Diffusion and adoption of improved rice and maize varieties in Tanzania: application of genetic fingerprinting technique

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Acronyms and Abbreviations

AGRA:	Alliance for Green Revolution in Africa
ARI:	Agricultural Research Institute
BeCA:	Bio-sciences for Eastern and Central Africa
BMGF:	Bill and Melinda Gates Foundation
DAICOs:	District Agriculture, Irrigation and Cooperatives Officers
DArT:	Diversity Arrays Technology Pty Ltd
DRD:	Department of Research and Development
DNA:	Deoxyribonucleic acid
IITA:	International Institute for Tropical Agriculture
ILRI:	International Livestock Research Institute
IPC:	Identified Primary Constituent
KATC:	Kilimanjaro Agriculture Training Center
MAFSC:	Ministry of Agriculture Food Security and Cooperatives
MARI	Mikocheni Agricultural Research Institute
NPGRC:	National Plant Genetic Resources Center
ODK:	Open Data Kit
PASS:	Programme for Africa's Seed Systems
SNP	Single Nucleotide Polymorphism
TASTA	Tanzania Seed Traders Association
TOSCI:	The Tanzania Official Seed Certification Institute
REPOA:	Research on Poverty Alleviation

Acknowledgements

We are grateful to the Alliance for Green Revolution in Africa (AGRA) and the Bill and Melinda Gates Foundation (BMGF) for funding this study. We also express our deep appreciation for the support and encouragement from the seed sector stakeholders in Tanzania; in the absence of which the present study would have been a non-starter. The AGRRA Country Office in Tanzania provided a home for the project. Dr. Mary Mgonja, the AGRA Tanzania Country Representative deserves special mention for her role as a Champion for this project. She was instrumental in obtaining the buy-in from key stakeholders, facilitated the inception workshop and coordination of activities from her office, and provided valuable technical inputs to the genomics component. From AGRA Head Office, Dr. David Ameyaw and Josephine Njau ensured compliance with AGRA's administrative procedures and smooth flow of funds. Equally critical to successful implementation of this project was the buy-in from the Ministry of Agriculture Food Security and Cooperatives; the Department of Research and Development (DRD). Dr. Mansour ensured that the project got all the necessary approvals at the Ministry while Dr. Nduguru the head of Mikocheni Agricultural Research Institute (MARI) provided the facilities and staff for DNA extraction. Dr. Arnold Mushongi and Dr. Sophia Kashenge identified and assembled high quality reference material in addition to contributing to the study design. John Mark and Ramadhan Lipala, research technicians from MARI did a marvelous job of extracting high quality DNA. The Biosciences for Eastern and Southern Africa (BeCA) stepped in to provide the platform for DNA extraction at their laboratory in Nairobi; this gesture is much appreciated. Finally, our sincere gratitude is extended to the team from Diversity Arrays Technology LTD led by Dr. Andrzej Kilian for providing advice on the grain sampling protocol, technical backstopping during the DNA extraction exercise and generating high quality data from DNA analysis.
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Executive Summary

This study was designed as part of the AGRA Outcome Panel Survey in Tanzania to assess the diffusion and adoption levels of improved rice and maize varieties. Borrowing from a similar study conducted in Ethiopia in 2014-2014; the present study combined data from DNA fingerprinting and farmer recall to generate more accurate estimates of varietal diffusion and adoption. Household socio-economics data and grain samples were collected from a representative sample of farm households in the following administrative districts; Kilosa; Iringa Rural, Kilolo, Mbarali and Sumbawanga. A reference library was developed from 79 maize and 18 rice varieties. The genetic composition of the test materials were compared to the reference library. Each test material was therefore identified and correctly classified based on the identity of the primary genetic constituent.

Results based on DNA fingerprinting analysis revealed widespread diffusion of improved maize and rice varieties and more precise estimates of adoption of specific varieties. Whilst only 46% of the maize growing households reported planting improved varieties in 2015, 95% were actually growing improved varieties based on the DNA fingerprinting results. The results from rice farmers were even more dramatic. Only 6% reported growing improved rice varieties while DNA fingerprinting classified 100% of the material as improved. The results further confirmed that individual varietal identification in the field based on farmer recall data is prone to misclassification bias. Only 18% of the maize and 23% of the rice samples were correctly identified by the farmers. In the case of maize, the most popular varieties were the Kitale hybrid series; *Kitale* H625 (44%),H628 (20%), Kitale H614D(16%). Supa India was by far the most popular rice variety comprising 97% of all the rice test samples submitted for DNA analysis. Other rice varieties identified were TXD 306 and TXD 85.

These results have some implications for agricultural development interventions by AGRA and the other partners. Given the technical feasibility and the modest cost of combining DNA fingerprinting with farm survey data collection, we recommend that this approach should be employed in all of the future studies that aim to establish diffusion and adoption levels of improved crop varieties. The high levels of misclassification by farmers reported in the present study calls for further interrogation of the existing evidence on varietal diffusion and adoption in Tanzania and possibly in other countries. Second, the reasons for the observed levels of misclassification should be examined as well. A deeper understanding of why some varieties are more popular compared to others could result in better targeting of productivity enhancing interventions. Likewise, a modified tracer study version of the present pilot could be conducted on selected seed value chains to assess their performance; specifically to establish whether farmers are receiving the recommended planting materials, and the relevant accompanying information.

Finally, there is scope for improving the efficiency and effectiveness of conducting a similar study at scale in Tanzania. All of the Tanzania based organizations who were tasked with delivering on the genomics component of the present study did a sterling job. With additional equipment and technical backstopping, the cost of DNA analysis should come down further. The organization tasked with administering the farm household survey and grain sample collection faced some challenges. It is our considered opinion that the performance of the said organization is not fair reflection of the existing capacity in Tanzania-there should be other research outfits in the country that are capable of collecting and analyzing farm household data. More importantly for the said organization, additional investments in automated data capture and management, and analytical capability should place it in good stead for a similar assignment in future.

1 Background

1.1 Rationale

In their endeavor to catalyze the African Green Revolution, both the Bill and Melinda Gates Foundation (BMGF) and the Alliance for Green Revolution in Africa (AGRA) have identified Tanzania as one of their anchor countries. Over the last 8 years, AGRA made significant investments in the southern highlands of Tanzania through the Breadbasket Transformation Programs. To highlight but a few achievements, 1,498 agro-dealers were trained, 6 seed companies supported to expand their businesses and the release or commercialization of 10 varieties of rice and maize (Tables 1 and 2).

Table 1: Southern highlands based seed companies supported by the PASS

Organization Name	Type of support (Grant in USD)
Beula Seed Company and Consultancy Limited	145,000
Tropical Seed (EA) Limited	149,982
Suba Agro-Trading & Engineering Co. Ltd	186,800
Kipato Seed Limited	150,000
Meru Agro-Tours and Consultants Co. Ltd.	223,900
Highland Seed Growers	Fund beneficiary

Source: PASS data 2015

Table 2: Rice and maize varieties whose release were supported by PASS

Crop	Variety Name (	Variety Type	Class	Year of Release	Commercialized (Y/N)
Maize	SARIH 208 (SARIH06A16)	Hybrid	Hybrid	2009	Yes
Maize	SARIH 308 (SARIH06A20)	Hybrid	Hybrid	2009	Yes
Maize	UHS5210	Hybrid	Hybrid	2009	No
Maize	UHS5350	Hybrid	Hybrid	2009	No
Maize	UHS 401	Hybrid	Hybrid	2015	N/A
Rice	Nerica-1	Self-Pollinated	Lines	2010	Yes
Rice	Nerica-2	Self-Pollinated	Lines	2010	Yes
Rice	Nerica-4	Self-Pollinated	Lines	2010	Yes
Rice	Nerica-7	Self-Pollinated	Lines	2010	Yes
Rice	WAB 450	Self-Pollinated	Lines	2010	Yes

Source: PASS data 2015

The focus on Southern highlands among other regions has been maintained in the Tanzania Business Plan 2016-2020. Whilst accounting for about 35% of Tanzania's agricultural output, there is potential for productivity gains in the Southern highlands if small holder farmers have increased access to; 1) improved production and post-harvest technologies and, 2) remunerative output markets. In addition to the regional focus, the Tanzania Business Plan 2016-2020 prioritizes rice and maize amongst the high impact growth drivers going forward (Box 1).

Box 1

AGRA and its partners have invested in significant maize seed varieties (their development, production and distribution) and knowledge of maize cultivation that can be scaled up effectively. In addition, AGRA is spearheading post-harvest management efforts to reduce post-harvest losses in the maize sector. AGRA is introducing and promoting hermetic storage solutions including cocoons, PICS bags, and metal silos. The second most common cereal in Tanzania, in terms of area under cultivation and tonnage, also presents a large potential for impact. The production is close to the demand in the country and the government is investing in the crop to tackle post-harvest loss issues, providing AGRA opportunities to leverage these investments.

Source: AGRA Tanzania Business Plan 2016-2020.

