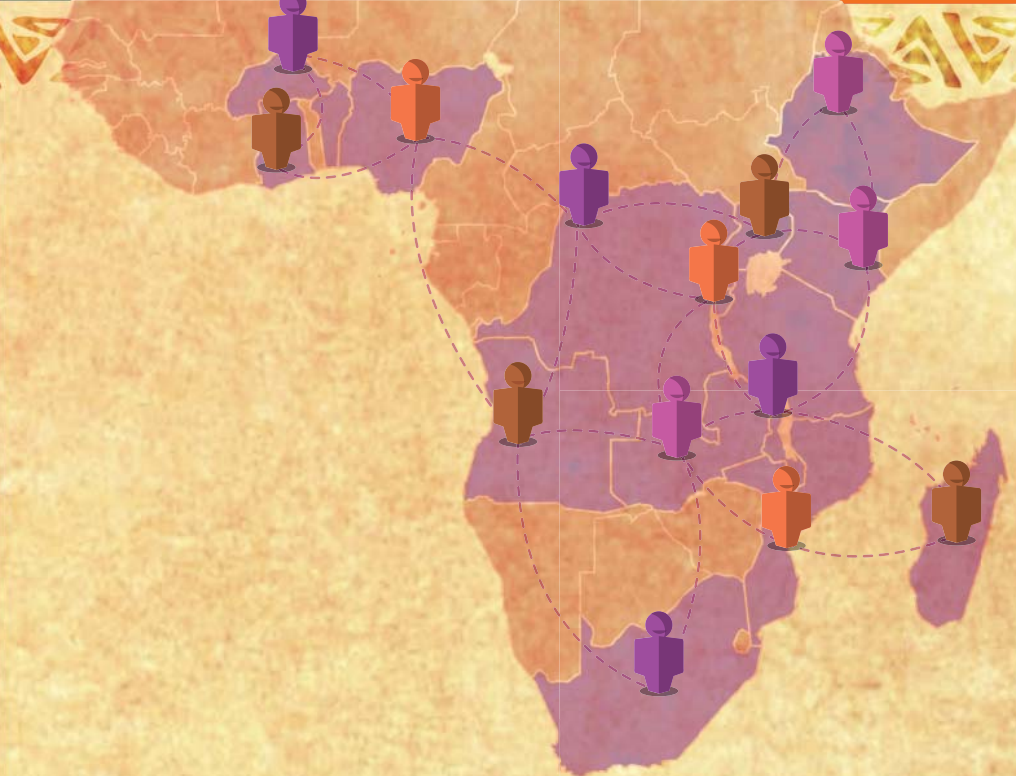




Sweetpotato SpeedBreeders and Genomics Community of Practice



Report of the 14th Sweetpotato Breeders' Meeting held at
Colline Hotel, Mukono-Uganda

June 2-5, 2015

Compiled by Charles Wasonga, Christine Bukania and Robert Mwanga



LIST OF ACRONYMS

ABS	Accelerated breeding scheme
ACCI	African Centre for Crop Improvement
AGRA	Alliance for a Green Revolution in Africa
AT	Advanced Trials
BecA	Biosciences eastern and central Africa
BMGF	Bill and Melinda Gates Foundation
BTI-CU	Boyce Thompson Institute- Cornell University
CGIAR	Consultative Group on International Agricultural Research
CIP	International Potato Center
CSIR-CRI	Council for Scientific and Industrial Research of Ghana – Crops Research Institute
DARS	Department of Agricultural Research Service
EBV	Experimentally estimated breeding value
ECA	East and Central Africa
GEBV	Genomic Estimated Breeding Values
GMO	Genetically Modified Organisms
GT4SP	Genomic tools for sweetpotato improvement
IPM	Integrated Pest Management
KEPHIS	Kenya Plant Health Inspectorate Service
KNUST	Kwame Nkrumah University of Science and Technology
LAMP	Loop-mediated isothermal amplification
MAB	Marker assisted breeding
MAS	Marker assisted selection
MSU	Michigan State University
NACRRI	National Crops Resources Research Institute
NARS	National Agricultural Research Systems
NCSU	North Carolina State University
NIRS	Near Infrared Spectroscopy
NPT	National Performance Trials
OFSP	Orange-fleshed sweetpotato
OFT	On-farm trial
OP	Open Pollinated Seed
PCR	Polymerase chain reaction
PDA	Portable Digital Assistant
PI	Principal Investigator
RNA	Ribonucleic acid
ROI	Return on investment
SASHA	Sweetpotato Action Security and Health in Africa
SNP	Single nucleotide polymorphism
SPCSV	Sweet Potato Chlorotic Stunt Virus
SPFMV	Sweetpotato Feathery Mottle Virus
SPVD	Sweetpotato virus disease
SPW	Sweetpotato weevil
SSA	Sub-Saharan Africa
SSP	Sweetpotato support platform
SSR	Simple Sequence Repeat
US	United States
WAAPP	West Africa Agricultural Productivity Program
WACCI	West African Centre for Crop Improvement

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A INTRODUCTION

The annual Sweetpotato Breeders' Meeting was held at Colline Hotel, Mukono, Uganda, from June 2-5, 2015. This was the 14th meeting since 2003 and the seventh since the start of the Sweetpotato Profit and Health Initiative (SPHI) in 2009. The meeting was opened by the Director General of National Agricultural Research Organization (NARO), Dr. Ambrose Agona.

In his opening address, Dr. Agona welcomed participants to Uganda and described the importance of sweetpotato for the food security and economy of Uganda and sub-Saharan Africa (SSA), and said that the crop is especially valuable among small-scale farmers and women. He commended the continued cooperation between the different institutions present and their Ugandan counterparts, and urged them to customize their work according to what end-users want and the market demands. In addition, he highlighted the progress made in breeding sweetpotato in SSA, and the challenges such as pests and diseases, and explained that the genomics team, which was attending the meeting for the first time, had come at the right time to develop genomic tools to solve some of these major bottlenecks and to accelerate sweetpotato breeding. In conclusion, he thanked the various institutions, farmers and donors who have been working to research and promote sweetpotato production in the region.

The following report captures the proceedings of the workshop, including a summary of all presentations and discussions and field visit. It also captures the feedback on on-farm trial protocols and suggestions for improvement.

The report, presentations and pictures from the 2015 breeders' meeting can be accessed at the Sweetpotato Knowledge Portal: <http://sweetpotatoknowledge.org/>

B PRESENTATIONS AND FIELD VISIT

1. REGIONAL SUPPORT PLATFORM AND COUNTRY REPORTS

1.1. Sweetpotato breeding at the East and Central Africa Sweetpotato Support Platform (SSP)

Mwanga, R., C. Wasonga, G. Ssemakula, J. Kreuze, J. Low, T. Zum Felde and W. Grüneberg

The objective of the breeding component of the support platforms under the Sweetpotato Action for Security and Health in Africa (SASHA) project is to breed new populations with new methods and varietal development. This is done by:

- ▶ Generating a radically expanded range of sweetpotato varieties that combine different quality traits with significant improvements in yielding ability
- ▶ Generating new improved sweetpotato populations to address users' needs, which are as follows:
 - a) Sweetpotato virus disease (SPVD) resistance (East Africa)
 - b) Drought tolerance (Southern Africa)
 - c) Non-sweet sweetpotato (West Africa)
 - d) Incorporate important traits e.g. high beta-carotene content, and dual purpose types for animal feed

The specific objectives of the breeding work under the East and Central Africa (ECA) SSP are:

- a) **To continue to improve sweetpotato population development in SSA through validation of improved breeding methods linked with participatory varietal selection at national level (Proof of concept for accelerated breeding scheme and heterosis).** This entails validation of new breeding approaches and strengthening breeding capacity in SSA. Emphasis is also placed on efficient population improvement using conventional and new molecular tools for breeding.
- b) **To breed for key biotic constraints in Africa. Population development work in Uganda aims to achieve high frequencies of resistance to SPVD (2 to 20%) in new varieties for the low to mid-altitudes.** The ECA breeding program seeks to: continue population improvement for virus resistance with 130 parents in two gene pools so as to ensure true seed supply for National Agricultural Research Systems (NARS) partners in high SPVD pressure zones; incorporate virus resistance into breeding populations; and to exploit heterosis in two virus-resistant pools using a small number of parents.

As part of the effort in population development for the SSP, two distinct gene pools (Population Uganda A and Population Uganda B that were previously separated using 18 simple sequence repeat (SSR) molecular markers) are used. Using parents from these gene pools, controlled crosses (inter- and intra-gene-pool) have been used for population improvement. Progeny resulting from the targeted crosses are evaluated in the field for responses to the biotic and abiotic factors prevalent in the test environments and also evaluated for quality in the laboratory using Near Infrared Spectroscopy (NIRS) to gauge quality traits such as beta-carotene, protein, starch, iron, zinc, glucose and sucrose.

The accelerated breeding scheme (ABS) used by national programs involves substituting the use of fewer sites over seasons with use of more sites at earlier stages of the breeding cycle. The sites used for ABS work in Uganda are Kachwekano (Kabale), Namulonge (Wakiso), Serere (Soroti) and Ngeta (Lira). To support the ABS work, new breeding lines are multiplied in screen houses, glasshouses, and irrigated fields to provide test clones for evaluation in multiple sites in the first year.

SPVD, which is transmitted by aphids and white flies and causes significant yield losses of 50-90% (or even more), has remained a challenge to sweetpotato production. No suitable resistance sources have been identified for deployment against SPVD as yet. At the ECA SSP, real-time polymerase chain reaction (PCR) is used to discriminate SPVD tolerant from SPVD resistant clones during clonal evaluation.

In 2014 specific crosses (29,778 seeds) were generated of which 10,063 seeds were from within Population A, 11,241 seeds from within Population B, and 8,474 seeds from targeted crosses between Population A and B). 697,339 open pollinated seed (OP), seeds were generated from Population A, while 605,654 OP seeds were generated from Population B. A total of 140,400 of the seeds were distributed to national research partners in Kenya, Uganda, Mozambique, Burkina Faso and South Africa.

The ECA SSP also continued to backstop national programs during the reporting period. The support entailed visits to the partners, and coordination of breeding protocols, proposal writing, and training on CloneSelector, on-station and on-farm trials, variety release and publishing of research outcomes. Support to partners included root quality analyses using NIRS in which 140 root samples from Ethiopia were analysed for beta-carotene, iron, zinc, starch, sucrose, fructose, glucose and protein. In 2014, with technical support from the platform, the Alliance for a Green Revolution in Africa (AGRA) awarded sweetpotato breeding and seed systems grants to national partners in Uganda (breeding), Burkina Faso (breeding), Rwanda (seed systems), Kenya (seed systems), Malawi (seed systems). Grant proposals for renewed funding by AGRA had also been submitted by Tanzania and Zambia. AGRA has supported 13 graduate students (10 PhD and 3 MSc) at the African Centre for Crop Improvement (ACCI), University of

KwaZulu-Natal in South Africa and at the West Africa Centre for Crop Improvement (WACCI), University of Ghana, Legon. By June 2015, eight (5 PhD, 3 MSc) had already completed.

The ECA SSP continues to coordinate and organise annual meetings and training of the breeders. Since 2009, six annual meetings have been held in different venues in the following order: Uganda, Mozambique, Ghent University, Rwanda, Malawi, and Uganda.

Discussion arising from the presentation

Following the presentation, some participants expressed their appreciation of the progress that had been made in the area of human capacity improvement through the PhD and MSc trainings.

The following is a summary of the questions that arose for the discussion and the responses:

- ▶ ***How often are the parents in the two populations changed?***
No change had been done after the two populations were grouped using molecular markers; changes will be made based on results from the heterosis and polycross vs. specific cross analyses.
- ▶ ***How much progress had been made to establish testers that will help to come up with heterotic groups for sweetpotato improvement?***
This was planned as a next step.
- ▶ ***What is the trade-off between SPVD resistance and yield?***
Getting the characteristics of SPVD resistance together with high yield has been difficult because of the recessive nature of sweetpotato feathery mottle virus (SPFMV) and sweet potato chlorotic stunt virus (SPCSV) resistance genes.
- ▶ ***Can the gene pools A and B could be considered heterotic?***
Yes, if the two pools were properly separated based on the molecular markers used.

1.2. Sweetpotato breeding activities in East and Central Africa for the year 2014/15

Kivuva B., G. Ssemakula, M. Anyanga, B. Yada, G. Kyalo, J. Namakula, C. Kigozi, R. Mwanga, L. Karanja, J. Malinga, S. Agili, E. Lukonge, K. Mtunda, H. Kulembeka, R. Amour, H. Musa, L. Lembris, B. Chirimi, L. Lyimo, M. Yongolo, H. Kiozya, F. Gurmu, J. Ndirigwe, D. Shumbusha, P. Rukundo, and L. Kankundiye

The presentation covered the East and Central Africa sub-region, Kenya, Uganda, Tanzania, Rwanda, and Ethiopia.

The key constraints to sweetpotato production in the countries covered are:

- a) **Tanzania:** Low yield, sweetpotato weevils and SPVD, drought, and low dry matter of orange-fleshed sweetpotato (OFSP)
- b) **Uganda:** SPVD, *Alternaria*, weevils
- c) **Ethiopia:** SPVD, sweetpotato weevils, low yield and low dry matter content of OFSP
- d) **Kenya:** SPVD, *Alternaria* and weevils, drought, low yield, low dry matter in OFSP, inadequate research funds, and few breeders.
- e) **Rwanda:** Low yield, dual purpose varieties, low dry matter, low beta-carotene, SPVD, weevils

The objectives of sweetpotato improvement research in the East Africa countries are to:

Uganda: <ul style="list-style-type: none"> i. Develop high dry matter, resistance to SPVD and <i>Alternaria</i> blight, and high beta-carotene sweetpotato varieties ii. Promote diversified utilisation, that is for food and processing iii. Promote linkages, and distribution of breeder seed to seed entrepreneurs iv. Promote technical and training support to community-based organisations (CBOs), non-government organisations (NGOs), and farmer seed producers 	Tanzania: <ul style="list-style-type: none"> i. Improve root yield production ii. Increase sweetpotato resistance to SPVD and weevil iii. Screen for drought tolerance iv. Improve beta-carotene and dry matter content of OFSP
Ethiopia: <ul style="list-style-type: none"> i. Improve beta-carotene and root dry matter content of OFSP ii. Improve resistance to SPVD and weevil iii. Improve root yield iv. Improve sweetpotato quality planting material production and seed system in the country 	Rwanda: <ul style="list-style-type: none"> i. To develop high yield dual purpose varieties ii. To improve root dry matter, and beta-carotene iii. To improve tolerance to SPVD and <i>Alternaria</i> iv. To breed varieties suitable for specific or wide adaptation, and/ with farmer preferences v. Breeding drought tolerant varieties vi.
Kenya: <ul style="list-style-type: none"> i. Develop drought tolerant sweetpotato varieties ii. Improve beta-carotene and root dry matter content of OFSP iii. Improve resistance to SPVD and weevil iv. Improve root yield of sweetpotato varieties adapted to broad and specific agro-ecological zones v. Promote production of quality planting material of sweetpotato and sustainable seed systems 	

At present many landraces and released varieties including OFSPs are grown in the different countries. These are summarized in Table 1. During the 2014/15 period, several sweetpotato research trials were conducted in the East Africa region. These are as summarised in Table 2.

Table 1: Important sweetpotato landraces, released, widely grown, and orange-fleshed varieties in East Africa

SWEETPOTATO CATEGORY	COUNTRY				
	Uganda	Rwanda	Kenya	Ethiopia	Tanzania
Important landraces	Ejumula, Kakamega, Semanda, New Dimbuka	Karibunduki, Mbiriwigisabo, Kigande, Mpakanjye, Mamesa II, Ndamirabana (old), Rukoma, Imbyo, Rukubikondo	Gatumbi, MarOoko, Mugande, Nyatonge, Kunyibuonjo, Bungoma		Polista, Mwanatata, Umeme, Isaka, Njugu Karoti, Kigambirenyok, Kilion, Berena, Mzondwa, Matege, Nzugu na tella, Bertha, Mbutu, Shangazi
Important released varieties	NASPOT 1, NASPOT 8, NASPOT 10 O, NASPOT 11, NASPOT 12	Mugande, Karebe, Rusenya, Wadada, Cacearpedo, Gihingamukungu, Giramata/RW11-1860, Terimber/RW11-2560, Ndamirabana/RW11-2910, Ukerewe, Vita, Kabode	KSP 20, KSP 28, SPK 004, SPK 031, Kemb 10, VITAA, KABODE, Kenspot 1, Kenspot 2, Kenspot 3, Kenspot 4, Kenspot 5	Kudade, Dubo, Falaha, Guntute, Damota, Bareda, Awasa-83, Belela, Temesgen, Beletech, Ordolo, Koka-12, Koka-6, Kulfo, Tulla, Kero, Mae, Berkume	Simama, Sinia B, Jitihada, Vumilia, Mavuno, Polista, Mazao, Kakamega, Mlezi, Ukerewe, Kiegea, Mataya, Mayai, Polista
Most widely grown varieties	NASPOT 8, NASPOT 11, NASPOT 12, New Dimbuka	Mugande, Karebe, Wadada, Seruruseke, Kwezikumwe	Bungoma, Kabode, SPK 004, SPK 031, Kemb 10, VITAA	Awassa-83, Kulfo, Tulla	
Most important orange-fleshed varieties	NASPOT 8, NASPOT 12, NASPOT 10		Kenspot 4, Kenspot 5, Kakamega, VITAA, KABODE	Kulfo, Tulla	Kabode, Mlezi, Kakamega, Jewel, Njugu Karoti, UKM 2001/05

Table 2: Sweetpotato research trials conducted in the East Africa region during the 2014/15 period

Trial	Country/No of clones				
	Ethiopia	Rwanda	Kenya	Tanzania	Uganda
Crossing block	7	2	-	16 (EZ)	27
Observation (OT)	25	760	-	2641	-
No. of checks	2	2	-	5	2
Preliminary yield (PT)	6	125	-	70	35
No of checks		2	-	2	2
No. of locations		3	-	2	3
Advanced yield (AT)		25-30	26,15	14, 15,17	19,15,12
No. of checks		2	4,2	2, 2,3	5
No. of locations		4	2,4	2,5	4
On-farm		12	3	34 (3 sets)	8

The variety trials were analysed using CloneSelector mainly. During the 2014 period, one sweetpotato variety was released in Kenya; in 2015 six clones are earmarked for release - two in Rwanda and four in Tanzania.

