen distribution database with direct links to appropriate national partners developed [2018]

SW2.6.5.7 Enhanced understanding of the impact of common symptomless (DNA) viruses in sweetpotato production [2018]

SW2.6.5.8 Development of a global database for the distribution of major sweetpotato insect pests (Cylas spp. and Acraea acerata) linked to risk maps for future pest distribution due to Climate Change [2017] SW2.6.5.9 The sweetpotato weevils and sweetpotato butterfly distribution, population dynamics, incidence and damage in different sweetpotato agro-ecologies understood and documented [2017]

SW2.6.5.10 Knowledge on the efficacy of cultural practices and plant characteristics to reduce Cylas sp. infestation enhanced [2017]

## **Reports – Two examples**

### Example 1

# SW2.6.4.2 Elaborate seed-related sweetpotato projects in different SSA agroecosystems [2017]

**Abstract:** The milestones ID 3764, 5282, 10033, 10034, 10035, and 10036 delivered for 2017 are completing this output on elaboration of seed systems in SSA. Main delivery reports are ID 3763 and 4176 in 2015 and 2016, respectively, on the status of seed systems in SSA. The first is a book chapter (28 Can Small Still Be Beautiful? Moving Local SP Seed Sys. to Scale in SSA by McEvans) and the second a working paper (Sweetpotato Seed Systems in SSA – A Review - ISSN 2309-6586). The tools, practices, and economics to conduct seed systems in different SSA agroecosystems are described in milestones ID 3765 (OFSP Investment), ID5282 (SP Vine Multi. In Lake Zone), ID10033 (SP Seed Systems - Everything you wanted to know), ID10034 (Tissue culture & Net Tunnels), ID10035 (Triple S System), ID10036 (Sandponics for rapid vine production). Output information in 2017/18 has been published in a journal article (M.A. MacEwan et al. 2017: Specialised Sweetpotato Vine Multiplication ... Vol 2: 64–69) and in a book chapter (R. Mwanga et al. 2017 Breeding in Sweetpotatoes. *In:* H. Campos & P.D.S. Caligari Genetic Improvement of Tropical Crops p.181-218).

## **Reports – Two examples**

### Example 2

SW2.6.2.5 "Optimization & calculating (GG) for later breeding stages" [2018]

Abstract: Towards Output SW2.6.2.5 "Optimization & calculating (GG) for later breeding stages" (for 2018) and Output SW2.6.2.6 "Description & and GGs for the accelerated breeding scheme (ABS) in early breeding stages" (for 2020) major milestones have been achieved / delivered. These are comprising variance component estimations in later breeding stages, model calculations for a wide range of variance components, and genetic gain estimates for various breeding scenarios in later breeding stages [ID5204], as well as a working paper / manuscript [ID5203]. A statistical module is under development called "Module for cooperators' guide on assessment of genetic gains (ID5831) to predict genetic gains for a breeding resource allocation in later and early breeding stages. This module is also a prerequisite for Output SW2.6.3.6 "Efficiency studies for polycross and controlled cross breeding" (ID 5225 - Variance component estimates are available). These outputs in the frame of selection theory (Output SW2.6.2.5, SW2.6.2.6, and SW2.6.3.6) are complemented by experimental genetic gain studies by modified demonstration trials in Southern Africa (Output SW2.6.2.2 for 2019), West Africa and East Africa (Output SW2.6.2.3 for 2019), and the humid topics of the Amazon basin (Output SW2.6.2.4 for 2019). These experimental studies are in the 2<sup>nd</sup> evaluation year and indicate so far a genetic gain across the past 10-15 years of 2 to 3% in storage root yield per year in world regions with investments into sweetpotato breeding.

## Innovations in breeding – breeding timelines shortened successfully

Breeding pipeline and timelines



### Allocation of breeding resources / later breeding stages

Breeding pipeline and timelines

Recommendation: Two-stage selection in later breeding stages and then entering into the variety release process



Fig. 4. Response to selection in standardized units for a phenotypic index (Elston) aggregating 8 key traits for 8 allocation scenarios to select the 3 "best" clones; A) total test capacity 2268 plots or B) 540 plots: ST1 = 1-stage selection, 42 clones; ST2 = 1-stage selection, 63 clones; OP1 = optimized 3-stage selection and 3 years testing; OP2 = optimized 2-stage selection and 2 years testing. Varcomp ratios: for index: 1 : 0.124 : 0.012 : 0.133 : 0.947 for Vg : Vgxl : Vgxs : Vgxlxs : Ve.