In addition to the Breadbasket Transformation Programmes, AGRA put in place a results measurement and learning system during the first strategic plan period, primarily to facilitate the tracking and documentation of its achievements and failures and to learn from them. Towards this end, the Outcome Panel Survey initiative was launched in 2013 primarily to periodically collect and analyze data on key intended outcome indicators[1]. In the case of Tanzania, the first round of data were collected from 1500 farm households out of the original sample of 1680 at the end of the main harvesting seasons in 2013 (Table 3).

Table 3: Outcome panel survey areas in Tanzania

Region	District	No of households
Kilimanjaro	Moshi rural	240
Morogoro	Kilosa	225
Iringa	Iringa rural	195
	Kilolo	195
Mbeya	Mbarali	195
Rukwa	Sumbawanga rural	210
Manyara	Babati	210
	Hanang	210

Source: AGRA outcome panel survey results 2014

The second round of the outcome panel survey was planned for 2015[2]. In order to improve on the quality of data on use of improved crop varieties, an additional component on tracking diffusion through genetic fingerprinting was added to the proposed outcome panel survey. Dr. Leonard Oruko[3], a private consultant who had conducted a similar study in Ethiopia was commissioned by AGRA in February 2015 to design and implement a study on:

> "Tracking the diffusion and adoption of improved maize and rice varieties in southern highlands of Tanzania with the aim of narrowing down on the varieties supported by AGRA"s Programme for African Seed Systems (PASS) Programme. This will involve superimposing the genetic fingerprinting component on the outcome panel survey and will focus on adoption / diffusion of improved rice and maize varieties."

The justification for use of genetic fingerprinting to validate reported diffusion and adoption data obtained from farmer recall surveys is supported by results generated from a pilot study in Ethiopia. Focusing on improved wheat and maize varieties, the results revealed that data generated through farmer recall underestimated the adoption levels of improved maize and wheat varieties. Only 9.3% of wheat and 49% of the maize growers correctly identified the varieties they cultivated based on a comparative analysis of the recall information with the DNA finger printings of the actual grain samples from their fields. The estimate for improved wheat varieties based on farmer recall information was 63%. The comparable figure from the DNA finger printing approach was 96%. Although less dramatic, a similar trend was observed in the case of improved maize varieties-the estimate based on farmer recall was 56% compared to 61% from DNA finger printing.

Following a detailed stakeholder consultation process, the following specific objectives were identified for the present study.

[1] Some of the indicators include target household demographics; farm inputs availability, access and use; and access to markets.

[2] This activity has since been pushed back to 2016.

[3] Leonard worked for the International Food Policy Research Institute (IFPRI) in Ethiopia from 2012-2015

- To provide more precise estimates of adoption of improved rice and maize varieties in the pilot study areas
- To develop the capacity of the Department of Research and Development (DRD) to conduct a similar study in Tanzania at scale
- To provide an estimate of adoption of improved crop varieties whose release were supported by the AGRA's PASS programme.

1.2 Implementation arrangements

During the project formulation stage, stakeholder buy-in was identified as critical to successful implementation and uptake of the project results. Towards this end, the consultant and a team from AGRA made several trips to Tanzania, primarily to sensitize key players in the agricultural development sector on the project. With the help of the AGRA Country Representative in Tanzania, endorsement of the present project was secured in good time from the Ministry of Agriculture, Food Security and Cooperatives. Besides being the principal implementing partner in Tanzania, the Department of Research and Development (DRD) was responsible for reference material collection and extraction of DNA from the material. Dr. Arnold Mushongi and Dr. Sophia Kashenge were assigned to collect both rice and maize reference material, respectively. Dr. Fred Tairo coordinated the DNA extraction work by staff from Mikocheni Agricultural Research Institute (MARI). MARI was also responsible for securing the necessary export permits / phytosanitary certificates for any plant material that was to be sent out of the country.

The Research on Poverty Alleviation (REPOA), an independent public policy research outfit has been working with AGRA since 2013 as an implementing partner for the Outcome Panel Survey in Tanzania. Based on the organization's experience, REPOA was tasked to collect grain samples together with the socio-economics data from households. Accordingly, REPOA identified sample farm-households, recruited enumerators and with help from the Consultant, trained field staff on data and sample collection.

The AGRA Tanzania Country Office played critical implementation support and thought partner roles. Within the framework of the Host Country Agreement between AGRA and the Government of the United Republic of Tanzania, the AGRA Country Representative organized and facilitated an Inception Workshop, arranged meetings with government officials and, provided transport to the field when necessary. In addition, being a plant breeder, the AGRA Country Representative was an important thought partner in the design of sampling strategy for genomics and other analysis components.

Diversity Arrays (DArT) PYT, a private laboratory based in Canberra Australia was identified as the preferred partner for DNA fingerprinting. Two decision variables informed this choice: 1) DArT uses high throughput technology Illumina 2000 and has developed the DArTSeq technique for analyzing the purity of test materials and comparing their identity with the reference materials using highly robust and reproducible single nucleotide polymorphism (SNP) molecular marker; 2) Compared to other laboratories in Africa, the cost per sample was most competitive.

2. Method and approach

2.1 The study areas

Initially designed to piggy back on the AGRA outcome panel survey whose primary objective is to provide information on the potential outcomes of AGRA's investments, the present study focused on administrative regions and districts where AGRA had made significant investments in the past. The first round of the AGRA Outcome Panel Survey was conducted in the following administrative districts; Moshi Rural, Babati and Hanang in Northen Tanzania; Kilosa in Central Tanzania and; Iringa Rural, Kilolo, Mbarali and Sumbawanga rural in Southern Tanzania. Owing to time and resource constraints, Kilosa in Central Tanzania and; Iringa Rural, Kilolo, Mbarali and Sumbawanga rural in Southern Tanzania were selected for the present study.

2.2 Sampling strategy

Initially, all of the 920 rice and maize growers from Kilosa, Iringa Rural, Kilolo, Mbarali and Sumbwanga districts were selected for the present pilot study. However, following consultation with REPOA, on the cost of data and sample collection compared to the allocated budget for the same, it was recommended that Iringa Rural should be dropped and Kilolo retained. Accordingly, a sampling frame was constructed from a listing of outcome panel survey households.

A series of consultative meetings with REPOA to flesh out the technical and implementation details on the sampling strategy, logistics of data and sample collection revealed that the total sample size based on the outcome panel survey data of 2013 was 671. A decision was made to re-introduce Iringa Rural (vijijini) in order to increase the sample size to 800 households based on a random selection from 840 farm households (Table4).

Table 4: Sample households by region

Region (district)	Maize only	Rice only	Both rice and maize	Total Sample Including Iringa Rural	Final sample
Morogoro (*Kilosa*)	166	26	22	214	206
Iringa (*IringaVijijini*)	153	4	12	169	161
Iringa (*kilolo*)	190	0	1	191	183
Mbeya (*Mbarali*)	44	52	95	191	183
Rukwa (*Sumbawanga rural)*	0	75	0	75	67
Totals	**553**	**157**	**130**	**840**	**800**

Source: Authors' compilation from 2013 AGRA Outcome Panel Survey collected by REPOA

.2 3 Test sample and household socio-economics data collection

Following the recent developments in the use of mobile devices for data collection, Andriod tablets programmed with the Open Data Kit (ODK) were deployed instead of the old fashioned paper questionnaires[4]. The Analyst developed the survey instrument and programmed the tablets for data collection based on the ODK platform by May 2015 The enumerator training was scheduled for the

[4] ODK allows data collection and submission to an online server, even without an Internet connection or mobile carrier service at the time of data collection

second week of May 2015, however, this exercise was pushed back to early June following a request from REPOA. In the interim, REPOA agreed to conduct the sample household identification exercise before the enumerator training.

Figure 1: Enumerator training-theoretical session

Figure 2: Enumerator training-pretest session

A theoretical training session for enumerators was held at the REPOA Conference Room on 18th June that focused on generating an understanding of the questions, including translation into Kiswahili, followed by the use of tablets for data collection (Figure 1). On 19th June, the team went out to pretest the questionnaire in Masaki Village, Kisarawe District, about 30 kilometers south of Dar-es-salaam (Figure 2). During the pre-test, the Consultant also demonstrated the procedure for grain sample collection.

Following the pretest, the questionnaire was revised and translated into Kiswahili and tablets reprogrammed accordingly. The consultant held a follow-up training with the supervisors and REPOA staff before commencement of the actual data collection exercise. A final dry run on data and sample collection, labeling and packaging was conducted just before the commencement of the field exercise (Figure 3). Since the actual farmer and plot identification had not been done, REPOA agreed to send out an advanced team who would identify specific maize and rice fields for sample collection.

Figure 3: Socio-economic data and grain sample collection

The original grain sample collection protocol was modified[5] Instead of small scoops of approximately 200 grains, the new protocol prescribed collection of 10 maize cobs and 30 panicles of rice per field. This approach assumed that sampling would be done when crops are in the field. When field survey and sample collection began on 15th July 2015 in Kilosa, a number of scenarios were apparent that necessitated a further modification of the sampling approach.