During the 2014/2015 period, the following 25 articles on sweetpotato were published:

1. Ssemakula G., C. Niringiye, M. Otema, G. Kyalo, J. Namakula and R.O.M. Mwanga 2014. Evaluation and delivery of disease-resistant and micronutrient dense sweetpotato varieties to farmers in Uganda. *Journal of Agriculture and Crop Sciences* 15: (2) 1-11.
2. Niringiye C.S., Ssemakula G.N., Namakula J., Kigozi C.B., Alajo A, Mpembe I and Mwanga R.O.M. 2014. Evaluation of promising orange-fleshed sweetpotato genotypes in different agroecological zones of Uganda. *Journal of Agriculture and Crop Sciences* 7: (13), 1312-1321.
3. Niringiye C.S., Ssemakula G.N., Namakula J, Kigozi C.B., Alajo A., Mpembe I. and Mwanga R.O.M. 2014. Evaluation of promising sweet potato clones in selected agro ecological zones of Uganda. *Time Journals of Agriculture and Veterinary Sciences* 2(3):81-88.
4. Rukarwa R. J., Mukasa S. B, Odongo B. , Ssemakula G. and Ghislain M. 2014. Identification of relevant non-target organisms exposed to weevil-resistant Bt sweetpotato in Uganda. *Biotech* 4:217–226.
5. Sefasi A., Ssemakula G., Ghislain M., Prentice K., Kiggundu A., Mwanga R. and Mukasa S.B. 2014. Transient expression of b-glucuronidase in recalcitrant Ugandan sweetpotato and putative transformation with two cry genes. *African Crop Science Journal* 22 (3): 215 – 227
6. Tumwegamire, S., Mwanga, R.O.M., Andrade, M.I., Low, J., Ssemakula, G.N., Laurie, S.M., Chipungu, F.P., Ndirigue, J., Agili, S., Karanja, L., Chiona, M., Njoku, J.C., Mtunda, K., Ricardo, J., Adofo, K., Carey, E., Gruneberg W. 2014. Orange-fleshed Sweetpotato for Africa. Catalogue 2014(Second Edition). International potato Center (CIP) Lima Peru 74pp.
7. Fekadu Gurmu, Shimelis Hussein and Mark Laing. 2015. Diagnostic assessment of sweetpotato production in Ethiopia : Constraints, post-harvest handling and farmers' preferences. *Research on Crops* 16(1):104-115.

8. Gurmu, F., Shimelis Hussein and Mark Laing. 2014. The Potential of Orange-Fleshed Sweetpotato to Prevent Vitamin A Deficiency in Africa. *International Journal of Vitamin and Nutrition Research* 84(1): 65-78.
9. Mekonen, S., Fikre Handoro, Fekadu Gurmu, Elias Urage. 2014. Sweetpotato Diseases Research in Ethiopia. *International Journal of Agriculture Innovations and Research* 2(6):2319-1473.
10. Lukonge, E.J., R. W. Gibson, L. Laizer, R. Amour & D. P. Phillips. Delivering new technologies to the Tanzanian sweetpotato crop through its informal seed system. Submitted to: *Agro ecology & Sustainable food systems* in 2015.
11. Ngailo, S., H. Shimelis, J. Sibiya and K. Mtunda (2015). Assessment of sweetpotato farming systems, production constraints and breeding priorities in Eastern Tanzania. *South African Journal of Plant and Soil* (In Press)
12. Lukonge E., Lembris L., Amour R., (2015). Lesson Learnt from research, DONATA and SASHA programmes. Marando Bora Workshop proceedings 27 – 28 January, 2015. mwanza
13. Mtunda, K., L. Lyimo, M. Yongolo, E. Mpaya and H. Kiozya (2015 in progress) Evaluation of promising sweet potato clones in selected agro ecological zones of Tanzania (To be presented in STI conference in June 17-19, 2015, Dar es salaam)
14. Kivuva, B. M., Stephen M. Githiri, George C. Yencho & Julia Sibiya. 2015. Screening sweetpotato genotypes for tolerance to drought stress. *Field Crops Research*; Final version published online: 23-NOV-2014, Full bibliographic details: *Field Crops Research* (2015), pp. 11-22. DOI information: 10.1016/j.fcr.2014.10.018. <http://authors.elsevier.com/a/1Q4eQ1M2tUyyrs>
15. Kivuva, B. M., Stephen M. Githiri, George C. Yencho & Julia Sibiya 2014. Combining ability and heterosis for yield and drought tolerance traits under managed drought stress in sweetpotato. *Euphytica* <http://www.springer.com/home?SGWID=0-0-1003-0-0&aqlid=2714195&download=1&checkval=cfd5c257532709a5fe658bbd6f401a0d>
16. Kivuva, B. M., Francis J. Musembi, Stephen M. Githiri, Craig G. Yencho, Julia Sibiya, 2014. Assessment of production constraints and farmers' preferences for sweetpotato genotypes. *Journal of Plant Breeding and Genetics*, 2(01):15-29. <http://escijournals.net/index.php/JPBG/article/view/524/389>
17. Kivuva, B. M., Stephen M. Githiri, George C. Yencho & Julia Sibiya. 2014. Genotype x environment interaction for storage root yield in sweetpotato under managed drought stress conditions. *Journal of Agricultural Science*. 6:41-56. <http://www.ccsenet.org/journal/index.php/jas/article/view/33268/22188>
18. Journal of Agricultural Science. 6:41-56.
19. Kivuva, B. M., Mburu M. W.K., Maina, J.M., Murdoch, A.J. 2014. The effects of planting density and weeding regime on maize light and water use. *Journal of Agricultural Science*, accepted for publication in august 2014.
20. Kivuva, B.M., F. Musembi, Mare E, Owenga P, Amata R, and Momanyi V. 2014. Enhancing sweetpotato production in Kenya through development and promotion of appropriate technologies. *Korean project on international agriculture annual report, Kenya, July 2013 - June 2014*, p. 76-121
21. Karanja, L., Joyce Malinga, John Ndung'u, Anne Gichangi, David Lelgut and John Kamundia (2014). Development and Evaluation of New Sweetpotato Varieties through Farmer Participatory Breeding for High Altitudes in Kenya. *CABI* (In press) 22.
22. Karanja L., Maura, S., Wachira F., Obonyo M. (2014) Effect of multiple virus infections on β -carotene and micronutrients levels in orange-fleshed sweetpotato. *International Horticultural Congress (IHC) 2014 Brisbane* (Conference proceedings)

23. Placide, R., H. Shimelisa, M. Lainga and D. Gahakwa 2015. Farmers' Perceptions, Production and Productivity Constraints, Preferences, and Breeding Priorities of Sweetpotato in Rwanda. HortScience 50(1):36-43.
24. Placide, R., H. Shimelisa, M. Lainga and D. Gahakwa.2015. Phenotypic characterisation of sweetpotato genotypes grown in East and Central Africa. South African Journal of Plant and Soil, 32(1):1-10
25. Shumbusha, D., J. Ndirigwe, L. Kankundiye, A. Musabyemungu, D. Gahakwa, P. S. Ndayemeye, R.O.M. Mwanga. 2014. 'RW11-17', 'RW11-1860', 'RW11-2419', 'RW11-2560', 'RW11-2910', and 'RW11-4923' Sweetpotato. HortScience 49(10): 1349-1352.

Discussions arising from the presentation

Two questions emerged from the presentation as follows:

► **What is the relative hectareage of the important sweetpotato varieties in the different countries?**

The data was not available at the time of reporting. However, the newly released varieties were not yet widely grown and their promotion had just begun.

► **Are systems in place to enable the testing of released varieties across different countries?**

At the time of reporting, the Kenya Plant Health Inspectorate Service (KEPHIS) was cleaning up sweetpotato material for exchange with other countries. For example, through this arrangement, Kabode and Vita, which came out of the breeding program in Uganda in 2006 had been moved to other countries including Kenya, and Tanzania. This year, varieties released by the breeding program in Mozambique were sent to other countries, including Uganda for testing.

While good breeding progress was noted, it was suggested that regional testing of materials needed to be implemented more systematically. One major challenge to that kind of work was limited funding.

1.3. Sweetpotato preliminary heterosis results from Uganda

Wasonga C., R. Mwanga, W. Grüneberg, and R. Eyzaguirre

This presentation focused on the preliminary results of a follow-up study designed to validate findings of earlier studies in Peru, which had demonstrated that there is exploitable heterosis yield increment in clonally propagated crops such as sweetpotato if crosses are made between parents drawn from distinct gene pools. The study made use of clones generated from two distinct populations, Uganda A and Uganda B with the objective of establishing yield gains in early generation sweetpotato clones derived from inter and intra population crosses of the two East African gene pools hypothesized to be mutually heterotic.

To generate the clones used in the study, eight parents were selected from each pool and controlled crosses between gene pools were made following A8xB8 factorial cross design; while within gene pools A8xA8 and B8xB8, a diallel cross design was followed. The parents were selected not on the basis of good combining ability to produce higher yields but on the basis of having other traits of interest such as resistance to SPVD, orange-fleshed colour and good taste. Seed from 120 cross combinations (families) were germinated and vines of generated clones multiplied in a screen house environment. Twenty clones were raised for each of the families. The sets of 20 clones from each of the 120 families were evaluated at two field sites (Namulonge and Serere) during seasons one and two of 2014. Three plants

were planted per clone and replicated twice per site. All the parents from the two gene pools were planted as checks. There were nine plots of three plants for every check in each of the two replications. Once the test clones and the checks were established, scores on SPVD and Alternaria disease incidences and severity were recorded since these were potential covariates that could affect root and biomass production especially on sensitive susceptible clones. At harvest, storage root and vine weights were recorded and yields computed. The storage roots were also scored for sweetpotato weevil damage.

Mean root and biomass yield data were calculated for the test clones and the checks (parents) and the values used to mid-parent mid-offspring heterosis. The mid-parent mid-offspring heterosis was calculated using the formula:

$$\text{Heterosis increment, \%} = \frac{[\text{Clone value} - \frac{1}{2}(P1+P2)] * 100}{(\frac{1}{2}(P1+P2))}$$

where P1 and P2 are means of parents one and two, respectively.

Results from the 64 families from the BxA crosses showed that fresh vine accumulation was 31.2 t/ha and was 5.5 times that of fresh storage root yield (5.7 t/ha). Fresh vine yield for the families was in the range of 14.5-40.5 t/ha with a median of 30.95t/ha while storage root yield was in the range of 1.8-9.4 t/ha with a median of 5.5 t/ha. The mean storage root for the parents were 6.6 t/ha for population A and 3.9 t/ha for population B while that of the BxA clones was 5.7 t/ha. The higher root yield in the population A parents was attributed to three exceptionally high yielding parents in this population, with storage root yields of 10-16 t/ha.

However, the median of 5.5 t/ha root yield for the BxA clones was higher than that of the two sets of parents – 4.1 t/ha for the parents in A and 2.9 t/ha for the B parents.

The heterosis increment for vine production ranged from -63% to 134% with a median of 26%. Storage root heterosis increment on the other hand ranged from -68% to 551% with a median of 2.9%. The heterosis increment associated with storage root yield was on average 62% while that associated with vine production was -21%. Storage root heterosis increment was positive in half of the of the 64 BxA families with 16 of these families showing increments of more than 100%.

The preliminary results from the reported study with the selected parents from the two populations indicate that there is exploitable storage root heterosis between the two populations that could be harnessed in the development of sweetpotato varieties with significant genetic gains in storage root yield.

1.4. The genome of cultivated sweetpotato contains functional Agrobacterium T-DNAs: an example of a naturally transgenic food crop

Kreuze, Jan

This presentation gave a background to a recent publication in the Proceedings at the National Academy of Sciences (PNAS) that showed evidence that in its evolutionary history the sweetpotato plant had incorporated Agrobacterium T-DNAs into its genome through a horizontal gene transfer.

First, distinction was made between sexual/vertical versus horizontal gene transfer. Sexual or vertical gene transfer happens between members of the same species, and thus the genes are closely related and have the same evolutionary history. Horizontal or lateral gene transfer on the other hand is when a gene gets transferred from one species to another, with which it's not normally sexually compatible.

Occurrence of horizontal gene transfer can be detected when a gene in a species is clearly different or related to other organisms as compared to all other genes from that same or related species. With advancement in the development of tools for genome analysis such occurrences have become easier to detect. Horizontal gene transfer occurs in nature and is believed to have even taken place in humans. Both vertebrate and invertebrate genomes express multiple horizontally acquired genes.

In nature DNA of the Ti plasmid of *Agrobacterium tumefaciens/rhizogenes* is transferred to the plants and integrated into the plant genome to produce plant hormones that cause the plant cells to proliferate and form a source of nutrition for the bacteria. This ability of the *Agrobacterium* to transfer its DNA into other species has been utilised by scientists to transfer favourite DNA segments into plants using the bacteria as the transfer agents resulting into transgenic plants. Natural transgenic plants exist as a result of horizontal gene transfer. For example Toad Flax (*Linaria vulgaris*), which is native to Europe and Asia as a weed and is also sometimes cultivated as cut flower, has recently been documented to have also had a horizontal gene transfer from *Agrobacterium*.

The discovery of the case of horizontal gene transfer from *Agrobacterium* into sweetpotato was made in 2008 when analysing the results of small RNA sequencing and assembly of sweetpotato cultivar, 'Huachano'. During this study, new viruses were discovered leading to a proof of concept of new generic diagnostic method. However, other sequences including bacterial genes were also found. The presence of bacterial genes was confirmed by PCR and Southern blot and screening BAC library and sequencing. Real time PCR was used to establish whether the genes encoded by the T-DNAs were expressed through mRNA. PCR testing of International Potato Center (CIP) and United States Department of Agriculture (USDA) sweetpotato collections was done to establish whether the bacterial genes were present in all sweetpotatoes. One of the bacterial gene sequences was found to be present in all the sweetpotato accessions tested. The next parts of the research then sought to establish whether these genes had any role in sweetpotato root development. Results from one of the studies significantly associated the presence of ORF13 with total root yield.

The study concluded that one (or two) ancestor(s) of sweetpotato were transformed through infection by *Agrobacterium*, integrating two T-DNA regions into the *Ipomoea* genome. One of the T-DNAs appeared to be fixed (it does not segregate) in cultivated sweetpotato as opposed to wild relatives. Because some of the genes are active, this provides the possibility that they may have conferred a trait that has been selected for during domestication. These findings therefore indicate that sweetpotato is naturally transgenic.

Discussion arising from the presentation

A question arose concerning the time when the gene transfer was likely to have taken place and whether it could have occurred before or after domestication. It was suggested that the transformation could have occurred 10,000 years ago and this was before domestication. Participants also expressed stated that the possible involvement of *Agrobacterium* genes in storage root development is an intriguing hypothesis.

1.5. How can we measure genetic gain in our applied breeding programs (can we measure it from 1993 – 2012?)

Grüneberg, Wolfgang

This presentation explored the question on whether it was possible to measure genetic gain in the applied breeding programs over long periods of time, say, 10 years or more. Available statistics are currently assembled by groups such as Food and Agriculture Organization (FAO) but there is need to have more robust approaches to gathering data that could give information on genetic gain as a result of sustained crop improvement efforts. The presentation discussed approaches to measuring genetic gain in applied breeding programs. It was pointed out that having genetic variation is a prerequisite for getting genetic gain which can also be considered as yield progress. Genetic variance is estimated to get response to selection.

In sweetpotato improvement in Africa there has been a question on whether it is possible to get 2-3% yield gain per year. The answer has been that this is possible but only if a correct determination is undertaken. Genetic gain can be estimated experimentally through heterosis experiments and also experiments comparing polycrosses with controlled crosses. In polycross versus controlled cross experiment, without discarding material for one selection step, it is possible to observe the response to selection or genetic gain. However, it is important to note that response to selection or genetic gain has a large biological error since it is a function of heritability and number of candidates in the selected fraction.

Genetic gain can also be measured under farm practice through a series of multi-environment trials (MET) usually over 2-3 years. For example, with the ended five years SASHA I project, it is possible to get three MET data sets which can (a) serve as variance component estimations in later breeding stages (b) the genetic gains (development of the mean in these METs) during this time period. However, this is still a small section of the long term genetic gain – 10 or 20 years. In practice with 10 to 20 years of METs from variety release time it would be possible to estimate long term yield trends and changes using data from eight to 18 METs. Estimation of long term yield trends using (METs data can be established by regression analyses or plots of year and/or genotype means against time that will allow for an assessment of the yield trends including gain components due to better practice. The estimates of gains in Uganda could be explored as a case in point.

Discussion arising from the presentation

The following points are a summary of the points that emerged during the discussion:

- ▶ There is need to compare generation with generation. Because of viruses there is need to compare materials of the same status.
- ▶ There are formulae that can be used to calculate genetic gain.
- ▶ Genetic gain is great but a more compelling way to measure using performance of released varieties.
- ▶ Apart from genetic gain, variety adoption is a way to measure productivity gain. In this case the number of people using a variety is what counts.
- ▶ A case could be built around OFSP varieties and efforts made to measure the gains that had been realised through their adoption. Using variety specific basis for measuring gain would be a more plausible approach.

1.6. Report of the Sweetpotato Support Platform – West Africa Demand-Driven Breeding and Germplasm Distribution

Carey, T., E. Obeng-Bio, R. Atuna, F. Amagloh, E. Dery, E. Owusu-Mensah, K. Asare, Y. Alhassan, D. Akansake, K. Adofo, K. Acheremu, K. Some, S. Afuape, J. Njoku, and E. Abidin

The SASHA breeding approach entails a population improvement program at a sub-regional level. The population is then linked with participatory varietal selection at the national level with a focus on the theme attributes of - less sweet sweetpotato (unsweetpotato) and reduced perishability.

