

A Case of Mistaken Identity? Measuring Rates of Improved Seed Adoption in Tanzania Using DNA Fingerprinting

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Abstract

Studies of improved seed adoption in developing countries are almost always based on household surveys and are premised on the assumption that farmers can accurately self-report their use of improved seed varieties. However, recent studies suggest that farmers' reports of seed varieties planted, or even whether the seed is local or improved, are sometimes inconsistent with the DNA fingerprinting results of those crops. We use household survey data from Tanzania to test the alignment between farmer-reported and DNA-identified maize seed types planted. In the sample, 70% of maize seed observations are correctly reported as local or improved, while 16% are type I errors (falsely reported as improved) and 14% are type II errors (falsely reported as local). Type I errors are more likely to have been sourced from other farmers, rather than formal channels. An analysis of input use,

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including seed, fertiliser, and labour allocations, reveals that farmers tend to treat improved maize differently, depending on whether they correctly perceive it as improved. This suggests that errors in farmers' seed type awareness may translate into suboptimal management practices. The average yield of seed that is correctly identified as improved is almost 700 kg per hectare greater than that of type I errors. This indicates that investments in farmers' access to information, seed labelling, and seed system oversight are needed to complement investments in seed variety development.

Keywords: *Agricultural systems; biotechnology; DNA fingerprinting; improved seed; maize; productivity analysis; Tanzania; technology adoption.*

JEL classifications: *O13, O33, Q12, Q16.*

1. Introduction

Crop yields in sub-Saharan Africa (SSA) have long lagged behind other parts of the world, including South and Southeast Asia and Latin America (Yu and Nin-Pratt, 2011; Otsuka and Muraoka, 2017). Growth in staple crop production in East Africa, including maize and rice, has generally stemmed from area expansion, rather than an increase in productivity (FAO, 2017, cited in Tegemeo, 2017). At the same time, adoption of improved seed varieties¹ in the region is relatively low. As of 2006/07, just 33% of the maize area in East Africa (and 18% in Tanzania) was cultivated with improved seed (Smale *et al.*, 2013). As improved seed varieties can be higher-yielding than local seed (or are designed to exhibit desirable traits, such as disease resistance or stress tolerance), the adoption of improved seed has the potential to enhance the farming outcomes and overall welfare of farm-households (Abate *et al.*, 2017; Alwang *et al.*, 2019).

For this reason, the literature is replete with studies of the effects of improved seed adoption on crop yield and farm-household welfare. By highlighting what is (or is not) effective, such studies capture the impacts of crop improvement research and guide what types of research might be prioritised (Walker and Alwang, 2015; Floro *et al.*, 2017). Authors overwhelmingly find that the adoption of improved seed varieties (or cuttings) and rapid varietal turnover can be welfare-enhancing in SSA (Kijima *et al.*, 2008; Kassie *et al.*, 2011; Asfaw *et al.*, 2012; Mathenge *et al.*, 2014; Shiferaw *et al.*, 2014; Khonje *et al.*, 2015; Zeng *et al.*, 2015; Manda *et al.*, 2017; Verkaart *et al.*, 2017; Jaleta *et al.*, 2018), although some reach a more nuanced conclusion (Alwang *et al.*, 2019). Many of these papers also probe the potential constraints to adoption of improved seed, ranging from challenges of access in a poorly developed seed system to a lack of information, liquidity constraints, or a lack of access to complementary inputs. Wainaina *et al.* (2017) further note the synergistic effects when improved seeds and agrochemical or management technologies are adopted simultaneously.

These studies almost always draw on household surveys and are premised on the assumption that farmers can accurately self-report their use of improved seed varieties

¹In this paper, 'improved seed' refers to seed that was originally developed in the research laboratory of a seed company or agricultural research centre and released to the public. 'Seed type' refers to the seed's status as being improved or local (landrace), and 'seed variety' refers to the specific variety of improved or local seed.

(Walker and Alwang, 2015; Maredia *et al.*, 2016; Abate *et al.*, 2017). However, recent evidence suggests that self-reports may be unreliable, as farmers do not always correctly identify the seed type they have used (Rabbi *et al.*, 2015; Maredia *et al.*, 2016; Floro *et al.*, 2017; Kosmowski *et al.*, 2018). Misidentification of seed type, especially if widespread, can potentially skew the detected rate of adoption of improved seed, an essential metric for agricultural research centres and development practitioners. Misidentification may also affect the results of studies regarding the farm-level effects of improved seed use. Depending on the research question being asked, this may lead to imprecise estimates, attenuation bias, or systematic bias if farmers' patterns of misidentification are not random (Hausman, 2001). Misidentification of seed type also has consequences for the farmers themselves if they allocate other inputs based on a false perception of what was planted, or if they make decisions regarding the adoption or dis-adoption of improved varieties based on faulty evidence.