In the case of rice, where households were found to have already harvested their crops farmers were asked to identify bags of the specific crops based on the field they were harvested from, especially where clearly identified varieties were stored in specific bags, followed by recording of farmer recall information on the same. . In other districts / regions where the harvested crop was mixed together in the storage bag, replacement farmers were randomly selected from a list of 3 nearby households who had not harvested their specific crops.

In the case of maize, the cobs had to be harvested from the field. Accordingly, sample households who had harvested their crop were replaced by neighbors following the aforementioned protocol applied to rice farmers.

The survey team was divided into two groups comprising 5 enumerators and a supervisor. Excluding travel time to different sites, the field data and sample collection was completed in 21 days.

2.4 Collection of reference material

During the Project Inception Meeting held at the Southern Sun Hotel in Dar-es-salaam on 31 March 2015, the participants identified the predominant improved varieties of rice and maize cultivated in the pilot study areas (Table 5).

Table 5: Reported maize and rice varieties grown in the study areas

District	Maize	Rice
Kilosa	TMV1, Situka M1, Kilima, Staha, ICS4, Pannar,Situka1, TANH600, TAN 250, Lishe K1, Meru Hb513, Tan 254, Pioneer	TXD 306 (SARO5), Supa (several versions), TXD88, TXD85
Mbarali	TMV1, Situka M1, Kilima, Staha, ICS4, Pannar,Situka1, TANH600, TAN 250, Lishe K1, Meru Hb513, Tan 254, Pioneer, TZM 523	TXD306(SARO5), Supa, TXD88, TXD 85
Kilolo	TMV1, Situka M1, Kilima, Staha, ICS4, Pannar,Situka1, TANH600, TAN 250, Lishe K1, Meru Hb513, Tan 254, Pioneer, UH6303, TMV1. Pannar 691, H614D, H625, H628 (from Kenya Seed); SC627, TZ H538, UH615	None Identified
Sumbawanga Rural	*Pannar 691, H614D, H625, H628 (from Kenya Seed);SC627, TZ H538, UH615, Meru HB 623*	TXD 306 (SARO 5), Supa, TXD 88

Source: Project Inception Meeting 2015

The original plan was to collect Breeder Seed and, in their absence, use Foundation Seed for reference material. Accordingly, the project team responsible for the collection of reference material contacted the following entities.

5 It was anticipated that small samples of up-to 200 grains would be taken from each farmer, based on experience from Ethiopia

- Maize and rice breeders from the Directorate of Research and Development of the Ministry of Agriculture Food Security and Cooperatives (DRD-MAFSC)
- Seed companies (local, regional and international)
- The Tanzania Official Seed Certification Institute (TOSCI),
- National Plant Genetic Resources (NPGR),
- Local Government Authorities especially the District Agriculture, Irrigation and Cooperatives Officers (DAICOs) in study the areas,
- Umbrella organization of private seed sector, the Tanzania Seed Trade Association (TASTA), farmers among others.

Based on an introductory letter from the Permanent Secretary of the Ministry of Agriculture Food Security and Cooperatives (PS-MAFSC), the DAICOs generated a list of improved maize varieties grown in their respective districts. TOSCI also provide a list of maize varieties released for use in Tanzania. The Breeders thereafter visited sources of improved maize varieties from DRD-MAFSC institutes and seed companies to collect seed samples, in addition to TOSCI in Morogoro and the National Plant Genetic Resources Center (NPGRC) in Arusha as possible alternative sources of authentic samples.

Since the majority of the variety owners were unwilling to give out breeder seed, certified maize seed from the seed companies were collected instead. A total of 71 varieties were collected for the development of maize reference library. In the case of rice, reference materials were obtained for all the 15 varieties in the Official Varieties Release List from TOSCI. The materials were collected from centers mandated for Rice Improvement (ARI – KATRIN and Dakawa Agro-scientific Research Institute – CHOLLIMA) and Kilimanjaro Agriculture Training Center – KATC). In addition, three varieties developed by Dr. Sophia Kashenge under the National Performance Trials (NPT were included as well. Breeder seeds grain samples for 15 released varieties was obtained, packed in paper bags, labeled and sent to Mikocheni Laboratory for grinding and DNA extraction. Tables 6 and 7 provide a complete list of assembled reference materials.

Table 6: Assembled rice reference material

Variety *(year of release)*	Aroma	Agro-ecological system
SUPA India	Aromatic	Rain-fed lowland
TXD 85 *(2000)*	Non	Rain-fed lowland and irrigated
TXD 88 *(2000)*	Non	Rain-fed lowland and irrigated
TXD 306 *(2001)*	Semi aromatic	Rain-fed lowland and irrigated
Mwangaza (2004)	Non	Rain-fed lowland and irrigated
Kalalu / Kalalo (2004)	Non	Rain-fed lowland and irrigated
Tai (2012)	Non	Rain-fed lowland and irrigated
Komboka / IR 05N221 (2012)	Semi aromatic	Rain-fed lowland and irrigated
IR54	Non	Rain-fed lowland and irrigated
KATRIN / IET 2397	Non	Rain-fed lowland and irrigated
NERICA 1 (2009)	Aromatic	Upland rain-fed
NERICA 2 (2009)	Non	Upland rain-fed
NERICA 4(2009)	Non	Upland rain-fed
NERICA 7(2009)	Non	Upland rain-fed
WAB 450-12-2-BL1-V4(2009)	Non	Upland
Sato 1 Sato 6 Sato 9	Varieties under National Performance Trials (NPT)	

Source: Authors' compilation from Kashenge 2015

Table 7: List of assembled maize reference material

Varieties from Directorate of Research & Development – Ministry of Agriculture Food Security and Cooperatives	**Varieties from Private seed companies**	
1. TMV 2 Open pollinated 2. UH 615 Top cross hybrid 3. UH 6303Three-Way Cross Hybrid 4. UHS 5210 Modified Single Cross Hybrid, Less commercialized 5. UHS 5350. Three-Way Cross Hybrid, Less commercialized 6. UHS 401. Single Cross Hybrid, Newly released 7. Staha-ST ,Composite 8. Kito,Composite 9. TMV 1, Open Pollinated 10. Bora ,Composite 11. Cholima 1, F1 hybrid 12. Kilima-ST, Open pollinated 13. Lishe - H1, Three-Way Cross Hybrid, Second inbred parent in hybrid composition collected 14. Lishe – H2, Double-Top Cross Hybrid 15. Lishe – K1,Open pollinated 16. Situka – M1,Open pollinated 17. Situka 2, Open pollinated 18. Vumilia K1,Open pollinated 19. Selian MH07,Three-Way Cross Hybrid, Female single cross parent collected 20. Selian H208,Three-Way Cross Hybrid 21. Selian H308, Three-Way Cross Hybrid 22. UCA,Composite 23. WE 2109,Hybrid,Newly released variety 24. WE 2112, Hybrid, Newly released variety 25. WE 2113, Hybrid, Newly released variety 26. WE 3102, Hybrid, Newly released variety 27. WE 3113, Hybrid, Newly released variety 28. WE 3117, Hybrid, Newly released variety	TanSeed International	1. TANH 600, Hybrid 2. TAN 222, Open pollinated 3. TAN 250, Open pollinated 4. TAN 254, Open pollinated
	Meru Agro Tours and Consultants Co. Ltd	1. HB 513, Hybrid 2. HB 623,Hybrid 3. HB 515, Hybrid 4. MERU IR621,Hybrid,Newly released variety
	Kibo Seed Company Ltd	1. Kitale H614D, Hybrid 2. Kitale H625, Hybrid 3. Kitale H628, Hybrid 4. Kitale H513, Hybrid 5. Kitale H515, Hybrid 6. Kitale PH4, Hybrid 7. Kitale DH04, Hybrid 8. Katumani, Composite
	SATEC	1. TZH 536, Hybrid 2. TZH 538, Hybrid 3. TZM 523, Open pollinated
	PANNAR SEED (Tanzania) Ltd	1. PAN 691, Hybrid 2. PAN 67, Hybrid 3. PAN 4M-19, Hybrid 4. PAN 4M-21,Hybrid
	Monsanto Hybrid Seeds Co.	1. DKC 8053,Hybrid 2. DK 8031, Hybrid 3. DKC 90-89, Hybrid
	Pioneer Overseas Corporation	1. PHB 3253,Hybrid 2. PHB P2859W, Hybrid 3. PHB 30G19, Hybrid
	SeedCo Tanzania Ltd	1. SC 627, Hybrid 2. SC 403, Hybrid 3. SC 513,Hybrid 4. SC 719, Hybrid
	East Africa Seed Co Ltd	1. KH 600-15A, Hybrid
	Aminata Quality Seed	1. NATA H104, Hybrid 2. NATA H105, Hybrid 3. Lishe K6Q, Hybrid
	Bajuta International/ZamSeed	1. ZMS 402, Hybrid 2. ZMS 606, Hybrid
	FICA Seeds	1. Longe 4H, Open pollinated 2. Longe 6H, Three-way Hybrid, single cross female parent collected
	Iffa Seeds	1. Lubango, open pollinated newly released.
	Charoen PorkPhand (T) Ltd	1. CPP 201(TSW5), Hybrid

Source: Authors' compilation from Mushongi 2015

2.6 Sample processing and extraction of DNA

Upon receipt at MARI, maize test samples (cobs) were immediately dehusked and sun dried inside screen house at 33-35^{0}C for 3 days, then threshed and pooled to make composite samples. The threshed grain were dried again at 33-35^{0}C for 3 days to further lower moisture content prior to grinding into fine flour. From the bulk composite samples, 1kg each was sampled and packed into paper bags and stored as analytical samples in dry place (Figure 4).