The sweetpotato breeding selection sites and target zones in Ghana are in:

- a) Ashanti region which is in the forest agro-ecological zone and is used mainly as a selection site;
- b) Central region in the coastal Savanna agro-ecology, where sweetpotato is grown as a commercial crop and selection is done
- c) Volta region, also in the Coastal Savanna agro-ecology, is also an area where sweetpotato is a commercial and food security crop
- d) Upper East region within the Guinea/Sudan Savanna agro-ecology, which is also used as a selection site given that sweetpotato is an important food security crop in the region.

In the accelerated breeding scheme in Ghana, the first year is spent generating seed crosses within the crossing block of 50 parents. In the second year, the generated crosses are raised in seedling nurseries followed by observation trials in Kumasi (a virus disease affected zone) and Tono (a key production area). Out of the observation trials, approximately 250 clones are selected. Top selections go back for recombination. In the preliminary trials carried out in the third year, 25 clones are evaluated at four sites: Upper East, Central, Volta and Ashanti regions. Advanced trials and on-farm trials are conducted during the fourth year, during which decentralized testing and multiplication are done. The superior clones are released in the fifth year as new varieties.

For the 2014/15 period work at the platform focused on unsweetpotato, consumer acceptance and breeding for quality attributes. Among the findings made during this period was that cooking influenced sweetness. Considering that Ghanaian sweetpotato is mostly utilised as a staple this had implication on amylase levels for processing. It was also found that women and children were less picky when it comes to sweetpotato quality attributes. The breeding selections were acceptable. The progress with the work on quality attributes at the program had been possible with the support of the NIRS lab which had been instrumental in generating data that was used in the making the selections. The progress in this area was expected to increase with a recent purchase of Rapid Visco analyser. The program had also adopted barcode labels and Portable Digital Assistants (PDAs) for use in data collection and management of field trials.

Work at the platform had also focused on storability/perishability. In this study, three sweetpotato varieties had been stored for a 10 week period in a sand box or moistened heap at sites around Bawku. Under these storage conditions, the varieties were monitored for percentage weight loss, sprouting, weevil damage and rot. Varietal differences were found to exist with regard to the parameters measured. Percentage weight loss and rotting of the storage roots was significantly higher with the moistened heap storage compared to sand storage.

In 2014 in Ghana, hybridization was undertaken at Fumesua in the Ashanti region and Nav+Bawku in the Upper East Region. There was one seedling nursery at Fumesua. Three observation trials, four preliminary trials and more than eight advanced trials were planted at different locations. For on-farm trials, 14 mother and baby trials were planted in the Volta, Central, Upper East, Northern and Upper West regions. All this work was done with funding mainly from SASHA and WAAPP.

The program is at present moving towards having more than one selection cycle per year (dry season seedling nursery; possibly trials); two populations, A and B, in order to exploit heterosis in coming years; separation of early and later-maturing material at preliminary trials in order to ensure advancement of OFSP; strengthened breeding capacity in northern Ghana through expansion of advance trials and on-farm trials linked to the seed program; and recurrent selection of breeding populations while also identifying good parents. However, the harsh West African environment consistently presents challenges to get more than one trial per year.

Work on capacity building focused on student training mainly through the WACCI program in collaboration with universities in Ghana with funding from AGRA. So far, a total of 10 students had either gone through the training program or were undergoing training, mostly at MSc and PhD levels. New WACCI cohorts will be from Nigeria, Burkina Faso and Ghana. Students from other programs include an entomologist who is a SARI scientist at Kwame Nkrumah University of Science and Technology (KNUST) and who will work on Integrated Pest Management (IPM) of weevil. An additional student will go to North Carolina State University (NCSSU) under the project and the Genomic Tools for Sweetpotato Improvement (GT4SP). There will also be a PEARL grantee from Benin or Ghana whose focus will be weevil resistance/bio-control.



Some of the people who participated in capacity building through WACCI program pose for a photograph

The seed systems research work of the program has focused on establishing a regional platform for safe and efficient exchange and maintenance of germplasm. This is achieved mainly through improved indexing, virus cleaning, *in vitro* maintenance and genetic fingerprinting in each sub-region and through upgrade of *in vitro* facilities and tissue culture staff to ensure safe receipt and shipment of germplasm. During the 2014/15 period work was undertaken at the platform to clean up and distribute germplasm. At the Council for scientific and Industrial Research of Ghana – Crops Research Institute (CSIR-CRI) 14 clones were cleaned up: Ghana (9), Nigeria (2) and Burkina Faso (3) in 2014. An additional 18 clones are targeted for clean up during the 2015/16 period. The focus is also on clean foundation seed which is considered integral to the success of the breeding effort.

Seed distribution from the platform in 2014 was as follows:

- ▶ Nigeria: 3650 – OP 24/PC 15 (NARS – 2850; SASHA – 800)
- ▶ Burkina Faso: 2750 – OP 24/PC 15 (NARS – 2200; SASHA – 550)

1.7. Sweetpotato Breeding in West Africa: Progress in Burkina Faso, Ghana and Nigeria

Afuape, S., K. Adofo, and S. Koussao

This presentation was made on behalf of the National Breeding programs in Ghana, Nigeria and Burkina Faso. The important constraints to sweetpotato production across these countries include:

- i. Susceptibility to *Cylas* spp, *Alcidodes* sp and SPVD
- ii. Drought and short rainy season (irregular rainfall pattern)
- iii. Low yields, root dry matter content, low beta-carotene levels in farmer preferred cultivars
- iv. Weak seed system
- v. Declining soil fertility
- vi. High post-harvest losses
- vii. Low level commercial utilisation
- viii. Less structured marketing system

In view of these constraints the objectives of the national breeding programs in these countries are to:

1. Develop high yielding and drought tolerant OFSP varieties adapted to the Sudano-Sahelian zone (BF).
2. Develop high and stable yielding, disease and pest (SPVD, *Cylas* sp., *Alcidodes* sp.) resistant varieties with high nutrition and processing qualities (dry matter, beta-carotenoids, starch, flour yield, minerals) and highly accepted, utilised and consumed (especially for Ghana and Nigeria).
3. Improve sweetpotato populations for earliness, high carotenoid, high dry matter, resistance to *Cylas* spp and SPVD.
4. Widen the genetic pool through introductions from other parts of the world.

At present several landraces and released varieties including OFSP are grown in the different countries. These are summarized in Table 3. During the 2014/15 period, several sweetpotato research trials were conducted in the West African region. These are summarised in Table 4. No varieties were released in the three countries during the 2014 period but three were earmarked for release in 2015 in Burkina Faso and two in Nigeria. Foundation seed was available in 2014 in Nigeria and Burkina Faso.

The national sweetpotato programs on breeding and foundation seed were undertaken with funding from donors and the respective country governments.

In 2014/2015, the teams from the three countries published three papers in journals and three others in conference proceedings:

1. Somé K., Gracen V., Asante I.K., Danquah E. Y., Ouedraogo J.T., Tignegre J. B., Belem J. and Tarpaga M.V., 2014. Diversity analysis of sweet potato (*Ipomoea batatas* [L.] Lam) germplasm from Burkina Faso using morphological and simple sequence repeats markers. *Afr. J. Biotechnol.*, 13(6):729-742.
2. Afuape, S.O., Nwankwo, I.I.M., Omodamiro, R.M., Echendu, T.N.C. and Toure, A. (2014). Studies on some important consumer and processing traits for breeding sweetpotato for varied end-uses. *Amer. J. Experim. Agric.* 4(1): 114-124.
3. Nwankwo, I.I.M., Bassey, E.E. and Afuape, S.O. (2014). Yield evaluation of open pollinated sweetpotato (*Ipomoea batatas* (L.) Lam) genotypes in humid environment of Umudike, Nigeria. *Global J. Biol. Agric. Health Sci.*, 3(1):199-204.
4. Breeding for high beta-carotene, dry matter content and yield in sweetpotato in Burkina Faso. CABI.
5. S.O. Afuape, S. Sa'ad, E. Ogbo and I.I.M. Nwankwo. (2014). Identification of important traits for consumer-targeted breeding for enhanced sweetpotato commercial product development in Benue State. *Proc. 48th Annual Conf. Agric. Soc. Nigeria (ASN)*, Univ. Abuja, 24th – 27th November 2014.
6. Afuape, S.O., Egesi, C.N., Kahya, S.S., Umezurumba, I.C. and Nkaa, F.A. (2014). Growth differential of cassava cultivars in the production of cassava organised embryogenic structure (OES) for cassava transformation. *Proc. 38th Annual Conf. Genet. Soc. Nigeria*, Bishop Kelly Pastoral Centre, Benin City, Nigeria, 19 – 24, Oct., 2014.

Table 3: Important sweetpotato landraces, released, widely grown, and orange-fleshed varieties in West Africa

Sweetpotato category	Country		
	Ghana	Nigeria	Burkina Faso
Important landraces	Blueblue, Akaten red, Jukwa orange, Shashango, Kuffour, Asamare, Sankase nabogro, Obare, Nanugungungu	Ex-Igbariam, Atsaka pupu, Buttermilk, Danzaria	Nakalbo, Saafare, Patate, Tiebele-2, Wosso-woule
Important released varieties	CRI-Okumkom, CRI-Faara, CRI-Sauti, CRI-Santom pona, CRI-Apomuden, CRI-Otoo, CRI-Ogyefo, CRI-Hi starch, CRI-Patron, CRI-Bohye, CRI-Ligri, and CRI-Dadanyuie	King J, UMUSP/2, Mother's Delight, TIS 87/0087, TIS 8164, TIS 2532.OP.1.13	
Most widely grown varieties	CRI-Okumkom, CRI-Faara, CRI-Sauti, CRI-Santom pona, CRI-Apomuden, CRI-Otoo, CRI-Ogyeto, CRI-Hi starch, Blueblue	Mother's Delight, TIS 87/0087, Ex-Igbariam, Buttermilk	Nakalbo, Saafare, Patate, Tiebele-2, Wosso-woule
Most important orange-fleshed varieties	CRI-Apomuden, CRI-Bohye	King J, Mother's Delight	Tiebele-2, Bagre, Joel, Nanyoumondo-1, Nanyoumondo-2

Table 4: Sweetpotato trials/number of clones planted during the 2014/2015

Trial	Country / No of clones		
	Burkina Faso	Ghana	Nigeria
Crossing block	20	18	15
Observation (OT)	272	6817	600
No. of checks	2	5	3
Preliminary yield (PT)		3	N.A
No of checks		3	N.A
No. of locations		3	N.A
Advanced yield (AT)	10	6	20
No. of checks	2	3	2
No. of locations	2	6	6
On-farm		-	N.A

Discussion arising from the presentation

A question was raised on the current size of the gene pools and the criteria used to choose material to add into the pool. In the response, the presenter explained that the criteria for addition into the gene pools include quality traits, such as high beta-carotene content, resistance to viruses and drought tolerance. Better performing materials are collected and used to improve populations. The materials used in countries such as Burkina Faso have been acquired from East and Central Africa, Southern Africa and West Africa on the basis of having unique traits of interest.

1.8. Genetic improvement of sweetpotato for beta-carotene and yield in Burkina Faso

Koussao Some

This presentation focused on the presenter's PhD findings from research work undertaken in Burkina Faso. Sweetpotato production in Burkina Faso increased from 27,366 tons in 2000 to 140,061 tons in 2011, and 377,728 tons in 2014, a rapid increase that was mainly attributed to increased production area. However, yield has been unstable over time.

The objectives of the reported study were to:

1. Identify the main production constraints and understand farmers' and consumers' preferences.
2. Assess the diversity of sweetpotato germplasm in Burkina Faso prior to selection of superior parents to be used in a basic breeding program.
3. Estimate the heritability of economically important traits as a guide to parental selection necessary for significant breeding progress.
4. Identify high yielding and beta-carotene rich clones specific to wide adaption to the local environments.

The major production constraints previously identified for sub-Saharan Africa apply to Burkina Faso:

1. Viral diseases
2. Lack of processing technology
3. Poor availability of quality planting materials
4. Lack of improved control of weevil
5. Short storage ability duration
6. Lack of improved cultivars with high and stable yield.
7. Unavailability of cultivars with high beta-carotene content which could help to address vitamin A deficiency

The diversity of sweetpotato germplasm from Burkina Faso was analysed using morphological and SSR markers. This was aimed at estimating diversity and developing a core collection for conservation and use in breeding programs. The study evaluated 112 genotypes for morphological and molecular characteristics using 30 descriptors and 30 SSR markers.

For morphological characteristics, the predominant flesh colour and leaf lobe number were found to have the greatest discriminating power. During the analysis, the accessions were grouped into 11 clusters, while 19 were identified as duplicates. Using the SSR markers, seven clusters were formed with nine of the accessions remaining as duplicates. There was no correlation between the SSR and morphological characterisation data. However, despite the poor correlation between morphological and molecular markers, both techniques were useful in characterising the sweetpotato germplasm.

Inheritance of yield components and beta-carotene in sweetpotato was analysed using parent-offspring regression. The aim was to estimate narrow sense heritability for economically and nutritionally important traits, and also to estimate the genetic gain from selection of the breeding product. Fifteen F1 families were generated from local sweetpotato accessions crossed with introduced orange-fleshed accessions (used as males). Among other things, the study found that the male parent CIP-199062-1 was an important parent to use in breeding for yield, dry matter and beta-carotene. Among the local accessions found to be useful in the breeding were BF77 (yield); BF59, BF82 and BF92 (beta- carotene); and BF24 (dry matter). Heritability for yield and yield related traits were low, indicating the need for more divergent sources to enable a significant improvement in these traits.

The genotype by environment interaction of OFSP analysis in Burkina Faso was done to assess whether the OFSP hybrids in question and their corresponding OFSP parents responded differently to environmental changes. Another aim of this analysis was to identify varieties with stable performance or specific environment adaptation that could be recommended to farmers. Through this study, better yielding genotypes were identified for different production regions in Burkina Faso.

The study concluded that sweetpotato germplasm in Burkina Faso has moderate (0.49) to high (0.73) diversity and can be successfully utilised in a breeding program. It was also concluded that promising OFSP must hierarchically combine high and stable yield, high dry matter content, good storability, early maturity and good shape. Compared to the local parent mean, the storage yield and beta-carotene content were respectively increased by 55.33%, 216.73, while the dry matter content (-11.54%) needed to be improved. The best OFSP F1 genotypes for yield (BF82xTainung-8) showed 82.99% increase over the best checks. The F1 OFSP BF82xCIP-11 and BF82xCIP-17 combined higher yield and higher beta-carotene content with dry matter content of over 28%.

Discussion arising from the presentation

One participant wondered whether it was right to state that West Africa has no capacity to make sweetpotato crosses. The response was that researchers from the region were getting more experienced in making crosses even though infrastructure had remained a limitation and would have to be developed over time. Wolfgang commented that sweetpotato is very easy to cross even though some people are more talented than others in making crosses. To further increase competence of the West Africa teams in this area, Wolfgang offered to assist by sending an expert to go to the region to find out how they could be assisted.

1.9. Development of end-user preferred sweetpotato varieties in Ghana

Ernest Baafi

This presentation was also based on the findings of a PhD study undertaken in Ghana through the WACCI program. The background leading to the reported study is that locally available clones have very sweet taste, which limits consumption as a staple food.

On the one hand, the sweet taste, which is attributed to sugars, is the central feature that significantly modulates the overall flavour. On the other hand, the recently introduced OFSPs have low dry matter. Because preference for sweetpotato varies with ethnic background and geographic location, there had been low adoption of improved sweetpotato varieties because consumer acceptability was not taken into consideration. The specific objectives of the reported study were therefore to:

1. Ascertain stakeholders' knowledge, perceptions, and preferences on sweetpotato end-user-traits in Ghana.
2. Assess genetic variation of sweetpotato genotypes in Ghana using agro-morphological, physico-chemical and SSR markers.
3. Assess self- and cross-compatibility in sweetpotato germplasm.
4. Determine the gene action involved in the control of beta-carotene, dry matter and sugar content of storage roots.
5. Determine level of heterosis for beta-carotene, dry matter and sugar content of sweetpotato storage roots.

To address objective 1, focus group discussions were held and semi-structured questionnaires administered in different areas of the country. It was found that the majority of the respondents preferred high dry matter sweetpotato types that are less sweet and have moderate beta-carotene content.

To assess genetic variation of sweetpotato genotypes in Ghana and their utilisation for breeding, phenotypic characterisation was undertaken on 115 sweetpotato accessions. Molecular characterisation was also done on 76 of the accessions using 25 SSR markers. Genetic parameters were estimated on 115 of the sweetpotato accessions. Analysis of molecular variance in the 76 accessions showed that the variance was highest within the groups than between the groups.

In order to address objectives 3 to 5 that covered compatibility status, gene action and population development, low and high beta-carotene parents were crossed with dry matter parents in a 12x12 full diallel while crosses were made in a 15x15 full diallel for sugars.

The study through which non-sweet, high dry matter hybrids were identified concluded that: (a) consumers in Ghana desire non-sweet, high dry matter sweetpotatoes with low or moderate beta-carotene content; (b) genetic variability was significant for the traits studied and much of this genetic variation was additive in nature; (c) significant negative heterosis for sugar content is very important in breeding for non-sweetness; (d) adding high beta-carotene content to these types may require many cycles of selection; and (e) lack of, or poor flowering was a problem.

Discussion arising from the presentation:

The discussion following this presentation focussed on the fact that with quality traits there is usually no heterosis increments.

1.10. Beyond yield: end user preferences

Jan Low and Robert Mwanga

This presentation shared experiences gained at the *Integrating End User Preferences into RTB Breeding Workshop, Munyonyo/Kampala, Uganda, 26-27 February 2015*. Prior to the presentation a questionnaire had been circulated among the sweetpotato breeders at the meeting; they were asked to respond to specific questions pertaining to their breeding programs. The questions were: key groups targeted by the breeding program; traits that met the needs of the target groups; how the preferences of the target groups were assessed; the stage in the breeding cycle at which the preferences of the target groups were assessed; the sweetpotato varieties in the programs that best met the preferences of the target groups; and how widely those varieties had been adopted.