There are several reasons why farmers may not correctly identify seed type, including both misinformation and mismeasurement. Farmers could have a poor understanding of what constitutes an 'improved' or 'modern' variety (Maredia *et al.*, 2016). Alternatively, where the formal seed system is characterised by weak oversight, supposedly improved seed may be adulterated before it is purchased from an agro-dealer or other formal seed sources (Bold *et al.*, 2017). At the time of purchase, farmers are unlikely to be able to visually confirm the seed quality or type (Spielman *et al.*, 2017). Quality-declared seed systems, in which smallholder farmers produce seed intended for sale within specific guidelines of quality assurance, may also be susceptible to quality lapses or ineffective oversight. Moreover, inexpensive seeds sourced through the informal system – including farmer-to-farmer seed exchanges – may be misrepresented, either because sellers have lost track of the seed variety being exchanged, or through wilful deception. As noted by Westengen *et al.* (2014), both local and farmer-recycled improved varieties are often sourced through these informal channels.

Farmers may also be unsure of the improved status of their seed due to the loss of genetic identity in the process of recycling (Morris *et al.*, 1999), or the 'creolization' of cross-pollinating crops (Westengen *et al.*, 2014). This occurs when improved varieties are hybridised with nearby local varieties, a phenomenon that may be either intentional (a result of farmer selection) or unintentional. Thus, farmers may feel confident of the improved status of newly purchased seed but could express uncertainty over how future generations of seed ought to be characterised. In addition, an improved variety that was released decades ago and has been passed along through farmer exchanges may be described as 'local', even though it was initially developed in a research laboratory (Kosmowski *et al.*, 2018). A final explanation for the incorrect identification of seed type could involve farmers planting multiple seed varieties within a single field as a risk management strategy (Spielman *et al.*, 2017), though a household survey might only collect information on the main variety used. At the level of seed variety, farmers may misidentify the specific variety if they are unfamiliar with variety names or if there is any inconsistency between the official versus locally adapted names (Floro *et al.*, 2017).

The misidentification of seed type could have several implications. Farmers make numerous management decisions around their perception of the seed type selected, including what field is used or how much fertiliser is applied. To the extent that the misidentification of seed type leads to suboptimal management decisions, it may result in lower yields or lower net farm returns. In addition, incorrectly identified seed type necessarily adds considerable 'noise' to the dataset on agricultural outcomes that each

farmer mentally builds over the course of their farming career. In this way, it could slow and distort the farmers' learning process. Finally, if a farmer intends to adopt an improved seed variety and sees poor outcomes only because the seed was misidentified, it could serve as a rationale for dis-adoption. This could hinder the agricultural growth that might be achieved with more widespread use of improved seeds.

In this paper, we examine how accurately farmers in Tanzania report on the type of maize seed they have cultivated. Farmer reports from a household survey are therefore compared with the results of crop sample deoxyribonucleic acid (DNA) analysis, which is considered to be the gold standard method for crop variety identification (Wossen *et al.*, 2019). Crop observations are categorised as 'true negative' (correctly reported as a local variety), 'true positive' (correctly reported as an improved variety), 'false negative' (type II error – incorrectly reported as local when the seed is determined, through DNA analysis, to be improved), or 'false positive' (type I error – incorrectly reported as improved when the DNA results indicate it is a local variety).

With this information, we quantify the rates of accurate reporting of seed types, as well as type I and type II errors (over- or under-reporting of improved seed use). We then examine the correlates of correct reporting of seed type, aiming to discern who is more likely to misreport and whether this seems to be a problem associated with the seed source, geography or farmer characteristics. To understand whether farmers seem to make different management decisions based on their perception of seed type, we also summarize the rates of input use and intensity across the four categories of seed. Although we cannot discern causality, we discuss whether the evidence is consistent with average yield differences across the four categories being attributed to variation in input use. Finally, we apply a yield function to estimate the yield premium associated with improved maize seed (a very common analysis) to determine whether the detected effect differs when we rely on farmer reports or DNA evidence.