Figure 4: Maize field samples being processed prior to DNA extraction

***Upper left- dehusking of maize; upper right -sun drying of cobs; lower left- threshed composite sample; and lower right - analytical sample.

Ten milligrams of maize samples were grinded into fine flour using magic bullets (Model NH 21PCS) and/or food blender (Model SHG296) at full speed for 20sec (Figure 5), shaken briefly to get a homogenous mixture and grinded again for another 20 seconds to obtain a fine flour. Maize reference samples were prewashed to clear them of dressing insecticides, dried briefly for 30 minutes and grinded. In the case of rice, both field and reference samples, were dehusked, winnowed, and grinded. Fine flour for both Maize and Rice were collected and stored. Two duplicates of 2g per samples were drawn from the 15mls tubes to create working samples.

Both MARI and the nearby International Institute for Tropical Agriculture (IITA) laboratories did not have a high density centrifuge, one of the critical equipment used for extracting DNA from flour. A decision was made to have technicians from MARI conduct the DNA extraction at the Bio-sciences for Eastern Africa (BecA) laboratories based at the International Livestock Research Institute (ILRI) Campus in Nairobi, Kenya (Figure 6).

Figure 5: Sample preparation at MARI biotechnology Laboratories

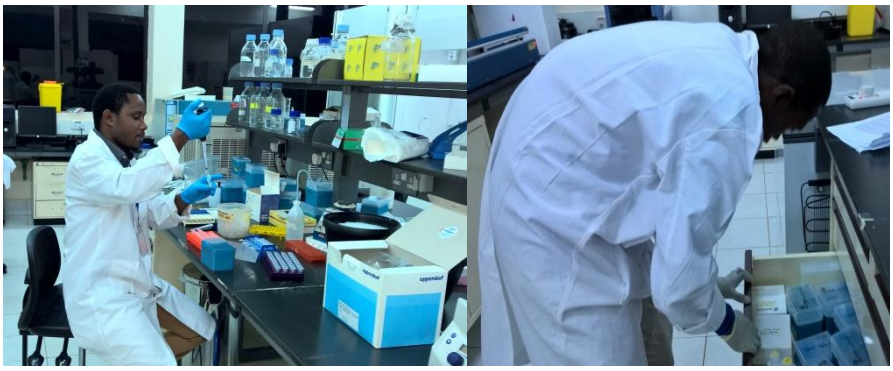

Figure 6: Technicians from MARI extracting DNA at BecA-ILRI lab in Nairobi, Kenya

One set of duplicate working samples were sent directly to BeCA-ILRI while the other one to DarT laboratories in Australia. Prior to the commencement of DNA extraction, the technicians from MARI attended a three day training session conducted by Dr. Andrzej Killian from Diversity Arrays laboratories in Nairobi, in June 2015. Thereafter, they spent all of September and part of October 2015 conducting

the actual extraction at BeCA in Nairobi. DNA extraction was done as per protocol for Bulk Seed DNA Extraction protocol (http//dev.diversity.arrays.com/protocol) with minor modifications.

The extracted DNA from reference materials and test samples was of good quality and no residue DNAse were seen following digestion with restriction enzyme, though few rice samples showed some degradation (Figure 7).

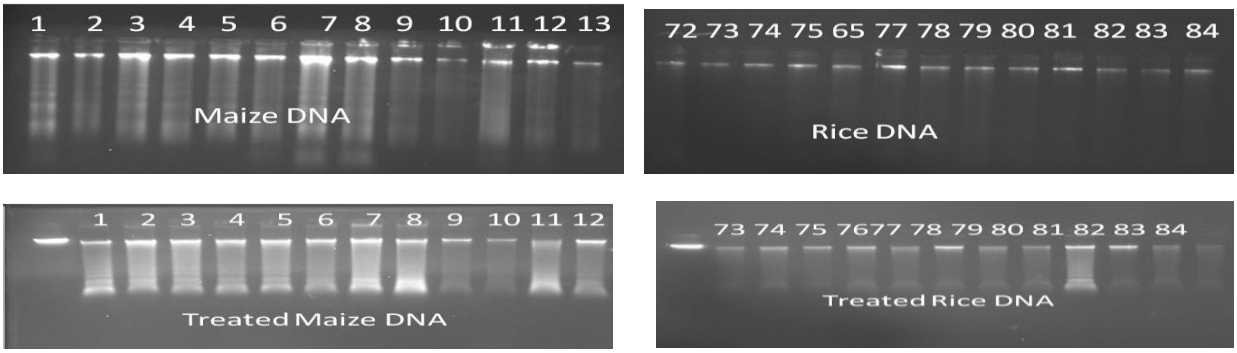

Figure 7: Agarose gel of the quality of DNA

The concentration of DNA was benchmarked with the reference materials using Nanodrop spectrophotometer (Thermo sceinntific, USA). The results showed appreciable purity ranges from 1.79 to 1.93 and 1.58 to 2.02 for Maize and Rice, respectively. Similarly, DNA concentration was also enough for downstream applications from both Maize and Rice reference samples (Table 8)

Table 8: DNA concentration of selected maize and rice reference samples

Sample ID	Crop	A260	A280	260/280	DNA Conc.(ng/µl)
7	Maize	2.216	1.183	1.87	110.8
8	Maize	1.797	0.964	1.86	89.9
11	Maize	1.087	0.594	1.83	54.3
15	Maize	1.395	0.739	1.89	69.8
18	Maize	1.297	0.722	1.8	64.9
23	Maize	1.058	0.573	1.84	52.9
30	Maize	1.253	0.651	1.93	62.7
68	Maize	1.004	0.539	1.86	50.2
70	Maize	1.082	0.582	1.86	54.1
71	Maize	1.064	0.562	1.89	53.2
73	Rice	0.445	0.224	1.99	22.3
75	Rice	0.426	0.214	1.99	21.3
88	Rice	0.513	0.261	1.96	25.6
89	Rice	0.513	0.254	2.02	25.6

3 Findings on adoption of improved varieties

3.1 Background to analysis

As indicated in the background section, the primary objective of the present study was to generate more accurate estimates of diffusion and adoption of improved rice and maize varieties using DNA analysis. Data were collected in the same areas as the original outcome panel survey. Based on socioeconomic data received from REPOA, 291 maize and 356 rice farmers from Iringa, Rukwa, Morogoro, Mbeya regions were interviewed in the present survey (Table 9). The 2015 survey information was used to analyze reported adoption / diffusion based on respondent recall.

Table 9: Distribution of maize and rice farmers in 2013 and present surveys

Crop/Region	Region/district	2013 panel survey	2015 survey
Maize	Iringa rural district	189	121
	Kilolo district	206	170
	Total	**395**	**291**
Rice	Morogoro	238	44
	Iringa	17	40
	Mbeya	290	184
	Rukwa	274	88
	Total	**819**	**356**

Source: Authors' compilation

In the case of DNA analysis, a reference library was developed from the submitted reference samples. The purity level of the Identified Primary Constituent (IPC) expressed as a percentage was the main criteria for variety identification (Table 13). Each test sample was analyzed and identified based on the IPC purity level. In the case of the reference samples for example, the submitted Hybrid 625 Kitale maize variety had 99.8% purity level while SUPA INDIA Rice variety had 100%. A test sample from one of the farm households had 93.8% purity level of Hybrid 625 Kitale, confirming that the farmer had correctly classified the genetic material in his plot. On the other hand, one of the test samples was identified as Pannar by the farmer but upon DNA fingerprinting, the material contained 62.1 % IPC of the Vumulia variety; this sample was therefore misclassified. Likewise two of the rice test samples (TXD306 and TXD85) were misclassified by the farmer (Table10). In sum, the DNA analysis only compared the test samples collected from the farmers' fields to the reference library. We adopt a relatively high IPC purity level of 70% as the minimum threshold for correctly identifying a variety in the present study. However, this threshold can be varied depending on the desired precision levels.