Subsequently, in the first part of the presentation participants were asked to respond to the question of who breeding is done for. A summary of the findings of the questionnaire were presented.

Twenty three breeders from the different regions responded to the questions. According to their responses, breeding was done for: farmers (10), poor farmers (2), children (6), women – mothers/pregnant women (4), smallholder farmers (4), commercial producers (2), national breeders (2), traders (2), processors (4), industry groups (2), consumers (7), malnourished people (1), urban consumers (1), health remedial centres (1) and supermarket ventures (1).

The response in on traits bred for were: yield (17), early maturity (5), virus resistance (6), biotic stresses (5), Fusarium resistance (2), soil rot resistance (1), root knot nematode resistance (1), weevil resistance (4), *Alternaria* resistance (1), drought tolerance/abiotic stresses (6), beta-carotene/nutrition (15), mineral nutrient content (3), good taste (3), and high dry matter (15). Other traits bred for included starch quality (3), non-sweet (2), sweetness (2), good cooking qualities (1), processing quality (1), storability/long shelf life (2), root shape (4), root size (2), high quality seed (1), vine vigour (2), leaf quality, (1), and dual purpose (2).

On the stage at which the preferences of the target groups were assessed the responses were: on-farm trial with farmers (10), advanced selection trials (10), various yield trials (4), uniform/multi-locational yield trials (4), demonstration trials (1), second year selection and onwards: NIRS chemistry (1); in the initial stage to inform choice of candidate clones for improvement (3) and before hybridization (1).

The presenters emphasised the need for sweetpotato breeding programs to better understand end user profiles. This is in view of the fact that Africa's population is projected to be 1.6 billion by 2030, representing 19% of the world's population. Urbanisation rate is presently the highest in the world and

it is estimated that by 2035 there will be more urban than rural residents. There is also shifting demographic balance and by 2030 there will be more young people of working age.

These changes call for a better understanding on how to breed better for now and for the future. There is need for sweetpotato breeders to learn from other projects (e.g. NextGen Cassava) and the private sector (e.g. Nestle and HZPC Holland). When breeding for quality traits, there is need for interdisciplinary engagements bringing together social scientists, socio-economists and breeders.



Plate 1: Groups discuss end user preferences
Bukania

Photo: C.

Often, varietal adoption decisions are the product of the interaction between characteristics/traits of the variety, characteristics of the end users and the characteristics of the socioeconomic environment. There is need to understand if there are engendered traits that have so far been unconsidered. The private sector has made more progress by developing typologies in which individuals are classified into types of end users (segments).

For example, there are several things that could be learnt from Nestle's approach. These are:

1. Having a consumer-centric approach. The end user is a key player;
2. Having an understanding on why consumers behave how they do (focus groups, individual interviews, ethnographic research);
3. Having trained assessors to monitor sensory attributes discover commonalities in consumer preference drivers to shape nationally- or regionally-accepted products;
4. Realising that sensory attributes do not vary much for traditional foods from village to town, it becomes more about prioritizing sensory against services, e.g. convenience.

However, in taking these lessons into consideration it should be noted that in the experience of the company only 50% of the ideas make it.

There are also several lessons to learn from HZPC's experiences and approaches:

1. Recognition of the fact that there is not one perfect potato: there are many perfect potatoes, depending on the clusters and many other factors;

2. Heavy investment in high-throughput texture analysis;
3. Realisation that 350 flavour components make or break the quality of the potato;
4. Realisation that sugar is the most important piece for processing trait profiling;
5. Realisation of the fact that most quality traits have medium to high heritability and are multi/polygenic in nature;
6. Experience during the development of SNP markers for potatoes that about 20-25 SNP markers may explain 80% of variance.

Reflecting on the quality attributes of sweetpotato, several lessons could be picked from the outcomes of a study/review on roots, tubers and banana textural traits commissioned by the Bill and Melinda Gates Foundation (BMGF). The review established that there was paucity of literature on sensory traits in SSA. With available publications, it was found that GXE interactions can affect textural traits making breeding more challenging. Starch, taste and sweetness were the most dominant sensory attributes for consumers. Starch digestibility and pasting qualities were found to vary widely by variety. Sugar composition changes were found to change upon cooking – more maltose.

Based on the experiences that have come from Marketing, Processing and Utilisation CoP, there is need to:

1. Start considering more nutritional attributes affecting processing and include them in the OFSP catalogue with traits;
2. Consider starch content, and reducing sugar content, amino acid profile (Asparagine has been found to cause browning), and moisture content (already reporting) for fried foods;
3. Pay attention to sugar content after cooking, amylase activity and fiber; stringiness for puree;
4. Have ability to retain beta-carotene after heating and more starch as a thickening component (dry matter) for flour production;
5. Explore ways by which odour can better be captured during breeding since this seems to be an issue especially with OFSP;
6. Breed more for shape (oblong) and form (no bumps) and size (200-300 grams).

Following the presentation, participants went into groups (on the basis of sub-regions/countries) to further explore the issue of developing consumer profiles. The groups sought to answer four questions:

1. What are 3 distinct market segments in your sub-region/country for which distinct sweetpotato varieties are needed now and in the future?
2. What are the key traits for each of these segments?
3. Which of these traits could be determined using Near-infrared spectrometry (NIRS) technology or another fast throughput method?
4. How should we approach confirming these consumer profiles and estimate the future size of the different market segments?

The findings of the group discussions are summed up below:

Group 1: East Africa (Ethiopia, Kenya and Rwanda)

Four distinct market segments in Ethiopia, Rwanda and Kenya for which distinct sweetpotato varieties are needed were identified:

1. Fresh storage root market for end users
2. Processing industry
3. Animal feed
4. Commercial “seed” for planting

For each of the market segments the following traits were identified as important:

- a) Fresh storage roots market: red skin colour, yellow or orange-flesh colour, high dry matter (30% and above), medium root size and regular shaped roots with no cracks
- b) Processing market (flour, biscuits, bread): for puree, the fibre content and type of starch are important; oval shaped roots are preferred; thick skin for better storability (long shelf life); and chemicals associated with weevil resistance
- c) Animal feed: dual purpose, biomass, digestibility, crude protein and fibre were considered crucial
- d) Commercial seed: virus resistance and vine vigour

Other additional traits that were considered important were: beta-carotene, iron and zinc, storability, weevil resistance, earliness, drought tolerance, transportability and taste

Among the listed traits proteins, beta-carotene, iron, zinc, starch, sugars, digestibility, crude protein and fiber could be determined using NIRS.

Group 2: Southern Africa

- 1 The identified distinct market segments in the sub-region for which varieties are needed are:
- 2 Population of women and children with VAD in drought prone areas
- 3 Freezing industry
- 4 Crisp and biscuits production
- 5 Sweetpotato puree and Juice

The important traits the different market segments are:

- a) **Women and children with Vitamin A Deficiency (VAD) in drought prone areas** - beta-carotene content, re-sprouting ability, survival ability, leaves (deeply lobed/narrow leaves with no tangy taste or bitterness, frost tolerance (early maturity to avoid frost could also be explored).
- b) **Freezing industry** - low oxidation, elongated roots, white/orange-flesh with purple skin and high dry matter were considered important.
- c) **Crisps and biscuits production** - beta-carotene content, low oxidation, low reducing sugars, high dry matter and smooth root shape
- d) Sweetpotato puree and juice production - orange-flesh, low oxidation after mashing, low fibre and medium dry matter

The group noted that gender played an important role in trait preferences with men being more interested in commercial aspect while women are more on nutrition security. Children may prefer low dry matter types while adults prefer high dry matter.

Group 3: West Africa

The distinct utilisation channels that the group identified included: fries, boiled/porridge, puree for bakery and confectionary products, and starch. These traits were considered important for the different channels

- a) Fries - high dry matter, texture (especially pectin component), flavour, colour, transportability and storability, shape and size. These traits were similarly important for consumption in the boiled form.
- b) Puree for bakery and confectionary products - high beta-carotene, good texture, high dietary fibre and transportability/storability
- c) Extraction of starch of notable importance - traits conferring flesh colour, starch granule size, amylose to amylopectin ratio (high amylose starch often better) and transportability/storability
- d) On the question of the approach to confirm consumer profiles, the group noted the need for better capacity for sensory analysis for the different consumers and uses. The use of detailed end-user targeted surveys administered by food and social scientists was suggested.

Group 4: East Africa (Uganda, Burundi, Tanzania)

The group identified four market segments: table stock, processing, specialty type and animal feed. For these market segments the important traits, which were also cross cutting were: yield, root shape, root size, uniformity of roots (especially for processing), resistance/tolerance to abiotic stresses, resistance to biotic stresses, vine production, nutritional content, sugars (glucose, fructose, sucrose), dry matter, taste and texture, freedom from discoloration (especially when processing), good shelf life especially for processed products, flavour (beta-carotene, fructose), time to maturity, micronutrient content (especially iron and zinc), and harvest index.

To identify consumer profiles and future market segments, the group suggested the use of focus group discussions with target groups, interviews with proprietors, and questionnaires.

2. The Genomic Tools for Sweetpotato Improvement Project – GT4SP

Craig Yencho

The presenter who is the lead Principal Investigator (PI) in the GT4SP, jumpstarted the discussion on how teams working in the SASHA and GT4SP projects could work together to enhance the potential of sweetpotato to contribute to better livelihoods in communities in SSA. He shared his continued fascination with sweetpotato: he had initially started a breeding program in the United States (US) with a focus on a few traits, but now the focus had expanded and included quality traits that demand the use of more refined techniques/tools during selection. He reported that in the US, sweetpotato production had increased through development and adoption of better varieties and better management practices.

Similarly, there is potential for growth in productivity in SSA through development and adoption of better varieties, coupled with adoption of better production practices. Funders like the McKnight Foundation and the BMGF have made remarkable contribution to creating an enabling environment for sweetpotato production through the SASHA project. The project has made efforts to: (a) breed and develop new sweetpotato varieties; (b) improve populations for sweetpotato improvement; (c) develop new breeding methods such as the accelerated breeding scheme; (d) studies initiated to explore exploitation of heterosis in sweetpotato, with potential application to other clonally propagated crops; (e) establishment of sweetpotato support platforms, each with a quality lab in three sub-regions in SSA to support sweetpotato breeding work, germplasm exchange, information exchange and project implementation in the sub-regions.

As a result of on-going efforts to improve sweetpotato and demonstrate its potential as a utility crop, it is now widely recognised, and it has generated much interest from following the realisation of its superior nutritional quality. However, there are a number of areas in which the crop still needs improvement through breeding. Progress in addressing outstanding challenges will be possible mainly through investments in the development and utilisation of better and modern breeding tools which at the moment are noticeably lacking.

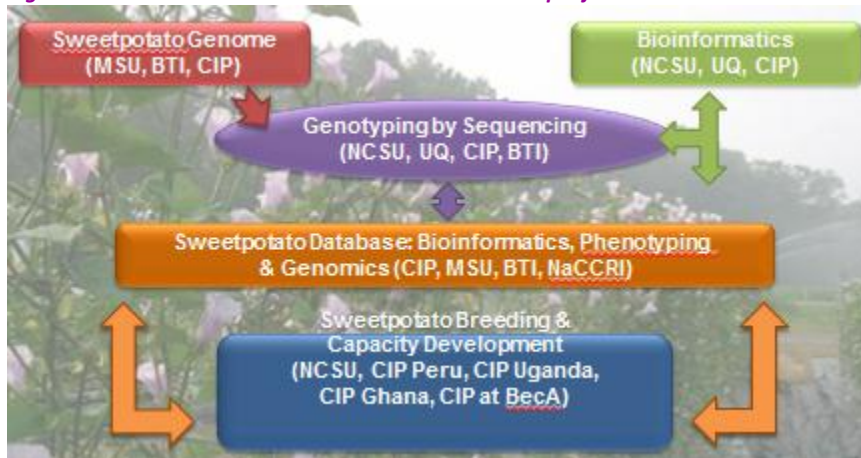
The development and utilisation of genomic tools in breeding offers much promise in addressing the outstanding bottlenecks to sweetpotato production, especially in Africa. These tools are expected to increase the efficiency and precision by which alleles associated with resistance to SPVD, and sweetpotato weevils are identified and selected. The tools would also be useful in the identification/selection of useful transgressive segregants.

Through the GT4SP project, a vision for marker assisted breeding (MAB) has been envisaged for Africa. This will entail investment in strategic areas in the breeding pipeline. These areas include:

1. **Genomic resources:** a reference genome; marker development; a robust set of SNP markers and a low-cost genotyping platform; advanced laboratory sequencing linked with developing country phenotyping and breeding activities; and 2x and 6x mapping, training and test populations.
2. **Bioinformatics, analytics and database resources:** improved web-based bioinformatic resources; new database, data collection and phenotyping options; new analysis resources.
3. **Human resources and capacity development:** continued assembly and development of a dynamic team of breeders and allied disciplines; training in the use of traditional and genomic breeding methods; promotion of effective communication and collaboration; and multi-institutional training and capacity development.

The collaborators and contributions in the GT4SP which seeks to sequence sweetpotato and develop modern breeding tools for a food crop that sustains millions of people in SSA are as summarized in the following Figure 1.

Figure 1: The collaborators and roles in the GT4SP project



The collaborators are: Boyce Thompson Institute at Cornell, Michigan State University, University of Queensland, Australia; CIP (CIP, Peru; CIP at BioSciences East and Central Africa, Kenya, CIP/Ghana, CIP/Uganda); National Crops Resources Research Institute (NaCRRI) Uganda; CSIR-CRI, Ghana.

The outcomes expected from implementation of the GT4SP include:

- ▶ An MAB breeding pipeline that utilises up- and down-stream breeding methods
- ▶ Genomic selection technologies integrated with the SASHA accelerated breeding program
- ▶ A new generation of sweetpotato breeders, and a new cadre of molecular geneticists and bioinformatics scientists interested in using the new tools to study sweetpotato.
- ▶ Linkage of genomic-based breeding to address the demand of new varieties and “products” will yield maximum long-term Return on Investment (ROI) on current sweetpotato crop improvement investments in SSA.

Discussion arising from presentation

In response to the question on how soon the reference genome could be available, the presenter said that it would possible be available next year.

The following comments were also made:

- ▶ We cannot expect genomics to solve all our breeding problems. Conventional breeding will still be the workhorse, but genomics will offer new solutions for difficult traits.
- ▶ There is need to learn from the private sector by developing and deploying better tools that enable smart breeding. The sequencing of a reference genome can be useful in starting to map complex traits in sweetpotato improvement. The BMGF is motivated by the need to avail new tools to breeders.

2.1. Sweetpotato reference genome sequencing

Zhangjun Fei

The presenter started by explaining that genome sequences are needed because:

- ▶ The genome contains all the genetic information of an organism, which determines its phenotype;
- ▶ High-quality reference genome sequence provides a foundation that can facilitate basic research, gene/QTL cloning, molecular marker discovery and marker assisted breeding;
- ▶ Genome sequences can help understand genome evolution and domestication history.

The utility of genome sequences is clear from the fact that the industry (growers, shippers, processors) depend on high quality, disease resistant cultivars. To respond to the needs of the industry, the breeding community (seed companies and public breeders) must develop these cultivars. The scientific community supports the work of breeders by developing knowledge to facilitate more effective plant breeding and train the next generation of plant scientists and breeders.

Under the sweetpotato reference genome sequencing, the objectives and the team members are as follows:

- 1) Development of the core genomic and genetic resources for sweetpotato improvement. This has the following sub objectives:

Objective 1.A. Whole genome sequencing of NCNSP-0323, a homozygous diploid sweetpotato progenitor of cultivated sweetpotato *I. batatas*. Lead Scientists: Fei - Boyce Thompson Institute-Cornell University (BTI-CU) and Buell - Michigan State University (MSU). Under this sub objective the focus will be on 1) genome DNA library preparation and sequencing; 2) genome assembly and annotation; 3) genome evolution and comparative genomic analysis of NCNSP-0323

Objective 1.B. Transcriptome profiling of multiple tissues of the sequenced NCNSP-0323 for genome annotation. Lead Scientists: Fei (BTI-CU) and Buell (MSU).

Objective 1.C. Development of diploid mapping populations for high density SNP genome sequence anchoring and QTL mapping. Lead Scientists: Grüneberg and Khan (CIP); Yencho and Quesada (NCSU), Fei (BTI-CU) and Buell (MSU).

Objective 1.D. Sweetpotato genome browser development. Lead Scientists: Buell (MSU) and Fei (BTI-CU).

An ideal system for whole genome sequencing requires highly homozygous plants such as inbred lines; haploids or diploids; relatively small genome sizes; and contain a small portion of repetitive sequences.

Sweetpotato genome sequencing on the other hand poses a challenge as the cultivated sweetpotato is an allo-auto-hexaploid ($2n=6x=90$) with two non-homologous genomes. It is a polyploid and highly heterozygous. To tackle the challenge the strategy that has been adopted by the project entails sequencing the closely related wild ancestors that are diploid and homozygous. Sequencing of NCNSP-0323, an inbred *I. triloba* line, derived from PI 618966 that is self-compatible is underway.

Discussion arising from the presentation

One question was raised on how the *Ipomoea trifida* genome will be applied to sweetpotato breeding. The presenter explained that having a reference genome enables development of better markers/new tools that would enable understanding of traits.

2.2. Genetic approaches towards marker-assisted and genomic selection, and the challenges in sweetpotato

Dorcus Gemenet

Revisiting the traits targeted in sweetpotato improvement (storage root yield, diseases such as SPVD, sweetpotato weevil, drought tolerance, quality, dual purpose and adaptation to low soil fertility conditions), this presentation gave a background to the genetic approaches towards MAB and genomic selection and then discussed the challenges in sweetpotato. It was clarified that genomic selection is aimed at speeding the breeding process using predictions based on the genome.