We make several contributions to the literature on improved seed use in SSA. First, we expand on the thin evidence base regarding patterns of seed type misidentification in household surveys (Labarta *et al.*, 2015; Maredia *et al.*, 2016; Floro *et al.*, 2017; Kosmowski *et al.*, 2018; Wossen *et al.*, 2019). We therefore shed light on the generalisability of others' results (from Colombia, Bolivia, Ethiopia, Ghana, Zambia and Nigeria) and whether patterns vary by crop. Second, by incorporating DNA analysis directly into a large-scale household survey, we offer insight beyond the smaller pilot studies that have been conducted, and further produce some practical lessons for future studies of a similar nature. Third, we extend the scope of existing studies by characterising seed prices and input intensities across observations that are correctly or falsely identified as local or improved. This provides insight into how farmers perceive their seed and whether farmers might be misallocating inputs when they miscategorise seed type.

The remainder of the paper is organised as follows: Section 2 details the methods available to gauge seed variety adoption, along with the rates of correct reporting found in other studies that incorporate DNA analysis. Sections 3 and 4 introduce the data and methods used in the analysis. Results are provided in section 5, with robustness checks presented in section 6. A discussion follows in section 7.

2. Background on DNA Fingerprinting for Seed Varietal Identification

Several methods are available to measure seed variety adoption. At the population level, expert elicitation and seed sales inquiries are used to gauge the diffusion of seed

types or varieties in a country or region (Walker and Alwang, 2015; Abate *et al.*, 2017). At the level of households or crop observations, household surveys with farmer reports are by far the most common method used to identify seed types and varieties (e.g. Kassie *et al.*, 2011; Shiferaw *et al.*, 2014; Alwang *et al.*, 2019). Surveys vary in the level of detail collected, as they may ask for the seed type only or may also ask for seed variety. Household surveys may also collect information on plant descriptors, or such surveys can involve the use of visual aids to assist farmers in variety identification (Maredia *et al.*, 2016; Kosmowski *et al.*, 2018). Another possible (though uncommon) augmentation of household surveys includes taking photographs in farmers' fields to facilitate expert identification (Maredia *et al.*, 2016).

The declining price of DNA fingerprinting and the application of this technology in surveys presents an opportunity to assess the accuracy of the more common methods of crop variety identification (Rabbi *et al.*, 2015; Kosmowski *et al.*, 2018). Several recent studies have endeavoured to do so, eliciting farmer reports of crop varieties in the usual manner, while crop samples are collected from farmers' fields and analysed in a laboratory.

Benchmarked against the results of genotyping, some studies find under-reporting of adoption of improved crop cultivars. In Zambia, Maredia *et al.* (2016) find that bean farmers under-report their use of improved seed, with self-reports ranging from 4% to 13%, while DNA results find this rate to be 16%. In Ethiopia, Tizale *et al.* (2015) measure rates of improved wheat adoption of 62% (based on farmer reports), as compared to 96% (based on genetic analysis). For maize, these figures are 56% and 61%. In Bolivia, Labarta *et al.* (2015) find the adoption rate of improved rice to be 42% with self-reports or 45% with DNA analysis. However, approximately 12% of farmer reports are either type I or type II errors. In Nigeria, Wossen *et al.* (2019) find that 54% of households report growing improved cassava, though DNA analysis indicates that the true adoption rate is 69%.

Other studies find over-reporting. In Colombia, Floro *et al.* (2017) analyse the cultivation of improved cassava varieties and find that farmers are likely to over-report their use of improved varieties. Specifically, while DNA evidence indicates that 9% of households in their study grew improved cassava, 17% of farmers self-identified as growing an improved variety. In a study of improved sweet potato adoption in Ethiopia, Kosmowski *et al.* (2018) find that the rates of type I and type II errors balance out, with 20% of farmers incorrectly referring to a local variety as being improved, and 19% incorrectly reporting an improved variety as being local. With the exception of Tizale *et al.* (2015) and Wossen *et al.* (2019), all studies summarised here were conducted on a pilot scale.

3. Data

This study draws from the Varietal Monitoring for Realized Productivity and Value in Tanzania survey, implemented by the Tegemeo Institute for Agricultural Policy and Development (Tegemeo Institute, 2017),² in partnership with Sokoine University of Agriculture (SUA). Household survey weights were generated with input from the Tanzania National Bureau of Statistics (NBS), although these are only used in a

²The Tegemeo Institute for Agricultural Policy and Development is a policy research institute under the Division of Research and Extension of Egerton University.

robustness check. Prior to the data collection, a reference library for maize varieties, including both landraces and improved varieties, was established by the Mikocheni Agricultural Research Institute (MARI) under a pilot project funded by the Alliance for a Green Revolution in Africa (AGRA). As part of the current study, genomic data were extracted by MARI and then sequenced by Diversity Arrays Technologies (DArT), based in Australia.