Table 10: A sample result of DNA analysis and classification of test materials

Crop	Reference samples			Test Samples		
	Identification by plant breeders	Identification from DNA analysis	% purity level of Identified Primary Constituent	Identification by farmer	Identification from DNA analysis	% purity level of Identified Primary Constituent
Maize	PANNAR 691	PANNAR 691	99.7	PANNAR	VUMILIA K-1	62.1
	H 625 KITALE	H625 KITALE	99.8	H 625 KITALE	H625 KITALE	93.8
	KATUMANI	KATUMANI	99.5	H628 KITALE	H625 KITALE	98.7
Rice	TXD 85	REF (5) TXD 306	99.0	TXD 306	SUPA INDIA	99.7
	TAI (IR 0334262)	REF (7) TAI (IR 0334262)	97.5	TXD 85	SUPA INDIA	99.9
	SUPA INDIA	REF 1 SUPA INDIA	100	SUPA INDIA	SUPA INDIA	98.1

Source: Authors' compilation

3.2 Diffusion of improved Maize varieties

3.2.1 Reported diffusion levels by Maize farmers

While screening the socio-economics dataset, a comparison was made for 2013 and 2015 figures on the use of improved maize seed in Iringa region. The results showed a general increase in the proportion of farmers who planted improved maize seed in the region from 38% in 2013 to about 46% in 2015[6]. Worthy of note, however, is that only 46% of the sample households reported planting improved maize varieties in 2015 (Figure 8 and Table 11).

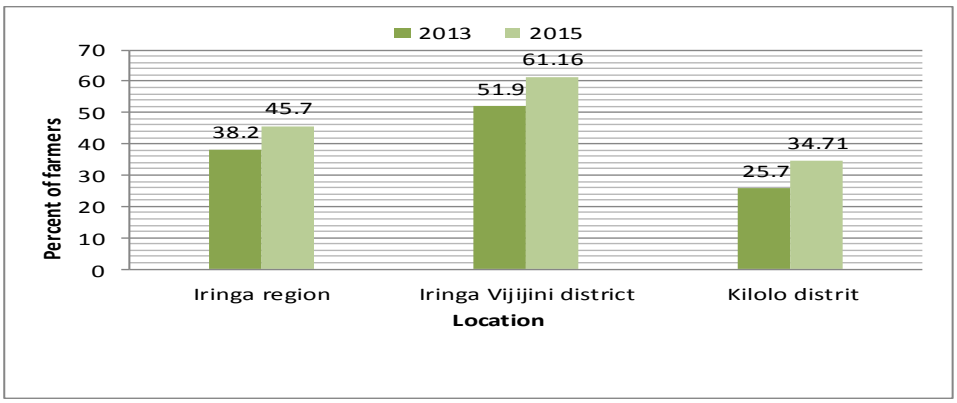

Figure 8: Self-reported use of improved maize varieties (2013 and 2015

Table 11: Maize farmers reporting use of improved maize varieties 2013 and 2015

	2013 non adopters	2013 adopters	2015 adopters	2015adopters
Iringa rural (vijijini) district	91	98	47	74
Kilolo district	153	53	111	59
Total for Iringa region	**244**	**151**	**158**	**133**

Source: Authors' compilation

Farmers were asked to state the criteria for classifying planting material as improved seed or otherwise. The majority (87%) who used improved varieties were confident that they had planted improved maize seed; only 12% were not sure whether the seed was improved or not. Of the surveyed farmers reporting use of improve d seeds, 74% believed that the maize seeds they planted in 2015 were improved because they were certified while about 13% reported that they purchased uncertified seed but from a reliable source (Figure 9).

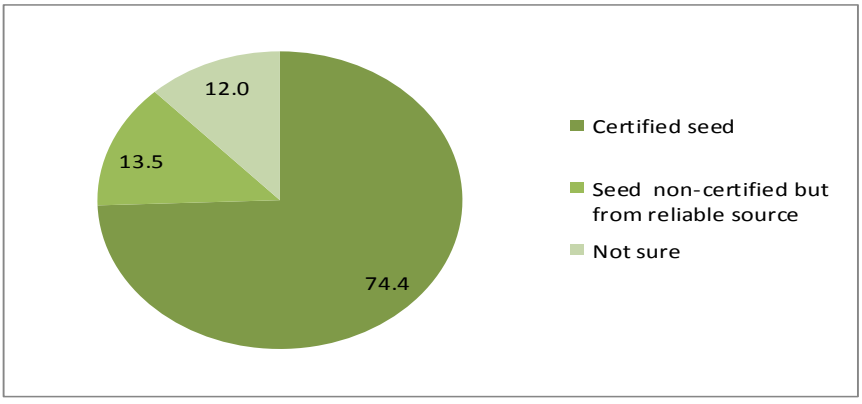

Figure 9: Criteria for identifying varieties by farmers (n=133)

[6] Given the differences in sample structure of the two surveys, these results should be treated with caution.

In addition to the classification of maize seeds as improved or non-improved, respondents were asked to identify the varieties by name (Figure 10). About 21% of the respondents reported growing the local variety (Kienyeji). A total of 31% of the respondents reported growing DK8053, Situka, Hybrid 625 Kitale and Kihehe as improved varieties with the percentage for each variety declining in the same order. The rest of the respondents reported growing a range of varieties that include the hybrid series (H614, H628, H626, H618, H698, H624), the DK series (*DK8051, Dk832*) and PAN series (*Pan413, Pan5M-35, Pan106, Pan 612, Pan 614*). The reported adoption levels of individual improved maize varieties were, however, low (less than 10% for most of the varieties). The most common improved varieties reported include *DK8051,* Hybrid625, pan691, KS 614, and H614 in that order (Figure 10).

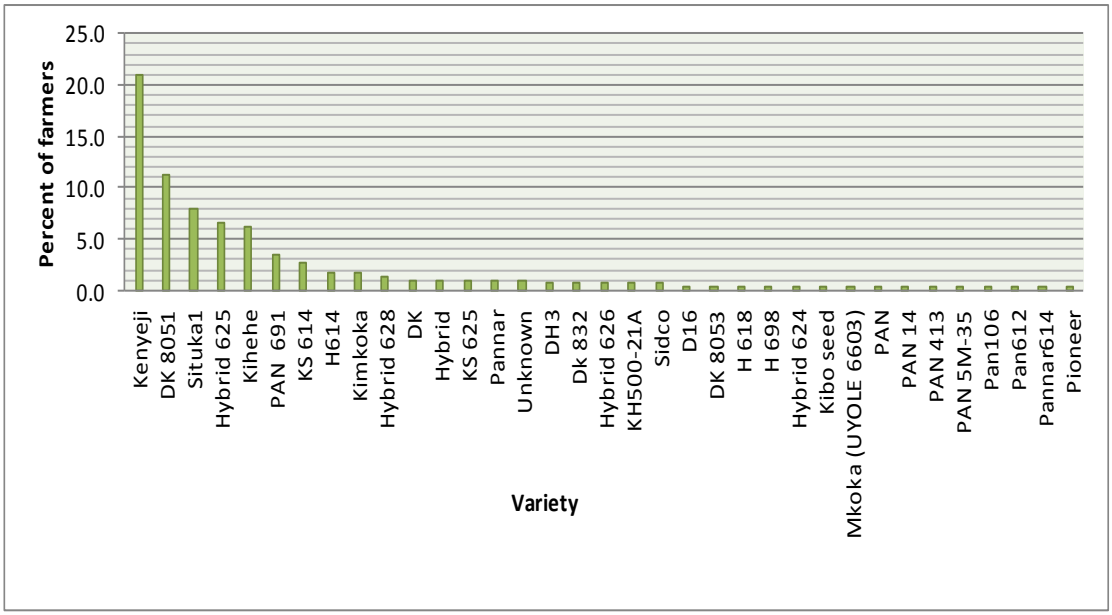

Figure 10: Reported use of improved maize varieties in Iringa (n=291)

During the inception workshop, the stakeholders identified the following varieties as the most common in Kiolo District; TMV1, Situka M1, Kilima, Staha, ICS4, Pannar, ***Situka1***, TANH600, TAN 250, Lishe K1, Meru Hb513, Tan 254, ***Pioneer***, UH6303, TMV1, Pannar 691, H614D, ***H625***, H628; SC627, TZ H538 and UH615. Out of this list, the respondents cited Situka 1 and HD 621 in addition to the pioneer series. These results would appear to suggest that varieties whose releases were supported by AGRA were not recognized. These varieties include SARIH 208 (SARIH06A16), SARIH 308 (SARIH06A20), UHS5210, UHS5350 and UHS 401.

The foregoing analysis by no means suggests the absence of these varieties in the farmers' fields. However, this may suggest that either the farmers are aware of them but the levels of adoption are way too low to be captured in the relatively small sample or the farmers may be more familiar with the popular nomenclature as opposed to the codes employed by professional breeders and seed specialist to identify the improved varieties.

3.2.2 Maize varietal diffusion estimates from DNA fingerprinting

Almost all of the maize samples submitted (96%) from Iringa region had 70% and above purity level of IPC (Table 12). In addition, the IPC purity level of the remaining 4% (13 samples) ranged from 60-69%.