At the moment there are several challenges when it comes to the genetic analysis of sweetpotato. These include:

- ▶ The crop being self-incompatible meaning there are no homozygous parents that could be utilised in genetic studies
- ▶ Lack of good quality sequence information on the crop
- ▶ Presence of multiple alleles at marker loci and at loci for traits of interest
- ▶ Different possibilities of allele dosages across homologous chromosomes
- ▶ Large amounts of unobserved marker data based on dominant markers
- ▶ Occurrence of both bivalent and multivalent pairing during meiosis
- ▶ Possibility of preferential pairing of different homologs
- ▶ Possibility of different recombination frequencies for different pairs of homologs
- ▶ Higher number of possibilities for the linkage phases between markers
- ▶ Possibility of double reduction during meiosis
- ▶ Lack of clear distinction in co-segregation due to same homologous chromosome and that due to two different homologs that end up together
- ▶ Current linkage approaches which put strong emphasis on single-dose loci are not appropriate
- ▶ Lack of appropriate software for hexaploids

2.3. Genomic-assisted breeding in sweetpotato: current status and future opportunities

Awais Khan

Phenotypic selection which is based on appearance and performance has several limitations:

- ▶ Difficult to separate environmental and genetic contribution
- ▶ Difficult to distinguish homozygous and heterozygous effects
- ▶ Needs large space and labour input
- ▶ Slow and time consuming

Genome-wide selection is a DNA based selection method in which several loci are selected using genomic estimated breeding values (GEBVs) based on genome-wide marker profiling. The phenotypes are predicted based on genotypes alone.

The present status of sweetpotato genetic and genomic resources can be summarized as follows:

1. There are 7,783 accessions at CIP's genebank (including breeding lines, improved varieties, landraces, and wild accessions)
2. There is great experience among breeders and scientists at CIP, NARs in SSA, NCSU, Louisiana State University (LSU), China, Japan and Korea, but limited community compared to many other crops
3. There are few genetic mapping populations and limited genomic resources – So far few linkage maps with SSRs and AFLP markers are available
4. QTL mapping has been done on Beauregard and Tanzania: Root-knot nematode resistance, beta-carotene content, dry matter, starch content, maltose and sucrose content, iron, zinc, calcium content
5. There is a 46 SSR marker based kit identifying 1029 alleles, 5 to a 23 alleles, averaging 11.5 alleles per marker.
6. A partially complete genetic linkage map (43 and 47 LGS) based on retrotransposon insertion polymorphisms has been published
7. Transcriptome of two sweetpotato cultivars Xushu 18 and Xushu 781 has been published
8. Whole-genome sequencing (de novo) of two lines of *I. trifida*, using the Illumina HiSeq platform. Assembled genome sequence from 513-712 Mb. 62,407 and 109,449 putative genes, 1,464,173 SNPs and 16,682 CNVs has been published.
9. There is an on-going project on "Transcriptome Analysis and Genome Wide Association Studies in Sweet Potato (*Ipomoea batatas* L. Lam)" (2014-2017 funded by USDA at University of Arkansas at Pine Bluff.

To be able to utilise genomic assisted breeding approaches in sweetpotato improvement we need

- ▶ Genome sequence
- ▶ Next generation molecular markers
- ▶ Dense genetic maps
- ▶ Clear breeding goals. These could be general (high storage root yield, taste/nutritional quality, resistance/tolerance to abiotic and biotic stresses) or specific (beta-carotene levels, mineral content, starch content, sucrose content, drought, salt, heat tolerance, SPVD resistance, weevil resistance etc.)
- ▶ High-throughput, precise, accurate and standardised phenotyping in multiple environments
- ▶ Database to store and access genotypic, phenotypic and environment data
- ▶ Analytical tools for trait analysis, rapid identification of markers from sequence data marker-trait associations and genomic selections (these tools have to be suitable for hexaploid and clonally propagated crops)

Discussions arising from the presentation

The summary of questions and responses arising from the presentation are as follows:

- ▶ ***How can this approach increase the frequency of variety release and how will breeders benefit from the mostly lab-based approach?***

Certain intractable traits need this type of technology. A practical application for breeders is for example in the selection of parents.

▶ **How cost-effective is the approach?**

The cost of genotyping has tremendously decreased and is expected to continue decreasing. Additionally, the technology/approach will save time. Even though at present the time may not be shortened, in future the benefits will be realised.

▶ **Why is the investment in research on SPVD still relatively low?**

In the GT4SP the strategy is to first develop appropriate tools then focus on the challenge. When it comes to complex traits such as SPVD resistance, it may be a good idea to start treating it as a quantitative trait and start selecting for clones with even some limited levels of resistance and so contribute to reducing virus titre in varieties which would be important for the number of cycles that a variety can be utilised before it completely degenerates.

Participants also made the following comments:

- ▶ It will be important for people to understand how to utilise genomics information in their breeding work.
- ▶ SPVD is extremely important in sweetpotato breeding. CIP has worked on the problem for 20 years but has not got long lasting success. However, results from recent work are showing some promising resistance with some crosses.
- ▶ Clearly there has been some good progress towards virus resistance as observed for example in a transgenic experiment on virus resistance. In the experiment a NASPOT variety that had been used as a check alongside the transgenic did better than the transgenic plants.

2.4. Combining phenotypic and genotypic data – issues and opportunities

Reinhard Simon and Lukas Mueller

The presentation highlighted that an integrated database was needed to support sweetpotato improvement work because:

- ▶ It acts as an information highway that is used by breeders to support development of new varieties with increased acceptability.
- ▶ It acts as a 'memory'. For example baseline data can be utilised to monitor genetic gain, track materials (reference list), and track environmental conditions (climate change). Raw data can also be re-used.
- ▶ It can be used as a collaboration tool. Through the database, it can be known who is doing what, when, where, how and why.
- ▶ It can be used as an integration platform. This is especially for linked data.
- ▶ It can be used as a base for data mining/market intelligence.

There are several issues (old and new) that need to be considered when working to combine phenotypic and genotypic data.

Old issues

- 1) There is need to manage identity and be pro-active by providing reference lists. Use characterisation and evaluation data to check if true-to-type (retro-active).
- 2) There is need to manage variation in data. This can be done by promoting best practices (standard concepts/ontologies, standard measurements/protocols, standard

documentation/meta-data, standard structure/forms). The less variability between batches the higher the quality. There should be consistency and completeness.

- 3) Information decay. The data should be used when it is fresh before it fades away.
- 4) Access and availability: open access – no more ‘data hugging’
- 5) Performance/responsiveness. There is need to have good physical infrastructure (server, bandwidth etc.). The database user interface should be optimized for search.

New issues

- 1) How to accommodate the contribution of high throughput technologies
- 2) High volume or big data
- 3) High dimensionality
- 4) Real-time: data anywhere anytime. Need to get better and faster at integration, analysis and decision making
- 5) Connecting scales – from SNPs to satellite imagery, from preferences to phenotype, from consumer profiles to choice of breeding parents

New options have emerged

- 1) The web is the way to connect ideas/information sources, cloud computing, operating system independent, device independent, the browser is the new office
- 2) Newer standards for concepts. Ontologies – a basic tool for knowledge creation. Facilitates logical operation on words
- 3) Newer devices – tablets, smartphones – with new ways of accessing, interacting and creating information
- 4) Newer use interaction paradigms – based on navigation (zoom, pan); touch (point) gestures; speech recognition
- 5) Increasing automation of computation

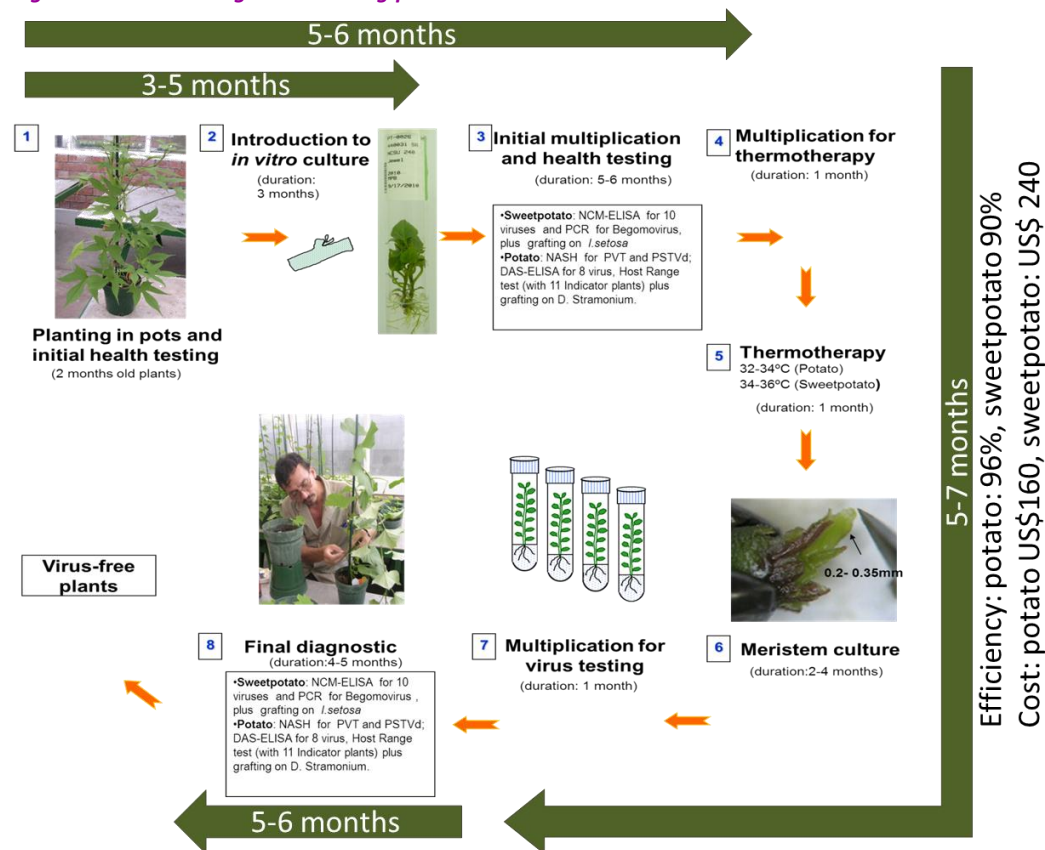
2.5. Best practices for clonal identity verification and health testing

Bramwel Wanjala and Jan Kreuze

It is important to have accurate and efficient ways by which sweetpotato clones can be identified. This is especially in consideration of the fact that genetic differences among clones have implications on potential utility in crop improvement, and consequently also in the response to challenges such as the need for high yielding, disease/pest resistant, more nutritious and better adapted crop varieties. Accurate identification of clones will enable preservation and utilisation of those clones with unique traits. Phenotypic/morphological, biochemical and molecular markers can be utilised in the identification of clones. Clonal identification methods need to be integrated, morphological and molecular. The phenotyping tools need to be standardised. It is important that the information generated on the different clones be properly managed.

The current virus testing protocols run for a period of virus testing and cleaning of up to two years and is costly as detailed in the protocol in Figure 2.

Figure 2: Virus testing and cleaning process



It is important the virus testing and clean up goes through such an extensive process because of:

1. Low virus titers in plants = unreliable detection directly from sweetpotato
2. Lack of adequate laboratory tests for some viruses
3. International guidelines for clonally propagated crops

There are on-going efforts aimed at improving the current process. Generic, highly sensitive and fast molecular tests on *in-vitro* plants are being explored. These approaches include: multiplex PCR; small RNA sequencing and assembly (towards universal viral diagnostics and sequencing); tube-arrays for sensitive detection of all viruses/pathogens of a crop at once (but this requires a laboratory); and field detection method with high sensitivity and ease of use (e.g. LAMP).

The current virus testing procedures are effective, but time consuming and expensive; hence they slow down germplasm exchange. The NGS sequencing data contributes to improving primer design for PCR and LAMP. Tube arrays are performing well and may be a useful tool for distribution hubs. Fast, sensitive and easy to use field based diagnostics is still a challenge, while isothermal amplification is the most promising (and flexible) solution.

2.6. Breeding for cold tolerant dual purpose sweetpotato

Benjamin Kivuva

Dual purpose sweetpotato varieties are needed in the East African highland due to diminishing pasture and crop lands. The reported study is aimed at developing cold tolerant dual purpose varieties with vine to root ratios of 1.5 to 3.0. To undertake the study 28,000 polycross seeds from 14 parents were germinated at Kiboko, Kenya. Selection was done at nursery stage against narrow leaved genotypes as these had low potential for use as livestock feed. Out of this initial selection 13,000 seedlings were planted and screened on station. Of the clones screened, 450 were selected for animal feed traits: without pubescence, vine pigmentation (green- against anthocyanin), with large non-serrated leaves and with large above ground biomass, and high storage root yield. Advanced and farmer participatory screening was undertaken for 49 clones together with one control planted at three on-farm sites and one on-station site. The sites were: Tea zones Runyenjes- Embu (very cold), Manyatta- Embu (cold), Kangundo (transitional coffee zone), and Kiboko (a semi-arid zone). Maturity period differed for the sites and ranged from 5-8 months.

From this study 13 clones were selected by farmers and did well in more than one site hence had some level of stability and would be advanced for cold tolerant dual purpose evaluation. The selected clones were: Kyembandula 3, Kyembandula 9, New Kawongo 7, Shock 5, Silklow 6, Bnd 1, Kigabali 16, Kigabali 17, Kigabali 6, Magabari 1, Magabari 3, and Naspot II 13. These clones are being further tested in three on farm sites and in an SPVD hot spot. The clones that perform well will be submitted for evaluation under the national performance trials (NPT) in preparation for their release towards the end of the year. More work will also be undertaken to analyse the nutritional quality of the clones in addition to doing work on animal palatability tests.

Discussion arising from the presentation

A question was raised regarding the genetic variation in the germplasm for cold tolerance, where the genetic variation came from and whether the weather data was analysed over a long period. The presenter explained that the sites used in the study were selected in a participatory manner with people working in agricultural extension.

2.7. Facilitated discussion: What do we need to do to make marker assisted breeding a reality in Africa?

Jan Low and Craig Yencho

The participants were first asked to mention ways by which their breeding programs had benefited from the use of molecular markers. Among the responses given were that molecular markers had been used to confirm genetic diversity, to confirm genotypes and to identify clones with traits of interest. The subsequent discussion then explored other areas through which the breeding programs in the region could benefit from the use of molecular markers.

It was observed that use of molecular markers in germplasm characterisation could be of benefit to the programs in countries such as Nigeria, Ethiopia, Rwanda, Ghana, Tanzania, and Zambia that at the moment were working to maintain local germplasm. Another area in which molecular markers could potentially be applied is in identification of male parents in polycross nurseries and testing for viruses

and identifying SPVD resistant clones in sweetpotato breeding programs. Many countries expressed interest in short term training on molecular marker technology. The lead PI in GT4SP indicated the intention of the project is to carry out such short trainings to increase the capacity of breeders in this area.

2.8. Sweetpotato breeding at the Southern Africa Sweetpotato Support Platform (SSP)

Maria Andrade

The objectives of the sweetpotato breeding and germplasm management in Southern Africa are to:

1. Generate drought tolerant OFSP that combine different quality characteristics with significant improvements in yielding ability
2. Maintain good quality material, establish community-based seed systems for good quality seed dissemination and develop and test strategies for the multiplication and dissemination of varieties

Research at Southern Africa Support Platform is supported by 16 screen houses, one kitchen lab, one quality lab (with a NIRS machine), one tissue culture lab, research stations and farmers' fields.

Under the SASHA II project the Southern Africa SSP was tasked with:

1. Undertaking studies that can demonstrate the achievement of significant genetic gain (2% per year in yield) in two years in early generations and 4 years for selected varieties;
2. Generating at least 150 thousand seeds with drought tolerance genes and disseminating to at least 10 NARS partners in SSA and SWCA;
3. Developing hybrid progeny exhibiting yield jump of 10 to 20% in hybrids from populations with drought tolerance and enhanced efficiency for drought tolerance breeding;
4. Clones with 200% RDA for young children of pro-vitamin A, 25% RDA of iron and 35% RDA of zinc under high intakes.

In 2012, activities to carry out studies commenced when two crossing blocks were established. The goal was to develop clones with population means of >8 t/ha root yield, >26% dry matter, >59% starch, >100 ppm beta-carotene, >18 ppm Fe, >9 ppm Zn. Clones with vine survival traits and weevil avoidance were also targeted. Seed was harvested from the crossing blocks and a series of trials were undertaken after the identification/selection leading to the release of 15 clones in 2011 under the accelerated breeding scheme (ABS).

From 2012-2014, 72 advanced clones were identified for more testing. In 2014, four multi-location trials were planted in Map, Chokwe, Gurue and Lichinga. The 72 clones were grouped into three categories (25 purple-fleshed, 20 dual purpose and 27 orange-fleshed). On-farm trials were conducted to assess varietal performance under farmer conditions and acceptance levels in Mozambique. During the on-farm trials, 253 farmers participated in the evaluation of cooked leaves and root tasting. Nutritional quality analysis was also done on the evaluated clones. Data from multi-location trials showed significant differences for total root yield, vine yield, dry matter, harvest index and nutrient content (beta-carotene, iron and zinc) among clones. Nine clones were identified for release: purple-fleshed (3), dual purpose (3), and orange-fleshed (3).

At the time of reporting there were several on-going trials. These included multi-location trials with 12 white and yellow-fleshed elite clones; advanced yield trials with 27 clones (planted in February 2015:

two treatments – irrigated and drought stress with each treatment having two replications); advanced yield trials with 37 clones (planted in May 2015: two treatments – irrigated and drought stress with each treatment having two replications); three different advanced yield trials with 27, (20 mixture of white and yellow-fleshed) and 26 OFSP under evaluation at Chokwe, Chibuto and Umbeluzi (2015); seven advanced yield trials at Gurue; one preliminary yield trial with 209 orange and purple-fleshed clones at Gurue; observation trials with 3,409 clones planted at Chokwe, Umbeluzi and Gurue; 24 on-farm trials in southern Mozambique; drought tolerance trial involving 54 clones. There is also an on-going trial at three sites on heritability of vine survival that involves 36 clones and is being carried out with the aim of estimating heritability of vine survival in a collection of genotypes.