The survey was conducted from October 2016–January 2017, with the household sample selected in three stages. First, in each region, three districts were selected in which a focus crop (e.g. maize) was dominant. Next, clusters (villages) were selected using probability proportional to size. A household listing exercise was then conducted in the selected clusters, and 15 households were drawn randomly in each cluster for inclusion in the survey.

The crop samples for this study were collected from survey households in June–August 2016, several months before the full household survey was conducted. Because the crop samples were generally collected in the Northern zone before harvest, though were not as well-timed in other zones, this study focuses on the three regions that comprise the Northern zone: Manyara, Arusha and Kilimanjaro (Figure A1 in the online Appendix). Furthermore, because maize is the most common crop in these regions, this study focuses only on maize.³ In total, the survey includes 1,548 households in the Northern zone, of whom 1,195 grew maize in the 2015/16 main season. The survey captured detailed information on crop production over the previous year, including crop choice, application of inputs and harvest quantities. Notably, farmers reported the seed type (local, hybrid, open-pollinated variety (OPV), or a combination) for each crop in each field. Note that the survey questionnaire defined recycled seed as ‘one that a farmer has saved from own/previous harvest, and the original material from which the first harvest was obtained was a new seed of improved/hybrid variety’. It follows that local seed was, by definition, *never* derived from a released variety. For all seeds that were reported as being improved, the farmers further specified the seed variety.

All households in the Northern zone were targeted for crop sampling, and samples were taken directly from the field toward the end of the main growing season. For this reason, samples could not be taken if the harvest was already complete at the time of sampling. If a household grew maize on more than one field, the respondent identified the field most important to the household’s food security (the ‘primary’ field), and this was selected for sampling. Thus, the data are not intended to be representative of all maize grown in the study site, and survey weights are not used in our main analysis. Samples were collected from 845 households or 68% of maize-growing households. There are 20 observations for which seed variety could not be identified through genotyping, and an additional four observations lack information on realised harvests. These have been dropped from the analysis, leaving a matched sample size of 821.

Crop samples were analysed by DArT, where the genetic match for seed variety and the level of purity were identified. The DNA material was compared with a reference library of maize varieties, using single nucleotide polymorphism (SNP) molecular markers, and an observation is considered to be an improved variety if the identified primary constituent (IPC) matches that of a released variety at a level of at least 70%.

³Across Tanzania in 2014/15, maize accounted for approximately 42% of the cropped area and was produced on 3.4 million farms (NBS, 2016).

The DNA analysis includes identification of the specific local seed variety, although, in the household survey, seeds reported as being local are not specified at the variety level. The year of release of various seed varieties found in the dataset was gathered from the Tanzania Official Seed Certification Institute (TOSCI 2017) and the Diffusion and Impact of Improved Varieties in Africa (DIIVA) project (ASTI 2017).

4. Method

As detailed above, crop samples are categorized as being either ‘true negative’, ‘true positive’, ‘false negative’ (type II error), or ‘false positive’ (type I error) by comparing farmer reports and the results of genetic analysis. Maize that is reported as improved and was recycled is considered to be improved in the main analysis, although we conduct a robustness check to explore whether results are sensitive to this decision. Hybrid and OPVs are pooled together as ‘improved’ because OPVs are quite marginal in the study site, with just 31 (farmer-reported) or 35 (DNA-determined) OPV observations. The four seed categories are then analysed descriptively to determine how they vary in terms of seed source, seed price, input intensities and realised yields.

To explore the correlates of a farmer correctly reporting a seed type as being improved or local, the following equation is used:

$$\text{Correct_ID}_i = \alpha + \mathbf{H}'_i \delta + \mathbf{I}'_i \omega + \varepsilon_i \quad (1)$$

where Correct_ID_i is an indicator of whether maize observation i is correctly classified by a farmer, \mathbf{H}_i is a vector of social and demographic characteristics that might influence one’s knowledge of seed type, \mathbf{I}_i is a vector of proxies for access to information and engagement with markets, and ε_i is a stochastic error term. Recall that each household has one sample, such that i indexes both the maize observation and the household. Because the correlates of correct identification may differ across type I and type II errors, this model is run separately for observations that are reported by farmers as being either local or improved.