Table 12: Purity of maize test samples by location

Region /district	70% and above IPC purity level		Less than 70% IPC purity level	
	No. of samples	%	No. of samples	%
Kilolo district (n=185)	174	94.1	11	5.9
Iringa rural district (n=138)	136	98.6	2	1.5
Iringa region (n=323)	310	95.98	13	4.01

Source: Authors' compilation from DNA data

Figure 11 presents the distribution of maize varieties grown by farmers, based on DNA fingerprinting data from samples with 70% and above IPC purity level. *Kitale* H625 is the most common improved variety (44% of the samples), followed by Kitale H628 (20%), H614D Kitale (16%), Pannar 691 (6%) and TMV-2 (4.5%). Notably, these findings confirm the expert opinion from breeders expressed during the project inception workshop.

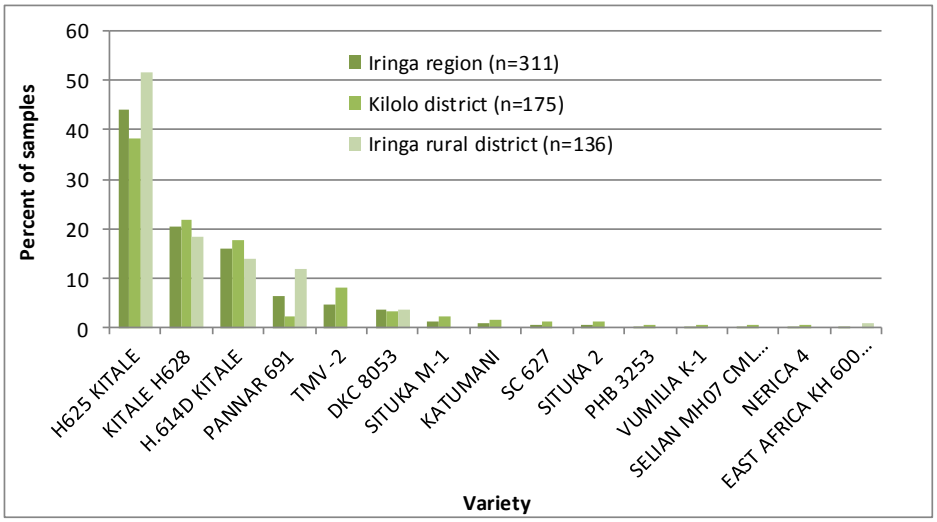

Figure 11: Diffusion levels of maize varieties based on DNA analysis

Comparing farmer reported adoption levels to those generated from DNA analysis reveals a high degree of variety misclassification by the respondents. Ignoring the 70% purity threshold, about 82% of the samples were not correctly identified by the farmers in the region (Figure 11).

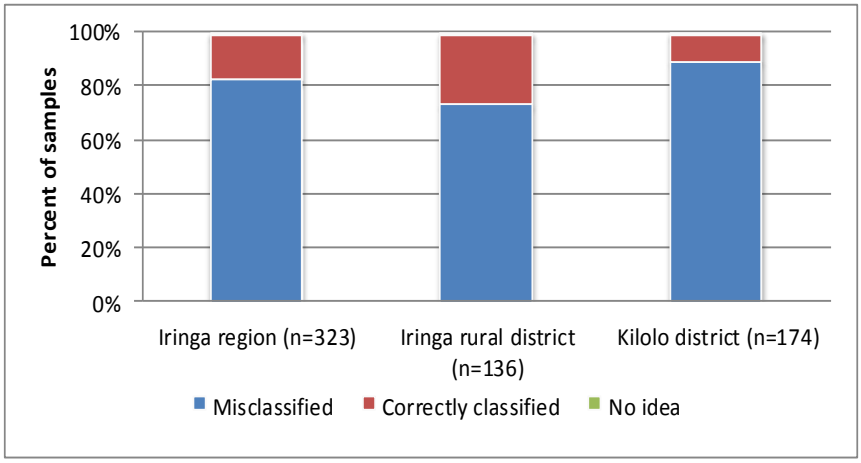

Figure: 12 Degree of misclassification of maize varieties by farmers

3.3 Diffusion of improved Rice varieties

3.3.1 Reported diffusion levels by Rice farmers

As was the case with maize, the initial screening of data compared adoption figures from 2013 outcome panel survey to those generated by the present survey. The results show a sharp decline in the number of farmers growing improved rice varieties in all the regions (Figure 12). This level of variability in reported adoption levels provides an even greater justification for conducting a DNA analysis. More importantly, only 5.9% of the surveyed households reported planting improved varieties in (Figure 13)..

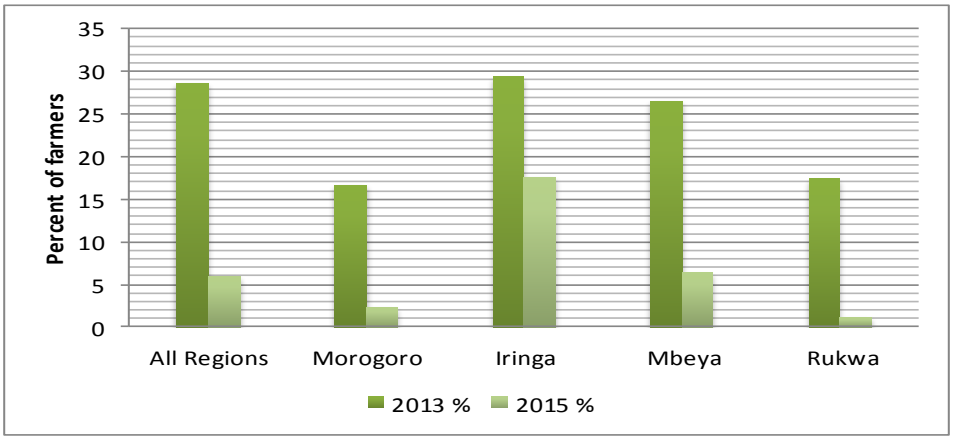

Figure 13: Reported changes in adoption of improved rice varieties 2013-2015[7]

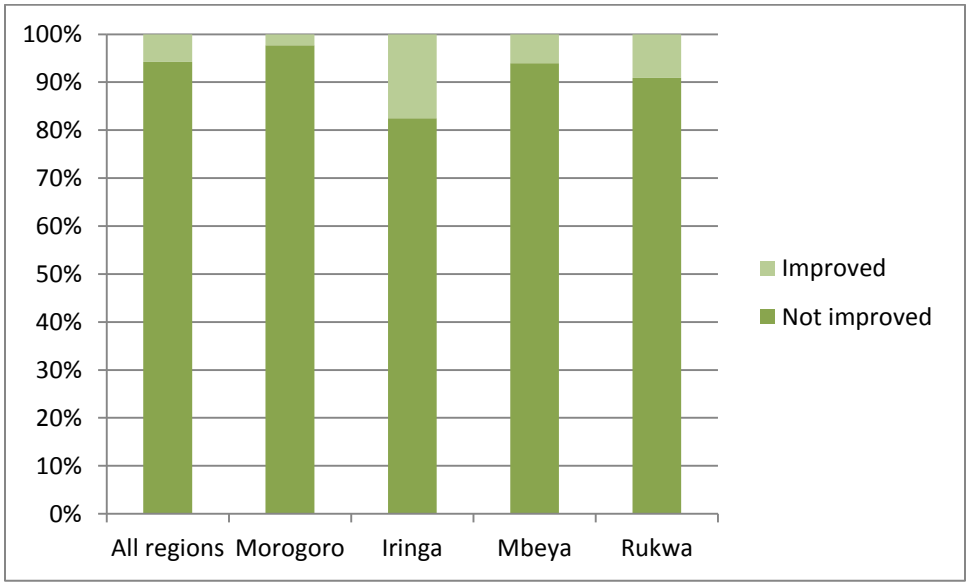

Figure 14: Reported use of improved rice varieties (n=328)

Figure 14 reports adoption levels of varieties named by farmers. The most popular varieties appear to be Zambia (26%), India Rangi Mkia (2%) and Faya / Faya dume (10%). Each of the remaining varieties was reported by less than 5% of the total sample (Figure 11). Worthy of note is the mode of identification using specific geography (India, Zambia, Kiombero, Mbeya); morphology / phenotype

[7] [7] Sample sizes are as follows: (a) in 2013: Morgoro (238), Iringa (17), Mbeya (290), Rukwa (274)
(b) sample size in 2015: Morgoro (44), Iringa (40), Mbeya (184), Rukwa (88)

(India rangi, Rangi Mbili , Mbegu fupi, Mbawambili) etc. In addition, it is possible that India, India Rangi Mkia and India Rangi could be making reference to the same variety.