To tackle the sub-objective on generating at least 150 thousand seeds with drought tolerance genes disseminated to at least 10 NARS partners in SSA and SWCA, two crossing blocks were established in January 2014 at Umbeluzi and Gurue. At Umbeluzi there are 60 female parents and eight males with five of the male parents from the released drought tolerant OFSP varieties. At Gurue, there are 50 females and six males. Manual crossing was done between May and July 2014. Seed harvesting was done between June and September 2014. A total of 34,929 seeds were distributed to seven national programs. Gurue planted 4,792 controlled crosses and 6,140 polycross, Chokwe 4,880 polycrosses, and Umbeluzi 1,541 controlled crosses. A total of 222,482 polycross (> 111 families) are in storage and 45,536 controlled cross seeds (>313 families) are available for sharing. An additional two crossing blocks were established in January 2015 in Umbeluzi and Chokwe and controlled crosses began in May 2015.

A total of 31,089 kg of sweetpotato vines were disseminated to different programs in 2015 and planting material was distributed to 19,000 families. The tissue culture laboratory maintained 107 clones and produced 32,485 plantlets. Also a total of 320 vines, 16 varieties, were received from Malawi for clean-up. Another set of 9 local clones were also subjected to thermotherapy for virus elimination, also 162 plantlets introduced into thermotherapy

Discussions arising from the presentation

The following sums up the questions and answers session:

- ▶ ***How is drought tolerance defined in the program?***
This defined by looking at yield, vine, vigour of the plant during drought.
- ▶ ***Is there a trade-off between genetic gain in root yield and dry matter content and should reporting on genetic gains be on dry matter basis?***
There is need to report data relative to checks so as to be able to gauge the genetic gains. Series of multi-environment trials of 2-3 years with information on check suffice.
- ▶ ***What are the three most important conditions for drought trials?***
Drought, absence of incidents of diseases (that would confound outcomes) and timely planting. The important traits to look for during evaluation for drought tolerance are vine vigour and growth rates and also rooting depth.

2.9. Sweetpotato report for Southern Africa 2014/2015

Laurie, S., B. Michelin, M. Chiipanthenga, G. Makunde, J. Ricardo, and M. Chiona

The Southern Africa sub-region covers Madagascar, Mozambique, Malawi, Zambia, and South Africa. The important constraints in the sub-region are:

1. Variable climate patterns: irregular rainfall, drought, floods.
2. Susceptibility to pests and diseases, mainly SPVD and sweetpotato weevil
3. Frost damage especially in South Africa and Madagascar
4. High post-harvest losses and limited value addition, especially in Malawi
5. Declining soil fertility especially in Malawi

The objectives of the breeding programs in the southern Africa countries are as summarized in Table 5

Table 5: The objectives of the breeding programs in the southern Africa countries

Madagascar	Mozambique	Malawi	South Africa	Zambia
•Food and nutrition securities	•Drought tolerant (CFSP) with high yield, high dry matter & tolerant to pests & diseases	•High and stable yields (≥ 20 t/ha) •Resistant/ tolerant to major and prevalent diseases (SPVD and Alternaria) and sweetpotato weevil	•Sweet taste & med high dry matter •High β -carotene content •High yield, good storage root quality and storability	•Tolerant to major pests and diseases with high yield and adaptable to various ecological conditions •Develop processing technologies
•To improve the livelihood of poor and especially vulnerable populations	•Increase availability of OFSP vines for farmers to mitigate the effects of droughts, floods and minimize the effects of VAD	•Desired root quality/color to meet local cooking and consumption requirements (high dry matter content, sweetness)	•Tolerance to Alternaria blight (OFSP); •Tolerance to Fusarium wilt (CFSP) •Drought tolerant	•Production packages for subsistence farmers •Identify post harvest problems;

Table 6: Important sweetpotato landraces, released, widely grown, and orange-fleshed varieties in southern Africa

Sweetpotato category	Country				
	Mozambique	Madagascar	Zambia	Malawi	South Africa
Important landraces	Xipone, Xitsekele, Cino Minutos, Mwambazambane, Manhissane, Chulamete, Canassumana	Galona/Sihanaka, Rakotozafy mijoro, Vony, Votavo		Zondeni, Yoyera, Kamchiputu, Babache, Mfumu	
Important released varieties	Irene, Ininda, Sumaia, Delvia, Bela, Gloria, Cicilia	Bôra (199062.1), Mendrika (199004.2), Naveto (440131), Zambezi, Ejumila, Ukerewe	Lukulu, Lukusashi, Lunga, Mulungushi, Kalungwishi, Chingovwa, Luapula, Kanga	Sakananthaka, Nyamoyo, Sungani, Chipika, Kadyaubwerere, Kaphulira, Mathuthu, Anaakwanire	Blesbok, Ndou, Monate, 199062, Impilo, Bophelo
Most widely grown varieties	Xipone, Xitsekele, Cino Minutos, Mwambazambane, Irene, Ininda, Sumaia, Delvia	Galona/Sihanaka, Rakotozafy mijoro, Ebokely	Chingovwa	Kenya, Mugamba, Yoyera, Babache, Kadyaubwerere, Chpika	Blesbok, Ndou, Bophelo
Most important orange-fleshed varieties	Irene, Ininda, Sumaia, Delvia	Bele Karôty	Olympia, Chumfwa, Chiwoko, Kokota, Zambezi	Chipika, Kadyaubwerere, Kaphulira, Mathuthu, Anaakwanire, Zondeni	Bophelo, Beauregard, Impilo, W-119

Table 7: Sweetpotato research trials were undertaken in the southern Africa region during the 2014/15 period.

Trial	Country/No of clones				
	Madagascar	Mozambique	Malawi	South Africa	Zambia
Crossing block	0	1 trial (68 clones)	30	20	30
Observation (OT)	2	2 trials (3203 clones)	87	216 + 3912 seedlings	5679
No. of checks	2	3	4	8	
Preliminary yield (PT)		2 trials, (175 clones)	43	8	100
No of checks		3	4	4	4
No. of locations		2	2	3	1
Advanced yield (AT)	9	2 trials, (53 clones)	39	16	22
No. of checks	2	3	5	8	2
No. of locations	4	3	2	3	1
On-farm	7	24 farmers (9 clones)	15	5 (6 clones)	

The Southern African team published the following resources:

Chipungu F., Grúneberg, W. et al. Breeding of efficient varieties for the changing environments in Malawi- an analysis of variance to predict selection of stable genotypes for root yield. Plant genetic resources.

Omotobora, B.O., Adebola, P.O, Modise, D.M., Laurie, S.M., Gerrano, A.S., 2014. Greenhouse and field evaluation of selected sweetpotato (*Ipomoea batatas* (L.) LAM) accessions for drought tolerance in South Africa. *American Journal of Plant Sciences* 21(5):3328-3339. Doi:10.4236/ajps.2014.521347

Mbengwa V.M., Mabuso JRM, Du Plooy CP, Laurie S and van Schalkwyk HD, 2014. Exploration of Sweet Potato cultivar markets availability in North West Province, South Africa. *International Journal of Biological, Veterinary, Agricultural and Food Engineering* 8(8):886-891

Laurie, S.M., Maja, M.N., Ngoben, H.M., Du Plooy, C.P. 2014. Effect of Different Types of Mulching and Plant Spacing on Weed Control, Canopy Cover and Yield of Sweet Potato (*Ipomoea batatas* (L.) Lam). *American Journal of Experimental Agriculture* 5(5): 450-458.

Hundayehu, M., Du Toit, E., Laurie, S., Steyn, M., Greyling, R., Myeza, N. 2014. Effect of long-term invitro sub-culturing on quality degeneration of sweet potato varieties: Morpho-anatomic assessment and simple sequence repeats (SSR) analysis. *Journal of Agricultural Science and Technology A&B* 4(10A):811-821.

Laurie, R.N., Laurie, S.M., du Plooy, C.P., Finnie, J.F. and Van Staden, J., 2015. Yield of drought-stressed sweet potato in relation to canopy cover, stem length and stomatal conductance. *Journal of Agricultural Science* 7(1):201-215 <http://dx.doi.org/10.5539/jas.v7n1p201>.

Laurie S.M. and Booyse, M., 2015. Employing the GGE SREG model plus Elston index values for multiple trait selection in sweetpotato. *Euphytica* <http://link.springer.com/article/10.1007/s10681-015-1359-6>.

Laurie, S.M., Tjale, S.S., van den Berg, A.A., Mtileni, M.M. & Labuschagne, M.T., 2015. Agronomic performance of new cream to yellow-orange sweetpotato varieties in diverse environments across South Africa. *South African Journal of Plant & Soil* 32(3). DOI:10.1080/02571862.2015.1014436

Woudenberg, J. H. C., Truter, M., Groenewald, J. Z., & Crous P. W. (2014). Large-spored *Alternaria* pathogens in section *Porri* disentangled. *Studies of Mycology*, 79, 1-47.

Laurie, R.N., 2015. Biochemical, physiological and agronomic response of various sweet potato cultivars to drought stress in rainout shelters and field conditions. PhD Plant Science, Research Centre for Plant Growth and Development, School of Life Sciences, University of KwaZulu-Natal.

Hundayehu MC 2015. Improvement of orange-fleshed sweet potato (*Ipomoea batatas* L.), *in vitro* propagation and vine conservation over prolonged drought seasons. MSc (Agric) Horticulture, Faculty of Natural and Agricultural Sciences, University of Pretoria, April 2015.

Malebana ME 2014. Induced mutation in sweet potato aimed at improved quality and drought adaptation. MSc, Department of Plant Sciences (Plant Breeding), University of the Free State, Bloemfontein, September 2014.

Naidoo SIM 2014. Genetic studies of yield and flesh color in sweetpotato. MSc (Agric), Department of Plant Production and Soil Science, University of Pretoria, November 2014.

Discussion arising from the presentation

Two questions arose after the presentation. The first related to the reason why varieties spread to different scales. Participants were informed that this is because the materials related to the varieties were not equally disseminated. The second one was on how to get varieties that were high in both beta-carotene and dry matter. The participants were told that this could be done by selecting for these types of clones which are present, though at a lower frequency; and that it also depends on the parents grown in the crossing block.

2.10. Preliminary results of the heterosis trial in Mozambique with clones derived from Ugandan inter- and intra- gene pool crosses

Makunde, G., M.Andrade, W. Grüneberg, and R. Eyzaguirre

The objective of this study was to demonstrate family means for inter gene pool crosses BxA (64 families) and intra-gene pool crosses AxA (28 families) and BxB (28 families) under drought stress conditions – in other words, heterosis increments under drought stress conditions. A total of 4317 clones were planted under irrigated and non-irrigated conditions in 1 m row plots, three plants per plot replicated two times. All clones from the three populations were randomized and planted together. Drought intensity index (DII) was calculated using the formula

$$DII = 1 - (\text{Mean [no irrigation]} / \text{Mean [irrigated]})$$

The AxB population had more good families than the AxA and BxB populations. The AxB population appeared to be more stable than the AxA and BxB population – especially under drought.

2.11. Heterosis in sweetpotato – what do we know, options and where to go?

Wolfgang Grüneberg

Heterotic gain or heterosis increment is considered to be present when the offspring is superior to mid-parent performance. In clonally propagated crops F1 offspring is the family derived from a cross – such F1s are segregating and so estimates of the mean across all clones of a family are used without selection. In heterotic cross combinations/families, one can still select for ‘the best’ clone. The aim is to efficiently generate better populations. Better for yield and yield stability (exploiting the phenomenon, heterosis) and better for quality and biotic stress resistance (by allowing more inbreeding within mutually heterotic gene pools).

In sweetpotato the heterosis increment studies that have been undertaken so far are:

Mega-clones (important clones across regions) – 4 x 12 crosses (48 families) – without separation of gene pools, without selection of recombining ability, without inbreeding. In this study the offspring means were clearly superior to that of the mid-parent.

- 1) PJ1 x PZ1 population (two populations at CIP developed independently since 2004) - 231 families clones (49 PJ parents and 31 PZ parents) - with separation of gene pools, without selection of recombining ability, without inbreeding. The two populations were found to be mutually heterotic gene pools without selection on combining ability.
- 2) B x A population with 8 x 8 parents (64 families) from Namulonge tested at Namulonge) - with separation of gene pools, without selection of recombining ability, without inbreeding. Overall heterosis increment of 7.6% was found in the BxA population. With respect to storage root yield 16 out of 64 cross combinations were observed with heterosis increments >100%. Heterosis increments of up to 74, 551, and 134.3% were observed for fresh biomass, storage root yield and vine yield, respectively. However, still further data checking is required to establish, for example which cross combinations generate extreme high heterosis increments.
- 3) A x B population with 8 x 8 parents (64 families) from Namulonge tested at Umbelusi / Mozambique) - with separation of gene pools, without selection of recombining ability, without inbreeding.
- 4) PJ and PZ populations (tracing back to 49 PJ parents and 31 PZ parents - with separation of gene pools, without selection of recombining ability, with inbreeding, ready to cross PJ” x PZ” to determine the gain of one complete reciprocal recurrent selection cycle.

The next steps for heterosis exploiting breeding schemes and/or better population improvement in sweetpotato would entail intensive data checking and publishing the results obtained so far. There would also be need to complete a reciprocal recurrent selection cycle and corresponding genetic gains. There would be need to make future large experiments more secure by planting checks more frequently within fields so as to capture more effectively possible within field variability – the check could take 10% of the test capacity. In the heterosis trial at Namulonge yield and SPVD resistance could be combined by crossing 40-50 parents from each gene pool and selecting 20-25 parents from each pool on the basis of offspring performance. An additional option would be to select testers on the basis of the 8x8 results – selecting 3-4 testers in each gene pool then crossing all clones in the two pools against these testers.

Discussion arising from presentation:

The next steps in the heterosis trial may need to focus on identifying testers; and there is need to isolate effect of virus on parents in assessing heterosis yield increments. It would be interesting to see the situation in families with some level of resistance

2.12. Short term training at BecA – vision and needs

Mercy Kitavi and Marc Ghislain

The objective of capacity building at BecA is to strengthen capacity of individuals and institutions to harness the latest biosciences technologies to improve sweetpotato production Africa. This entails:

- ▶ Improving breeders' skills and their access to research information and resources;
- ▶ Supporting breeders to regularly and effectively play a role in policy making; and
- ▶ Providing support to improve areas where there are gaps in skills.

The program is aimed at research managers, team leaders and breeders who need to familiarise themselves with the concepts and practices of the use of genomic tools in sweetpotato breeding. The capacity building is targeted at individuals, organisations and institutions.

The program at BeCA supports capacity building through research placements (that especially target graduate students), short term trainings of 3-6 months on the use of sweetpotato genomics for applied breeding, individual and small group training, and institutional capacity building. Training workshops, conferences, creation of linkages, information sharing and creation of awareness are all avenues through which the objectives of the program are addressed.

2.13. CloneSelector, Accudatalogger, and laboratory barcode identification: demonstration and updates

Luka Wanjohi

CloneSelector 1.0 is an Excel based program for field book design and analysis using R. Since initial release, new updates have been released. At present, there is CloneSelector 3.1 which has more statistical designs and also integrated NIRS data. Intensive in-country trainings have been undertaken to familiarise users with the program. So far over 200 trials have been generated using CloneSelector. Labelling of trials and samples from trials has been improved through the use of barcodes. There has also been work exploring electronic data collection using AccuDataLog.

At the BecA laboratories a Barcode KIT (comprising of a mobile computer for lab or field, a mobile barcode printer, and a barcode scan reader) has been adopted for use in *in vitro* potato genetically modified organisms (GMOs). Plants/samples are scanned instead of reading labels to reduce delays and eliminate human errors. Labels are printed instead of hand written. The automation of daily procedures has increased efficiency and allows personnel time for other activities.

2.14. Discussion and reporting on on-farm trial protocol improvement, check clones, and systematising feedback on performance of shared germplasm

Ted Carey and Jean Ndirigue

The participants were divided into four groups and tasked with reviewing and discussing the current on-farm protocols, the situation with check clones, and how to systematize feedback on performance of shared germplasm.

Based on the feedback reports from the groups on the farm protocols participants emphasized the need to ensure that during on-farm trials farmers are always adequately facilitated for smooth working relationships that will ensure effective contributions to the outputs of the trials undertaken or planned for the future. On the issue of check clones the need to use clean plants was pointed out and that for trials conducted in different locations there was need to have common check varieties such as Tanzania and Censa.

2.15. RTB Project reporting – a global reporting on sweetpotato progress (Theme 2, 2012)

Wolfgang Grüneberg

The RTB challenge research program of the CGIAR Consortium has seven themes under which research is undertaken:

1. **Gene bank and Germplasm** (conserving and accessing genetic resources)
2. **Breeding** (accelerating the development and selection of varieties with higher, more stable yield and added value)
3. **Disease and Pest Management** (managing priority pest and diseases)
4. **Seed Systems** (making available low-cost, high-quality planting material for farmers)
5. **Food Security and Health** (developing tools for more productive, ecologically robust cropping systems)
6. **Post-Harvest** (promoting postharvest technologies, value chains, and market opportunities)
7. **Impact** (enhancing impact through partnerships)

Sweetpotato breeding is captured under theme 2. In the RTB program, sweetpotato breeding is divided into five product lines:

Product line 2.5.1. Breeding tools, strategies, and approaches: sweetpotato. At the time of reporting this product line had 11 products. Two of the products here are: (a) molecular tools to characterise gene pools in use and documented at all sweetpotato breeding platforms and (b) magnitude of heterosis exploitation in sweetpotato breeding based on grouping breeding populations into two gene pools available for two breeding programs by 2016.

Product line 2.5.2. Trait capture and gene discovery: sweetpotato. This product line has four products. Two of these are: (a) genotypes and QTL gene(s) for heat and drought resistant sweetpotato identified by 2017 and (b) genotypes and gene(s) for early bulking (the <100 day sweetpotato) identified by 2016.

Product line 2.5.3: Population development and pre-breeding sweetpotato. This product line has seven products. Some of the products here are: (a) OFSP breeding populations for drought prone areas in SSA with emphasis on Southern Africa developed by 2016 and (b) Reciprocal recurrent selection to determine the potential selection progress and limits for high iron and zinc in an experimental high iron and zinc hybrid populations tested by 2017.