### Allocation of breeding resources / later breeding stages

Breeding pipeline and timelines

Table 1 Response to selection in standardized units (R) for the three best genotypes.

Scenario	TG <sub>1</sub>	TG <sub>2</sub>	$TG_3$	LOC <sub>1</sub>	LOC <sub>2</sub>	LOC <sub>3</sub>	REP <sub>1</sub>	REP <sub>2</sub>	REP <sub>3</sub>	R	R <sub>rel.</sub>
Standard I	42	42	42	9	9	9	2	2	2	1.826	100.0
Standard III	63	63	63	6	6	6	2	2	2	1.956	107.1
Opti. 3-stage Sel., TG <sub>1</sub> <= 500, LOC <= 12, REP <sub>1</sub> = 2	498	64	5	1	9	12	2	2	2	2.746	150.4
Opti. 3 stage Sel., TG <sub>1</sub> <= 500, LOC <= 12, Rep <sub>1</sub> = 1	500	36	5	3	9	12	1	2	2	2.753	150.8
Opti. 3-stage Sel., $LOC_1$ >= 3, $REP_1 = 2$	334	12	5	3	6	12	2	2	2	2.613	143.1
Opti. 3-stage Sel., LOC <sub>1</sub> >= 3, REP <sub>1</sub> = 1	500	36	5	3	9	12	1	2	2	2.753	150.8
Opti. 2stage Sel,, LOC <sub>1</sub> >=3, REP <sub>1</sub> = 2	338	10	0	3	12	0	2	2	0	2.606	142.7
Recommended I: Opti. 2 stage Sel., LOC <sub>1</sub> >=3, Rep <sub>1</sub> = 1	500	32	0	3	12	0	1	2	0	2.734	149.7
Recommended II: Opti. 2- stage Sel., $LOC_1 \ge 2$ , $TG_2 \ge 25$ , $REP_1 = 2$	454	25	0	2	9	0	2	2	0	2.682	146.9

### **Released OFSP varieties**

Breeding pipeline and timelines

**CIP 2018** 



Fig. A6 and A7 Released OFSP varieties by country and names given to varieties

### **Released OFSP varieties**

Breeding pipeline and timelines

### **Table 2** Released / launched OFSP varieties and available by CIP's genebank

Accession number	Name(s) used	Health Status CIP genebank Lima	Current location of material
<u>CIP105085.2</u>	Benjamin	HS2	CIP genebank Lima
<u>CIP105086.1</u>	Arne	HS2	CIP genebank Lima
<u>CIP105523.1</u>	Sumy	HS2	CIP genebank Lima
<u>CIP106090.1</u>	IDIAP C9017	HS2	CIP genebank Lima
<u>CIP106603.1</u>	IDIAP C0317	HS2	CIP genebank Lima
<u>CIP106906.1</u>	NN	HS2	CIP genebank Lima
<u>CIP194540.5</u>	Abigail	HS2	CIP genebank Lima
<u>CIP199004.2</u>	UMUSPO/1	HS2	CIP genebank Lima
<u>CIP199062.1</u>	Dagga, INTA Nutritivo, 199062.1, CRI-Bohye	HS2	CIP genebank Lima
<u>CIP440014</u>	BARI-SP-12	HS0	CIP genebank Lima
<u>CIP440132</u>	Beauregard, ICTA Pacifico	HS2	CIP genebank Lima
<u>CIP440136</u>	Caromex	HS2	CIP genebank Lima
<u>CIP440185</u>	ICTA Dorado	HS2	CIP genebank Lima
<u>CIP440254</u>	CRI-Apomuden	HS0	CIP genebank Lima
<u>CIP440293</u>	UMUSPO/3	HS2	CIP genebank Lima
<u>CIP441768</u>	SPK-004_Lima	HS2	CIP genebank Lima

CIP 2018

### **OFSP** farmer farmer / breeding lines from CIP's genebank

Breeding pipeline and timelines

Table 3 OFSP accessions / landraces, farmer varieties, old varieties, or lines available by CIP's genbank

Accession number	Name(s) used	Health Status CIP genebank Lima	Origin
CIP106861.3		HS2	PER breeding line
CIP187020.1	ATACAMA	HS2	PER breeding line
CIP420014	Jonathan	HS2	PER
CIP440001	Resisto	HS2	USA
CIP440280	85002-103	HS2	TON
CIP105058.2	PZ120	HS2	PER weevil tolerant breeding line







## **Thank-you for your Attention**