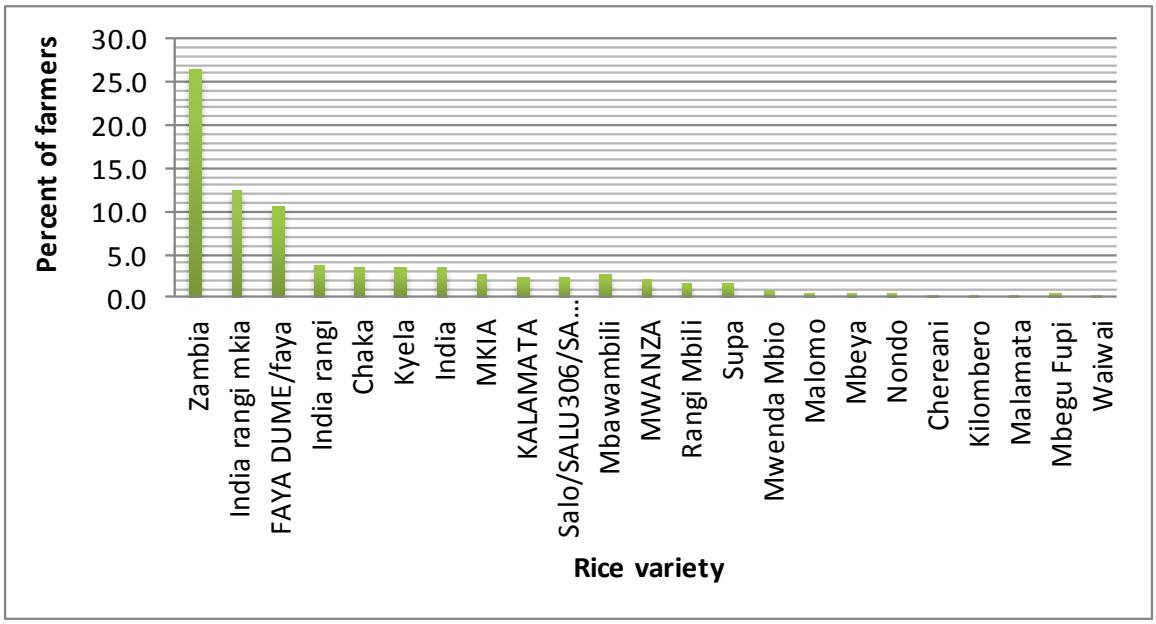

Figure 15: Farmer reported adoption of improved rice varieties (n=365)

3.3.2 Rice varietal diffusion estimates from DNA fingerprinting

A notable outcome from the rice DNA analysis is the high purity levels of the Identified Primary Constituent (IPC) for the entire set of submitted test samples; all of them were 99% and above. More importantly, 97% of the test samples were identified as SUPA India with the remaining 3% comprising TXD 306 and TXD 85(Table 13). Given the consumer preference for the aromatic SUPA India variety in Tanzania, the results are not altogether surprising.

Table: 13 Diffusion levels of Rice varieties based on DNA analysis

	Name of rice variety					
Region	SUPA INDIA		TXD 306		TXD 85	
	N	%	N	%	N	%
All regions (n=444)	430	96.85	12	2.7	2	0.45
Iringa (n=48)	46	95.83	2	4.17		
Mbeya (n=219)	200	91.32	9	4.11	1	0.46
Morogoro (n=72)	72	100				
Rukwa (n=103)	101	98.06	1	0.97	1	0.97

Source: Authors' compilation from DNA data

Not surprisingly, the majority of the farmers failed to correctly classify the rice varieties in their fields based on their genetic make-up. Only 23% of the rice samples collected in the four regions were correctly identified by the farmers. The level of misclassification was highest in Iringa region (about 87.5%) followed by Rukwa region (81.6%) then Mbeya (52%); and lowest in Morogoro at 37% (Figure 15).

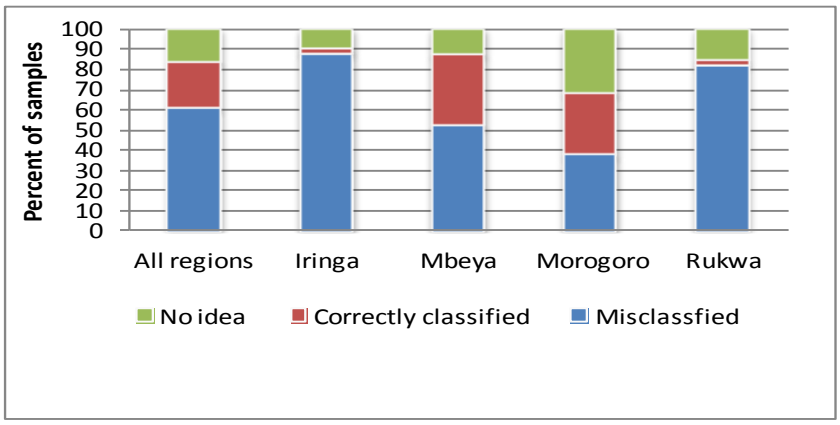

Figure: 16: Degree of misclassification of rice varieties by farmers

**N=444 Total sample, 48 Iringa, 219 Mbeya, 72 Morogoro 103 Rukwa

3.4 Discussion

The present study aimed to establish the status of adoption of improved maize and rice varieties in central and southern Tanzania. In the case of maize, Kitale hybrid series (H625, H628 and H614D) were the most predominant varieties. In the case of rice, the aromatic Supa India variety comprised closed to 97% of the test samples picked from the households. Owing in part to the limited geographic coverage and the small sample size, the present study did not pick out the rice and maize varieties whose releases were supported by AGRA. Nonetheless, prominent role of Agro-dealers as the primary source maize seeds, and could be attributed to AGRA's interventions over the last 8 years (Figure 17). In the case of rice farmers, although the cooperatives remain the predominant source of seed, the emerging role of agro-dealers is worthy of note (Figure 18).

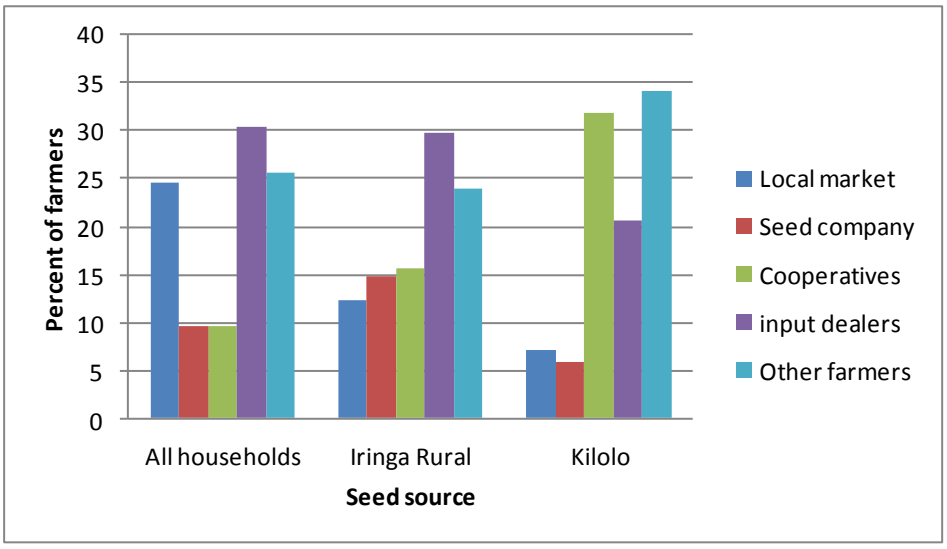

Figure 17: reported sources of maize seed

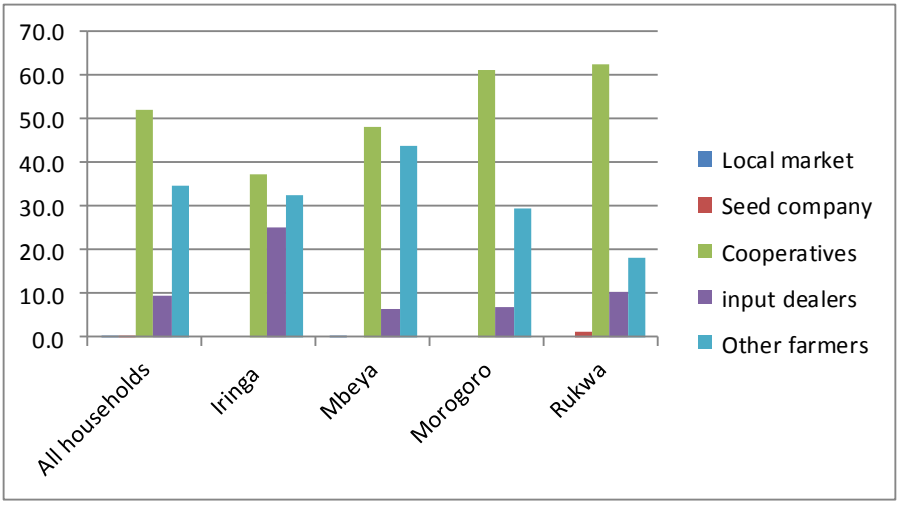

Figure 18: Reported sources of rice seed

Comparing the varietal identification results from DNA analysis to those from farmer recall revealed a high degree of misclassification. In the case of maize for example, varietal identification using DNA fingerprinting estimates diffusion levels of improved higher than the 46% reported by the survey respondent. In fact, one would argue that, all of the maize farmers in the sample survey were growing improved maize varieties based on the list of reference materials submitted. These results suggest that the genetic material that farmers refer to as local varieties are in fact improved and therefore, the diffusion levels of improved maize varieties could be higher than those reported in the literature. By the same token, only a small proportion of rice farmers reported planting improved varieties yet the submitted material was classified into 3 distinct improved varieties through genetic fingerprinting. The degree of misclassification of individual varieties by farmers were equally high, although less dramatic when compared to maize farmers.