Product line 2.5.4: Variety development sweetpotato. This has four products. Two of the products are: (a) early released sweetpotato varieties (4 to 5 years instead of 8 to 10 years) from CIP population improvement with IT status for global dissemination by accelerated breeding scheme (ABS) and farmer participatory selection developed and tested by 2016 and (b) early released sweetpotato varieties (4 to 5 years instead of 8 to 10 years) from CIP population improvement realised for different variety types by 2017.

Product line 2.5.5: Aligning research with farmers' and end-users' priorities: sweetpotato. This has five products. Two of the products here are: a) bi-annual communication and press releases of material and tools published (2012 to 2016) and (b) next generation OFSP (dry and starchy) variety disseminations and follow up of breeding target in farmer participatory approaches by 2017.

3. FIELD VISIT

During the 2015 sweetpotato breeders meeting which for the first time brought together partners engaged in SASHA and GT4SP projects, participants were taken on a field trip to NaCRRRI on June 4, 2015. The Acting Director of NaCRRRI, Dr. Godfrey Asea received the participants upon their arrival at Namulonge. The main purpose of the field visit was to acquaint the participants/breeders with skills on gauging sweetpotato end users' perceptions and preferences through focused group discussions and participatory variety/product evaluation and selection. While at the station the participants were also taken through a demonstration on preparing sweetpotato seed for germination.

3.1. Profiling of end user preferences

During the first session of the visit the participants gauged the perceptions and preferences of different sweetpotato end users. This was done by five different groups of the participants separately interacting with different categories of sweetpotato end users. The categories were: a) women farmers, b) urban consumers, c) traders, d) rural producers, e) livestock/ animal feed, and f) children. The groups had already done some preparatory work on the previous days, including development of questions to guide discussions and allocating of roles such as group leader and note-taker to the members.

The group that profiled end users that utilise sweetpotato as **animal feed** interviewed nine farmers. The livestock kept and average numbers kept were as follows: cattle (5), goats (3), chicken (small scale – 20,



Meeting participants discuss with the livestock keepers

Photo: C. Bukania

commercial – 500), pigs (5) and rabbits (4). All the farmers interviewed grew sweetpotato on land areas of one acre. Among the sweetpotato varieties grown were NASPOT 8, NASPOT 11, NASPOT 12, NASPOT 13, Dimbuka, New Kawogo and +Vita. The key positive attributes of sweetpotato among the farmers were its production of vines which was used as livestock feed to increase milk production, the hardiness of the crop, longer storage period, and its being a source of income. The farmers consumed sweetpotato roots and either sold or gave away vines as feed for livestock. When preparing sweetpotato as cattle feed, farmers harvested and stored vines for

approximately three days to reduce moisture content. The farmers emphasised that reducing moisture prevented cattle from getting gut problems. They also noted that from their experience, animals are not able to feed on a sweetpotato-only diet for a long time. Pigs were fed on fresh vines. Sweetpotato root peelings and small roots were mixed with other feed before being fed to livestock. Also sweetpotato dried roots chipping were milled and mixed with other feed. In the farmers' experience, the livestock fed had a high preference for sweetpotato as they aptly summarized "When an animal breaks loose it will bypass all other fodder and feed on sweetpotato if it's available." The farmers in this group preferred varieties with multiple benefits: high yields, nutritious, early maturing and dual purpose.

Discussion with the **rural producers group** brought together 10 producers (four males and six females). Among the crops that these farmers grow are maize, beans, cassava and sweetpotato on farm sizes ranging from 1.5-4 acres. They had been involved in sweetpotato production for home consumption, livestock feed and for commercial purposes. Surplus fresh roots are sold rather than stored. They grow white, yellow and orange-fleshed varieties (on average 3-4) with the orange-fleshed types occupying 25% of the areas planted with the crop. In the production of sweetpotato, the farmers used mounds rather than ridges to reduce water retained in the fields. The farmers source planting materials from their own fields and new releases from NaCRRRI. Sometimes they buy from fellow farmers. The seed is conserved in the wetlands during the dry season. The major problems encountered during production of the crop are leaf pests especially during drought, weevils,

drought, root rots and low market prices. For home consumption they eat sweetpotato in boiled and fried forms. For consumption the farmers prefer high dry matter varieties which are sweet, low in fiber, have good flavour and red skinned among other traits.



Children respond to questions during discussion

Photo: C. Bukania

The discussion in the **children's group** brought together 10 five-year old school going children from BK Junior School, near NaCRRI. The children identified their most preferred food as Irish potato, rice, sweetpotato, posho (maize meal), cassava, beans and bananas (not in order of preference). Four of the children preferred sweetpotato because it is orange, while six said they liked rice most. Sweetpotato was mentioned as the most consumed food. The reason given by the children who did not like sweetpotato was that they did not find it sweet. The children knew that sweetpotato flesh colour varied from white to orange and majority of them (seven) preferred the orange-flesh type that is soft. They

preferred to eat the sweetpotato steamed/boiled, fried or mashed. Only one of the children had eaten sweetpotato leaves as a vegetable. Four of the children do not like sweetpotato but gave no reason, while eight like soft sweetpotato – either fried or steamed. Two of them prefer to have sweetpotato as often as three times a week. Six of the children knew that food came from the garden. The specific crops they knew were found in the garden were maize, groundnuts, sweetpotato, beans, and cassava.



A woman states her mind during the session

Photo: C. Bukania

The **urban consumer group** brought together eight consumers (four female). The initial discussion sought to establish the perception of the consumers about sweetpotato. All the respondents said it is food that has several advantages including the fact that it is easy to grow and can be harvested from the farm in piece meal. They also mentioned the health benefit that orange-flesh types have, especially on children. All the respondents said that they regularly consumed sweetpotato at breakfast, lunch or supper, three to seven times a week. Sweetpotato is consumed in various forms: boiled, roasted, steamed, fried, mashed (especially for children), raw/fresh, chips, flour used to make doughnuts. Most consumption was in the

steamed form.

Some consumers sourced sweetpotato from the market and others grew it in their own gardens. Still others consumed ready prepared ones in restaurants. The respondents felt that sweetpotato supply in markets in their part of the country did not significantly fluctuate so they did not experience a lot of price changes. When asked about what informed their choices of the types of sweetpotato they bought from the market they mentioned preference for the red skinned, high dry matter, and white fleshed types. They liked medium sized roots arguing that large roots did not taste good, while the small roots were often immature. Some of them were able to predict high dry matter types by looking at the kind of sap coming out of a broken storage root – thick and greyish sap was often found in the high dry matter types. Some rejected the orange-fleshed types because of its flavour, softness and being less sweet. None of the consumers had a problem with the time it took to cook sweetpotato and rejected an idea of breeding for faster cooking types arguing that this could

have a penalty on some quality trait – they would only accept if nothing is lost on the side of quality. None of the respondents were aware of GMOs but stated that they would not mind eating them as long as they were safe.

3.2. Demonstration on preparing sweetpotato seed for germination

The objective of this demonstration was to familiarize the participants with the best practices in handling and treatment of sweetpotato botanical seed to maximize germination and hence number of clones be evaluated. The demonstration covered cleaning of seed, scarification using concentrated sulphuric acid, the environment and precautions during the scarification, the duration of the scarification, cleaning and sowing of the scarified seed. To reduce chances of getting low germination, the importance of ensuring that the seed is scarified for the correct duration (not too short and not too long [by experimenting with a small seed sample for different times (30 minutes to 1 hour) in the acid]) was emphasized and that the seed is sufficiently rinsed with water after the scarification and thereafter the seed is planted at the correct depth.



Demonstrating preparation of seed for germination
Photo: C. Bukania

to

first

3.3. Participatory evaluation of sweetpotato leaf as a vegetable (with farmers as the evaluators)



Farmers use a voting system to rank the different sweetpotato leaves dishes
Photo: C. Bukania

Sweetpotato leaves were cooked as a leafy vegetable and presented to farmers alongside a popular leafy night shade vegetable dish. The dishes were evaluated for appearance, taste, tenderness and overall acceptability. The farmers ranked by way of coloured votes the dishes for the different parameters as either 'liked', 'moderately like' or 'do not like'. An overall ranking was determined by a show of hands during discussion time. The reasons cited for selection of the most preferred dish included its being tasty, not slimy, having a likable bitter taste, good appearance, easiness to swallow.

3.4. Participatory storage root evaluation (with breeders as the evaluators)

Storage roots of five sweetpotato varieties were cooked (boiled/steamed) and then presented to the breeders to taste and evaluate visually and by taste for appearance, taste, starchiness fibrousness and overall acceptability. On tasting panels the identity of the varieties were hidden. Of the varieties evaluated Ejumula was the most preferred because of its good taste, texture, good appearance and taste.



Breeders evaluate storage roots
Photo: C. Bukania

Annexes

3.5. Annex 1: Opening Address, 14th Sweetpotato Breeders' Annual Meeting, Colline Hotel, Mukono, Uganda, June 2-5, 2015

Dear Participants,

I am very pleased to welcome you to this 14th Annual Sweetpotato Breeders' Meeting, here in Mukono, Uganda, to be held for the next four days, June 2nd to 5th, 2015. This is the second Annual Sweetpotato Breeders Meeting to be held in Uganda; the first one was held, June 22-25, 2010.

Some of you are visiting Uganda for the first time, you are most welcome; all of you, please, enjoy the green vegetation, the rich insect and bird variety you can see in the mornings and evenings, and the friendly people around; feel at home. If we consider a decade back to date, I am right to welcome you to the second capital of sweetpotato production in the World after China (about 2.5 MT Uganda vs 117 MT China annual sweetpotato production). In terms of volume and consumption, sweetpotato comes after cooking bananas, and cassava, so sweetpotato is very important to us as a staple (85 kg per capita consumption) in Uganda as well as our neighbours and, and is increasingly becoming very important in sub-Saharan Africa. Customize your work according to what the end-user wants and what the market demands. Sweetpotato is a staple food in Uganda, and in light of the devastation caused to the banana by the wilt disease and to cassava by the mosaic, and brown streak, it is bound to be a major source of carbohydrates and income for small scale farmers. This is through sale of storage roots, vines and processed products in rural and urban markets, and for animal feed mostly pigs. We should increase the productivity of sweet potatoes focusing on the orange-fleshed ones that are naturally bio-fortified, virus resistant and not moist. The average yields are still quite low and the amount of food is not enough to match with population growth. As in other parts of SSA, sweetpotato in Uganda is predominantly grown by poor smallholder farmers, especially women.

Most of you are probably aware that the Sweetpotato for Security and Health in Africa (SASHA), now in its second phase is part of the ten-year Sweetpotato for Profit and Health Initiative (SPHI). SASHA is led by the International Potato Center (CIP) and partners such as our National Agricultural Research Organization (NARO), here in Uganda, targeting 17 countries. SASHA was launched on October 26, 2009 at Namulonge (the National Crops Resources Research Institute/NaCRRI). It was a day-long event highlighting farmer involvement and agro-processing, scientific findings and awareness creation through primary schools.

I am aware that SASHA Phase 2 continues to emphasize breeding progress as its core but also has components on seed systems and postharvest handling. The reason you are here for this meeting is to focus on the breeding component, which includes developing efficient population improvement programs at a sub-regional level in SSA as well as participatory varietal selection at the national level. This approach enables rapid ongoing development of new varieties to contribute to improved farmer incomes and to deliver nutritional benefits to consumers, especially women and children. I am glad that CIP breeders work in collaboration with our national partners in the region at the Sweetpotato Support Platform (SSP) at Namulonge, supported by efforts at CIP headquarters.

A lot of progress has been made since the launch of SASHA in 2009, and that you should be proud of, e.g.

Eight SSA countries have released 46 new sweetpotato varieties, 37 of which are orange-fleshed

- a. 10 PhDs and 3 masters graduated at the S. African Centre for Crop Improvement and the West African Centre for Crop Improvement in Ghana. Many thanks to the Alliance for a Green Revolution in Africa (AGRA) for funding the training programs
- b. AGRA has awarded nine breeding and four seed systems grants for sweetpotato activities, so these national sweetpotato breeding programs are active.
- c. You are contributing enormously to unleashing the potential of sweetpotato.

However, challenges such as devastating sweetpotato weevils, the tricky problems of virus and drought tolerance, the lack of reliable markets for sweetpotato in many areas where sweetpotato is produced, meeting a growing range of consumer preferences, and the limited range of storability of sweetpotato in most countries, means that sweetpotato breeders and other scientists and development partners still have a lot to do.

I am also aware that this time you have a joint meeting, the Sweetpotato Speed Breeders with participants on the new Sweetpotato Genomic Tools for Sweetpotato Improvement Project. The genomics team has come at the right time to develop genomic tools to solve some of these major bottlenecks and to accelerate sweetpotato breeding.

This meeting provides a timely and important opportunity to reflect not only on the objectives, result areas and anticipated outcomes of the project, but also on the wider developmental challenges afflicting African farmers. I hope you find your deliberations exciting, informative and inspiring.

The SASHA project complements our efforts and the government of Uganda is therefore committed to providing support to the project. We are here at Mukono today to re-affirm our commitment to contribute to solving the problems affecting the farmers on the African continent.

We have developed partnerships since SASHA started; we need to deepen relationships with all stakeholders to ensure food security and alleviate malnutrition and poverty through addressing the major constraints affecting sweetpotato production and utilisation in Africa. SASHA offers some of the resources and intellects necessary to achieve our goal. It also provides the opportunity to enhance our capacities in science and technology to facilitate the development and deployment of science-based solutions.

SASHA is part of the 10-year, multi-donor SPHI, which seeks to reduce child malnutrition and improve smallholder incomes and livelihoods among 10 million African households by 2020 through greater awareness, expanded market opportunities, and the diversified use of sweetpotato in SSA. It is important for these two projects and others to work together coherently, deliver, and leave a footprint in the project participating countries. This calls for commitment and focus of you scientists and our governments. Thanks to SASHA and the stakeholders in SPHI contributing to working together for a better future.

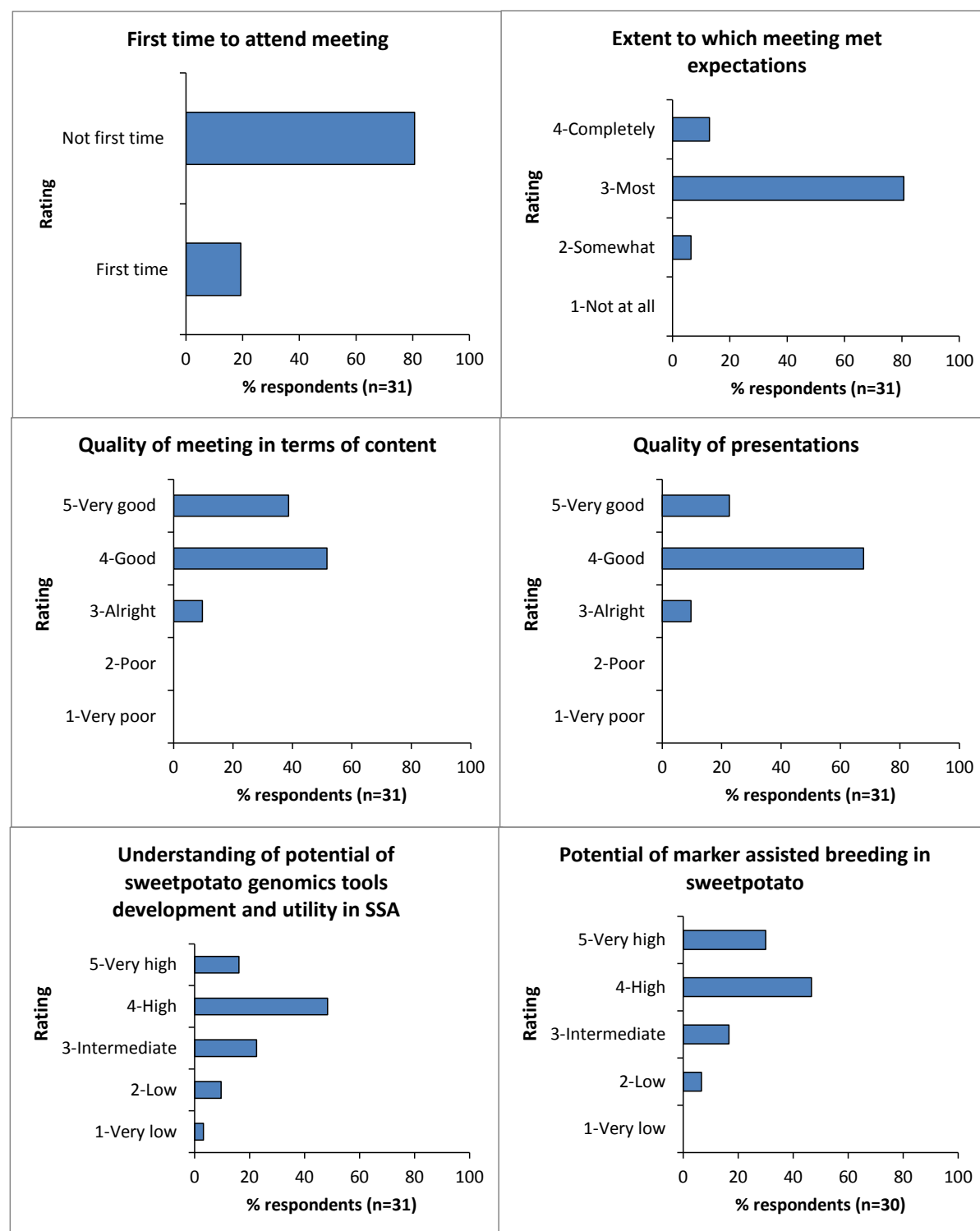
I would like to extend our gratitude to our development partners, such as the Bill & Melinda Gates Foundation, AGRA, USAID, the McKnight Foundation and the national governments of the 12 countries you represent in the region for their support for research for development, in addition to all the value chain actors you work with, and of course, to the farmers with whom we all work together with to find solutions to improve the food security, health, and wealth of families in SSA.