Linear regressions are used to identify the correlates of maize yield, with the key regressor being either the self-reported improved seed status or the status determined through DNA analysis. The equation is:

$$Y_{ijr} = \alpha + \pi [\text{Improved}_{ijr}] + \mathbf{M}'_{ijr} \sigma + \mathbf{X}'_{jr} \delta + \mathbf{H}'_{ir} \theta + \gamma_r + \varepsilon_{ijr} \quad (2)$$

where Y_{ijr} is the yield (kg/ha) of crop observation i on field j in region r , Improved_{ijr} is the improved seed status (1 = improved, 0 = local), \mathbf{M}_{ijr} is a vector of input intensities for crop observation i , \mathbf{X}_{jr} is a vector of characteristics of the field, \mathbf{H}_{ir} is a vector of household and farm characteristics, and γ_r is a region fixed effect. In light of the two-stage sampling strategy, standard errors are clustered at the village level.⁴

A linear regression is also used to determine whether correct reporting of improved status is a statistically significant correlate of yield, after controlling for other inputs and field characteristics. The equation is:

⁴In regression analyses, standard errors are clustered at village level to account for potential correlation of seed channels or yield-related shocks (weather or pests) within the same village. The 821 maize plots in our sample were found across 78 villages, with an average of 10.5 observations per village. Results tend to be consistent when standard errors are clustered at a higher level or are not clustered.

$$Y_{ijr} = \alpha + \mathbf{Cat}'_{ijr}\boldsymbol{\beta} + \mathbf{M}'_{ijr}\boldsymbol{\sigma} + \mathbf{X}'_{jr}\boldsymbol{\delta} + \mathbf{H}'_{ir}\boldsymbol{\theta} + \gamma_r + \varepsilon_{ijr} \quad (3)$$

where Y_{ijr} is yield and \mathbf{Cat}_{ijr} is a vector of categories, including true positive, false negative, or false positive (with true negative as the base group). Once we have controlled for input intensities and other management decisions, we would expect yields to be determined only by the seed's actual (not perceived) status as local or improved. If the yields of false negative or false positive seeds do not conform to this expectation, it may imply that the seed in this category differs systematically from other local or improved seed.

5. Results

Table 1 provides the rates at which seed type is correctly reported in the household survey. 73% of sampled maize observations are characterised as being improved, while the results of the DNA analysis of these same maize observations reveal that 71% are improved. (Among all 1,185 primary maize fields, including those that were not sampled and are therefore excluded from this analysis, households report that 71% are improved. Moreover, among all 1,565 maize fields, including those that were not listed as being the primary field, households report that 72% are improved.)

Overall, 72% of observations are correctly reported by farmers as being local or improved. This leaves a considerable portion of observations that are miscategorised as either false positives (type I errors) or false negatives (type II errors). It is somewhat more common for an observation to be falsely categorised by farmers as improved: among observations that are truly improved (according to the DNA analysis), 81% are correctly reported as improved, and among those that are truly local, 52% are correctly reported as such. At this coarse level of categorisation, it seems that maize farmers are more likely to believe that they have sown improved seeds.

For seed that was classified by the farmer as being improved, the survey also captured details on the seed source and history. This information provides at least a partial view of why type I errors may be so common. Table 2 shows that it is common (at 81%) for seed that is sourced through relatively formal channels to be correctly reported as improved. At the same time, it is more common for seed that is sourced from other farmers, or seed that had been recycled by the respondent, to be falsely reported as improved (a type I error). Specifically, 31% of seed observations that were

Table 1
Rates of local/improved maize seed identification

	% seed
Reported rate of improved seed use	72.7%
True rate of improved seed use (DNA-identified)	70.7%
Rate at which seed is correctly identified as local or improved	71.6%
True negative	14.1%
False negative (type II error)	13.2%
False positive (type I error)	15.2%
True positive	57.5%
Observations	821

Table 2
Seed sources for farmer-reported improved maize

Source of seed	Source of seed (all)	% improved from this source (DNA results)
Agro-dealer	64.1%	80.9%
Local shop	16.3%	82.5%
Recycled	10.4%	69.4%
Ministry of Agriculture	6.0%	77.8%
Other farmers	2.4%	56.3%
Cooperatives	0.5%	66.7%
Community-based organisation	0.3%	100.0%
Observations	596	
All formal sources (Agro-dealer, local shop, ministry of agriculture, cooperatives, community-based organisation)	87.3%	81.0%
Test	<i>P</i> -value (two-sample <i>t</i> -test)	
% improved formal = % improved other farmers	0.027	
% improved formal = % improved recycled	0.032	

Note: Information is missing for one observation.

characterised as improved and had been recycled were determined, through DNA analysis, to be local, which implies that farmers may lose track of seed type in the process of recycling. It also suggests that seed type uncertainty may stem from ambiguities in the informal seed system, in which farmers (perhaps unintentionally) mischaracterise the seed being sold or exchanged amongst themselves.