These findings appear to confirm that the varietal adoption and diffusion estimates derived from farmer recall data are less accurate compared to those generated through DNA fingerprinting. More importantly, the actual varietal identification is highly prone to misclassification bias. The findings on varietal misclassification are not surprising given the possible motivational factors for small holder farmers to correctly identify varieties. Whilst breeders, seed companies and agro-dealers have direct interest in promoting specific varieties, small holder farmers could be more interested in the phenotypic attributes expressed through *inter alia;* yield gains, tolerance to stress and consumer preference. Accordingly, complex scientific codes such as PANAR 691 are typically lumped together as PANA by farmers. Likewise, SUPA INDIA rice variety is simply referred to as INDIA, INDIA RANGI or SUPA by farmers. Needless to say, the foregoing are “hypotheses” that require testing through a rigorous objective scientific enquiry.

Finally, the non-improved varieties as defined by farmers would appear to be different from the classical landraces. Most of what maize farmers classified as local (Kienyeji) could be matched with the reference material at varying degrees of purity.

4 Lessons and implications

4.1 Implications for AGRA and other agricultural development initiatives in Tanzania

The present study provides a snapshot of the status of diffusion and adoption of improved maize and rice varieties in the study areas. For AGRA, these results could provide baseline scenarios for framing results measurement questions during the implementation of the Tanzania Business Plan 2016-2020. It is also our hope that AGRA will lead the stakeholder process of interrogating these results. Starting with the dissemination workshop planned for early 2016, a set of second generation questions could be validated from the present pilot. Some of the questions include the following.

- Whether the preponderance of the Supa India variety is a manifestation of consumer demand. If this is the case, is the crop improvement programme and input delivery system organized to respond to this demand? Furthermore, are the strategies for improving rice farmers' access to remunerative output markets informed by this preference?
- Likewise, in the case of maize, what explains the popularity of the Kitale hybrid series compared to the other varieties?
- The findings reveal that farmer recall data could generate misleading results on status of diffusion and adoption of improved varieties. We therefore recommend that typical adoption studies should combine farmer recall information with DNA analysis. The challenge going forward is how to improve the efficiency of conducting a similar study at scale and whether there is scope for applying DNA fingerprinting to evaluate the performance of seed value chains.

Analysis of data from the second round of the AGRA Outcome Panel Survey could speak to speak to the second generation questions posed above. We also intend to conduct further analysis in order to identify the determinants of the observed misclassification and their implications for agricultural productivity enhancement programmes in Tanzania.

4.2 Feasibility of combining DNA fingerprinting and farm-household survey

The present study was premised on a well thought out conceptual and implementation framework. Building on the AGRA Outcome Panel Survey, combining data from DNA analysis with a rich set of socio-economics data from sample households going back to 2013 would generate more robust estimates of adoption and better insights on triggers and drivers of the same. Likewise, the choice of REPOA as an implementing partner aimed to address the typical logistical challenges associated with designing a new farm household survey from scratch; including sampling design, data collection and management. Borrowing from the Ethiopian experience, DRD was identified as the main implementing partner from Tanzania for the genomics component. By the same token, the Australian based DArT Laboratories with excellent credentials as a service provider for genomics analysis was responsible for the DNA Assay work. In addition to providing the overall technical backstopping, DArT also conducted the DNA fingerprinting analysis for the Ethiopian study.

4.2.1 Organizational and institutional capacity

The first primary learning question on the feasibility of conducting adoption studies using DNA fingerprinting and household sample surveys is framed around the capacity of in-country organizations, and the prevailing institutional environment to do this. The AGRA Country Office in Tanzania was the champion in the mobilization of stakeholders, especially the Government Officials and seed value chain actors to endorse the project. In the absence of this mobilization, obtaining the reference material and processing the samples for export would have been a herculean task. Being Beneficiaries of PASS grants and staff of DRD, both Dr. Sophia Kashenge and Dr. Arnold Mushongi agreed to collect the reference

materials at cost. Furthermore, the two research scientist delivered the reference material to MARI way before the agreed deadline with minimal supervision from the Consultant.

The AGRA Country Representative introduced the Consultant to Dr. Nduguru, the Director MARI who in-turn appointed Dr. Tairo, a molecular geneticist, to coordinate the sample processing and DNA extraction. Even though MARI lacked some critical equipment for DNA extraction, the team exhibited world class professionalism in discharging their obligations. They remained flexible, innovative and cheerful even when faced with unforeseen challenges; processing and delivering high quality DNA to DArT laboratories in Australia on time.

REPOA had the experience and the infrastructure to lead both the household socio-economics data and grain sample collection. The organization was contracted directly by AGRA and was expected to conduct a second round of the AGRA Outcome Panel Survey thereafter. After a seemingly protracted negotiation process with AGRA on the budget for grain sample and data collection[8], the subsequent enumerator training sessions provided earlier indications that REPOA had the requisite capacity. Failure to stick to the agreed protocol for grain sample collection and use of the ODK platform for household socio-economics data collection and management therefore came as a surprise. It is our opinion that REPOA needs to do the following; tweak its organizational capacity by embracing and mastering the use of electronic data capture technology; develop a deeper understanding of agricultural household sample surveys and; boost its data management and analytical capability.

Based on lessons from the present study, the present partnerships arrangements that AGRA has forged with the public sector, private seed companies and the civil society provides a good environment for conducting a similar study at scale. More importantly, MARI and the wider DRD network have the capacity to lead the genomics component of a similar study at scale, if they can be facilitated to acquire the High Density Centrifuge and some technical backstopping from DArT.

4.2.2 Improving operational efficiency and effectiveness

The second primary learning question revolves around the operational efficiency and effectiveness. One of the key lessons from the present study is how to structure partnership arrangements and workflow process informed by clear deliverables. At the outset, the demand for the final product was articulated through an inclusive process. The buy-in from the seed value chain actors and the Government of Tanzania was secured in good time. In the absence of typical financial incentives, opportunity for learning by doing at a pilot scale and the probability of scaling out the project thereafter was a major incentive for all the implementing partners.

The partnership arrangements for implementing the present pilot were also anchored on the principles of mutual accountability. Although the Consultant had a typical Principal Agent contractual relationship with AGRA, he forged a different relationship with the implementing partners. A more flexible and facilitative “Activity Implementation Support Agreement” was crafted between the Consultant, DRD breeders, MARI and DArT. Accordingly, a greater degree of mutual compliance to the targets and quality of deliverables was realized from all of the above partners.

From a technical feasibility standpoint, we pick out a number of lessons as well. From the genomics component, we need to refine the grain sampling protocol. A scaled up version of the present study could consider combining the crop-cuts for yield estimates approach that was used in Ethiopia with the

[8] The sample size was reduced in order to accommodate REPOA’s concerns

field sampling techniques used by molecular geneticists[9]. The primary aim would be to reduce the amount of grain delivered for DNA extraction. Also, the MARI laboratory does need additional equipment, especially the High Density Centrifuge, for DNA extraction[10]. If possible, the MARI laboratories should be equipped to conduct DNA profiling using SNP markers.

Keeping tabs on the big picture, the foregoing discussion highlights some of the necessary steps for delivering quality data and information at a reasonable cost-value for money. Coordination and technical support would appear to be the other critical piece. The Consultant assumed the coordination role with AGRA providing the institutional home for the present project. Combining coordination with technical backstopping functions and, being housed by AGRA in Tanzania reduced the coordination costs substantially. Furthermore, the project was perceived as neutral by all of the Tanzania based organizations, thereby circumventing the potential adverse effects of organizational rivalry. The coordination unit of any scaled up version of this pilot should have the necessary legitimacy and flexibility in partnership arrangements to ensure timely delivery of quality results. We are yet to compute the full cost of implementing the present project[11]. However, given the input from the project implementing partners, the actual cost could be higher than what was proposed in the original budget.

The original plan was to collect samples from all of the rice and maize growing households in the Outcome Panel Survey. We maintain that bundling sample collection for DNA analysis with household farm surveys is both efficient and effective[12]. The observed challenges from the present study could be addressed through a more detailed planning process, building the capacity of the service provider and if necessary, rigorous supervision.

[9] The crop cuts for yield estimates method entails harvesting grain from a small proportion of the field and using the harvest to estimate the yield.
[10] MARI is well equipped to extract and profile DNA using SSR markers as opposed to SNP markers
[11] This will be done after submission of all the invoices by the implementing partners
[12] In the case of Ethiopia, a similar study was super-imposed on the Annual Agricultural Sample Survey.