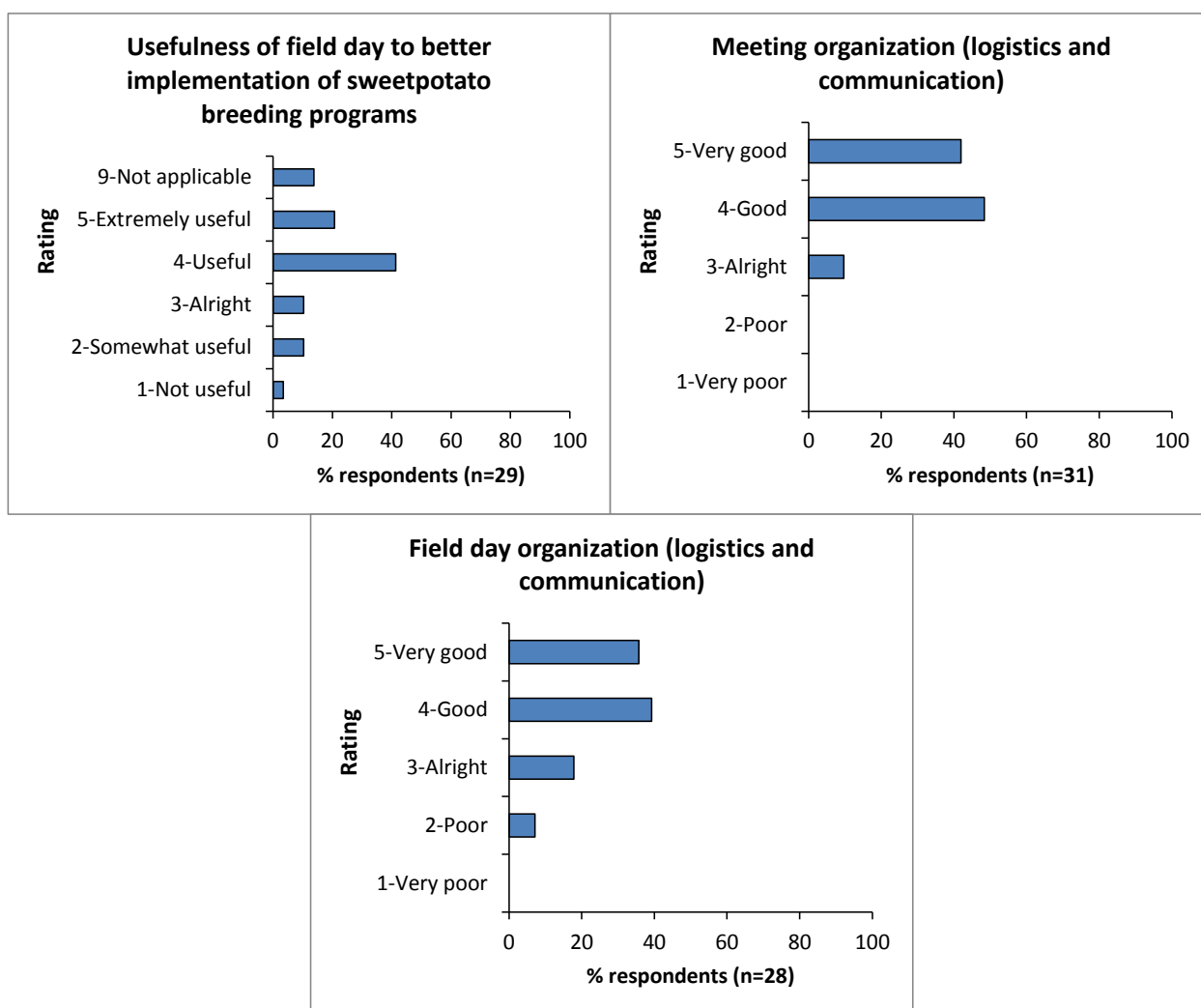
The national bird for Uganda, the Uganda Crane, is on the Uganda flag; it is a lovely bird. Ugandans are also friendly people, you are invited to find some time off your busy schedule while you are here to view them. I wish you fruitful deliberations. Finally I would like to thank all of you for gracing this occasion with your presence and together we pledge our commitment towards its success of the two projects

It is now my pleasure to declare this meeting officially open.

Dr. Jim Lorenzen, Senior Program Officer of the Bill and Melinda Gates Foundation, Dr. Jan Low, and Sweetpotato for Profit and Health Initiative (SPHI) Leader and Sweetpotato Action for Security and Health in Africa (SASHA) Project Manager, and Dr. Craig Yencho, emphasized the importance and role of the growing Community of Practice of the SSA sweetpotato breeders and their contribution to improvement in changing the livelihoods of the poor.

3.6. Annex 2: Evaluation of Speed Breeders Meeting held in Mukono, Uganda June 2-5, 2015





Parts of the meeting that were considered most useful

- 1) Meeting genomics and database team members
- 2) Meeting regional breeders
- 3) Sweetpotato base
- 4) Genetic gain presentation
- 5) Heterosis presentations and the discussions on the way forward
- 6) End user profiling methods
- 7) Constraints for sweetpotato in SSA
- 8) Discussions on various topics including breeding methods
- 9) Scientific presentations. The presentations/talks on breeding and scientific progress were very informative. Sharing of research results through presentations
- 10) Networking with fellow colleagues
- 11) Interaction with farmers during the field day
- 12) Presentation about completed reference diploid genome
- 13) Understanding what breeders require in their breeding programs
- 14) Hearing from rural producers
- 15) Meeting breeders from NARS
- 16) Side discussions with scientists
- 17) Introductions with other participants

- 18) Leadership shown by senior breeders and SASHA staff
- 19) Connecting SASHA and GT4SP projects
- 20) Discussion with end user groups
- 21) Better understanding of the different components of the genomics projects
- 22) Adapting genomics to sweetpotato breeding. Linkage of breeding to genomics
- 23) Interaction with farmers and other groups in the sweetpotato market chains
- 24) Progress on genomics work
- 25) Field day
- 26) Learning more about sweetpotato
- 27) Best practices for clonal identity verification
- 28) Marker assisted breeding in sweetpotato
- 29) Combining phenotypic and genotypic data
- 30) Scientific/professional experiences sharing by senior breeders
- 31) Establishing new linkages for collaboration
- 32) Overview of GT4SP
- 33) Presentation on estimating genetic gain
- 34) Determination of other useful traits beyond yield and their quantification
- 35) Meeting new attendees. Networking with new people
- 36) Exchanging ideas about the challenges in SP breeding
- 37) Sharing of results from PhD studies
- 38) Progress reports from SSP and NARS
- 39) Nice mix of topics. Great to have GT4SP
- 40) Nice practical during field day. Taste test during field day
- 41) Increasingly relevant topics and discussion by the CoP
- 42) Presentation on breeding for drought tolerance
- 43) National sweetpotato breeding
- 44) Group work
- 45) Field day
- 46) Genomics important for breeding
- 47) Marker assisted breeding in sweetpotato
- 48) On farm trial protocol improvement

Parts of the meeting that were considered least useful

- 1) Sequencing efforts
- 2) Genomic tools. Some genomics presentations were barely understandable by many breeders
- 3) Same format of the presentations. No insight on science behind the improvement of traits
- 4) The database talk needed to better address breeders
- 5) Country reports. Would be better to focus talks on improved breeding
- 6) Cold tolerance studies in sweetpotato
- 7) Field day
- 8) Part of country presentations on landraces in each country. This has remained repetitive over the last three years and is not likely to change in the coming years
- 9) Presentation on best practices for clonal identity verification was not very specific
- 10) The microphone was not working properly
- 11) Improving work plan
- 12) The field day did not cover all the aspects of the visit to NaCRRI
- 13) CloneSelector was not understood at all

Suggestions on areas for improvement in content or organization

- 1) The hotel venue was too far from the airport. Need to have better accommodation and internet
- 2) Meeting room was poorly arranged for size of group. Meeting room was too hot.
- 3) Gene sequencing efforts
- 4) Genomic tools
- 5) Breeders presentations should include more science
- 6) Need to have at least an afternoon off from the meeting to view/understand country or city especially for first time visitors
- 7) There is need for consensus on how to report data on fresh weight or dry weight
- 8) There is need for better organization and communication of field trip. It would be nice to know what to expect by way of a detailed program
- 9) Field demonstration
- 10) Perhaps we should focus more on topics of interest/new breeding tools for future sessions and drop country reports as presentation reports. These could be written reports so that there is more time for issues
- 11) Characterisation of local landraces by countries as it is now has too many holes
- 12) Presentations need to be improved. At present these are guided and not creative and do not reflect what happens in each country.
- 13) Need to observe time allotted for making presentations
- 14) Better setting of audio equipment
- 15) CloneSelector needs enough time. Presently many people are not using the program because of lack of expertise on the same.
- 16) Need for more time on genomics and molecular markers
- 17) Visit to fields, labs
- 18) Arrangement of subject areas by days of presentation
- 19) Group discussion on identified production challenges
- 20) Data documentation
- 21) Data reuse
- 22) Harmonize the descriptors and vocabulary used
- 23) Harmonize work between SASHA and GT4SP
- 24) Incidentals given to NARS invitees could be scaled up
- 25) During field day include visit to crossing block/breeding trials
- 26) Should reconsider if regional presentations should be so very prescribed or can contain highlights of other activities
- 27) Statistical designs for large number of entries
- 28) Maintenance of genotypes true to type over time and in tissue culture
- 29) Database development
- 30) Review of plan of activities
- 31) Conference hall was not very conducive – was very warm
- 32) Further elaborate GT4SP for non-professionals
- 33) Strengthen collaboration to implement and share genomic findings
- 34) Let other projects working on SP breeding also report what they are doing e.g. AGRA
- 35) It would be nice to go somewhere else to see ongoing program activities
- 36) Breeding for cold tolerance dual purpose
- 37) Virus identification

Suggestions on topics to be included in next year's meeting

- 1) Sweetpotato breeding progress in Burundi

- 2) More tutorials on trait evaluations
- 3) Basic concepts on marker assisted breeding in a presentation. More details on MAB
- 4) Workshop on new tools for data collection
- 5) Possibility of developing U-Tube Training videos
- 6) Revision of characteristics to go into the catalogue
- 7) Participants bring on-farm data and jointly compare analyses
- 8) Open discussions on sizes of mapping populations
- 9) A plant breeding statistics lab
- 10) CloneSelector in depth
- 11) Basis for selecting parents for crosses and understanding the genetics of the traits of interest
- 12) The use of genomic tools
- 13) More methods in data visualization and prediction
- 14) Data management irrespective of the tools
- 15) Software knowledge in analysing data from marker assisted selection
- 16) Various field designs, when to use them, how to analyse the data and where to seek help within the platform
- 17) Present more detail on Illumina and use of software
- 18) Refresher training on CloneSelector and program and Sweetpotato Knowledge Portal
- 19) Climate change coping
- 20) New tools/approaches, transgenics and genome editing
- 21) More presentations on dual purpose varieties
- 22) Sweetpotato seed system experiences. Tissue culture work on sweetpotato
- 23) Application of genomic tools to speed breeding of sweetpotato in reality

Other comments

- 1) Breeding is considered an art or science? If we are to consider it a combination of both, then it is better to discuss the rationale behind the traits, scientific reasoning for improvement and contribution of other traits
- 2) When new knowledge portal is available need to see active use by CoP and training at the next meeting
- 3) Need for more communication outside the meeting sharing relevant information on sweetpotato
- 4) Need to improve information on sweetpotato database
- 5) Share survey questions and problem topics to members
- 6) More tools for breeders
- 7) May be email update of major happenings on quarter basis to keep the countries at par with platform and CIP people
- 8) Encourage exchange visits between programs to share notes at either trial establishment or data collection events
- 9) Possible support for uniform trials over locations which would involve sharing of germplasm among programs
- 10) Have at the next meeting a practical session on basics on virus detection and cleaning
- 11) Harmonize techniques used in the community

3.7. Annex 3: Agenda

The 14th Sweetpotato Breeders Meeting, Colline Hotel, Mukono, Uganda, June 2-5, 2015

	June 1, Monday, Arrival (Colline Hotel , Mukono)	Martha Ameru
	June 2, Tuesday	
8:00-8:30	Registration	Martha Ameru and Ann Tomko
8:30-9:00	Introductions	
9:00-9:30	Opening	DG, NARO Dr. Ambrose Agona
9:30-10:00	Overview of the meeting	Robert Mwanga
10:00-10:30	Health Break and Group Photo	Christine Bukania
	Moderator – Ted Carey, Notetaker – Benard Yada (presentation/discussion)	
10:30-10:55	Sweetpotato breeding at the East and Central Africa SSP (15/10)	Robert Mwanga
10:55-11:20	National Sweetpotato Breeding in East & Central Africa (15/10)	Benjamin Kivuva
11:20-11:45	Sweetpotato preliminary heterosis results from Uganda (15/10)	Charles Wasonga
11:45-12:10	Sweetpotato, example of a naturally transgenic food crop	Jan Kreuze
12:10-13:00	How can we measure genetic gain in our applied breeding programs (15/35)	Wolfgang Grüneberg
13:00-14:00	Lunch break	
	Moderator – Kiddo Mutunda, Notetaker – Solomon Afuape	
14:00 -14:25	Sweetpotato breeding at the West Africa SSP (15/10)	Ted Carey
14:25 – 14:50	National Sweetpotato Breeding in West Africa (15/10)	Adofo Kwado
14:50 – 15:15	Genetic Improvement of sweetpotato for β -carotene and yield in Burkina Faso - Salient results of doctoral thesis research (15/10)	Some Koussao
15:15 – 15:50	Development of end-user preferred sweetpotato varieties in Ghana – Salient results of doctoral thesis research (15/10)	Ernest Baafi
15:50 – 16:15	Health Break	
16:15 – 17:30	End user (consumer) profiling	Jan Low
	Wed, June 3	
	Moderator – Marc Ghislain , Notetaker – Merci Kitavi	
8:00 – 8:45	Overview of the Genomic Tools for Sweetpotato Improvement (GT4SP) project (35/10)	Craig Yencho
8:45 - 10:00	Update on sequencing efforts with <i>I. trifida</i> and <i>I. triloba</i> - Why is a reference genome important for breeding? (60/15)	Zhangjun Fei
10:00-10:30	Health Break	
10:30 – 12:00	Marker-assisted breeding in SP - What do we need to do to get there and what sorts of traits are appropriate? (75/15)	Awais Khan
12:00 – 13: 00	General discussion	
13:00-14:00	Lunch break	
	Moderator – Zhangjuni Fei, Notetaker – Jan Kreuze	

14:00-15:00	Combining phenotypic and genotypic data into an integrated database platform - issues and opportunities, with examples from Cassavabase, Sweetpotatobase and other applications /brainstorming what is currently available (60)	Lukas Muller & Reinhard Simon
15:00 - 15:45	Questions and general discussion	
15:45 - 16:10	Health Break	
16:10-16:35	Best practices for clonal identity verification and health testing	Bramwel Wanjala & Jan Kreuze
16:35-17:05	Evaluation of sweetpotato for cold tolerance (15/10)	Benjamin Kivuva
17:10 - 17:45	Facilitated Discussion - What do we need to do to make marker-assisted breeding (MAB) a reality in SSA	Craig Yencho & Jan Low
17:45-18:15	Preparation for field day: Questions for end user groups	Group Leaders
	Thurs, June 4	
Thurs, June 4	Field day to Namulonge	Robert Mwanga & Gerald Kyalo
	A. Welcome from Director of NaCCRI B. Learning Opportunity from End users 1) Urban consumers (men & women): Laura Karanja (chair) & Charles Wasonga 2) Traders: Bernard Yada (Chair) & Ted Carey 3) Rural producers: Maria Andrade (chair) & Koussou Some 4) Women Farmers: Margaret Chiipanthenga (chair) & Godwill Makunde 5) Children: Robert Mwanga (chair) & Merci Kitavi 6) Animal Feed: Benjamin Kivuva (chair) and Bramwel Wanjala C. On-farm trial protocol review 1) Leaf evaluation with end users: Sweetpotato leaves vs. local leaf 2) Root evaluation with meeting participants	
	Fri, June 5, Moderator – Martin Chiona, Notetaker – Laura Karanja	
8:00-8:25	Sweetpotato breeding at the Southern Africa sweetpotato support platform (SSP) (15/10)	Maria Andrade
8:25 – 8:50	National Sweetpotato Breeding in Southern Africa (15/10)	Sunette Laurie
8:50-9:15	Sweetpotato preliminary heterosis results from Mozambique (15/10)	Godwill Makunde
9:15-10:30	Heterosis options and next steps (15/30)	Wolfgang Grüneberg
10:30-10:55	Health break	
16:10 –17:10	Short term training at BecA - Vision and needs (30/30)	Mercy Kitavi & Marc Ghislain
11:20-13:00	CloneSelector, Accudatalogger, and laboratory barcode identification: demonstration and updates	Luka Wanjohi/ Mercy Kitavi
13:00-14:00	Lunch break	
14:00 -15:45	Working table topic discussion and reporting (on-farm trial protocol improvement) (45/30)	Ted Carey and Jean Ndirigwe
15:45-16:10	Health break	
16:10-17:10	RTB Project reporting – a global view of sweetpotato progress (40/20)	Wolfgang Grüneberg
17:10-17:30	Wrap up	Robert Mwanga
Sat June 6	Departure	

3.8. Annex 4: List of participants

No	First Name	Title	Institution	Country	Phone	Email	Skype Address
1	Kwadwo Adofo	Research Scientist (Sweetpotato Breeder)	CSIR-Crops Research Institute	Ghana	+233 208198214	kinfodda@yahoo.com	adofo001
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12	Godwill Shimbarashe Makunde	Post Doc Breeder	CIP-Mozambique	Mozambique	+258 825 135177	g.makunde@ciar.org	g.makunde1
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The **Sweetpotato for Profit and Health Initiative (SPHI)** is a 10-year, multi-donor initiative that seeks to reduce child malnutrition and improve smallholder incomes through the effective production and expanded use of sweetpotato. It aims to build consumer awareness of sweetpotato's nutritional benefits, diversify its use, and increase market opportunities, especially in expanding urban markets of Sub-Saharan Africa. The SPHI is expected to improve the lives of 10 million households by 2020 in 17 target countries.



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