An analysis of the rate of correct seed type reporting, broken down by district, also sheds light on the extent to which type I and type II errors have a geographic basis (see Figure A2 in the online Appendix). Across districts, the share of farmers who report that they had planted improved seed that were correct (with results confirmed by DNA analysis) ranges from 57% in Same district to 85% in Babati and Babati Mjini districts. For districts with low rates of correct reporting of improved seed types, it is possible that the seed acquired from a major seed supplier in the district town had been adulterated. Along these lines, seed sellers in districts with less competition in the seed market may be more willing to cheat their customers if they face a lower risk of losing a customer in the following season. Among farmers who reported planting a local seed type, the rate at which they were correct ranges from 38% to 75%. This heterogeneity over space might be explained by geographically distinct rates of seed recycling if farmers tend to lose track of their seed type during the recycling process, or by localised preferences for seed varieties that are commonly misidentified.

We next use regression analysis to explore the household-level correlates of correctly identifying the seed type. Summary statistics of most variables used in the analysis can be found in Table A1 in the online Appendix. Several demographic variables may be correlated with the farmer's likelihood of correctly reporting seed type: 72% of field managers completed primary school, and 18% of field managers (the primary decision maker for cultivation) are women. Several other variables can serve as

Table 3
Correlates of correct identification of seed type (probit models)

	(1)	(2)	(3)	(4)
	1 = Farmer's report is correct			
	Local seed (farmer reports)		Improved seed (farmer reports)	
1 = Field manager is a woman	-0.12 (0.13)	-0.14 (0.11)	-0.06 (0.20)	-0.04 (0.45)
Age of field manager	0.00 (0.44)	0.00 (0.59)	-0.00 (0.29)	-0.00 (0.58)
1 = Field manager completed primary school	-0.00 (0.95)	-0.03 (0.64)	0.04 (0.36)	0.04 (0.28)
Value of household assets (log, shillings)	-0.03* (0.09)	-0.04** (0.04)	0.00 (0.88)	0.00 (0.89)
1 = HH accessed extension services		-0.01 (0.90)		-0.07 (0.18)
1 = HH is member of farmer group		0.17 (0.31)		0.03 (0.75)
Distance to nearest hybrid maize seed seller (km)		-0.01 (0.19)		0.00 (0.39)
1 = HH used inorganic fertiliser		0.03 (0.74)		-0.03 (0.53)
1 = HH hired some agricultural labour		0.05 (0.54)		0.01 (0.69)
Proportion crop value produced that was sold		-0.09 (0.46)		0.17** (0.03)
Observations	224	224	597	597

Note: Average partial effects; *P*-values in parentheses; standard errors clustered at village level; ****P* < 0.01, ***P* < 0.05, **P* < 0.1.

proxies for access to agricultural information, including whether the household accessed agricultural extension services (14%) or is a member of a farmers' group (3%).

The correlates of correctly identifying the seed type are identified with equation (1) and presented in Table 3.⁵ Column (1) is limited to maize observations that are reported as being local, with social and demographic factors included as explanatory variables. While the coefficient on a female field manager is negative, this is not statistically significant at the 10% significance level (*P* = 0.13). Interestingly, wealthier households are less likely to correctly identify local seed. It is possible that type II errors (reported as local when the DNA results indicate they are improved) are related to recycling, with farmers losing track of the seed type over time (or regarding seed as 'not improved' and therefore 'local' when it has been recycled over several seasons). Among farmers reporting local seed, wealthier households may be more likely than others to have, at one point, cultivated newly purchased improved seed. In column (2), variables related to access to information and engagement with input and output markets are included.

⁵Results of this analysis are extremely consistent when using linear models.

Contrary to our expectations, there are few correlations between observed factors and the likelihood of being correct about local seed type. In columns (3) and (4), this exercise is repeated for seed that is reported as being improved. Farmers are more likely to correctly identify improved seed if they are more commercially oriented (selling a greater share of crop value), which may be a proxy for being a more market-savvy farmer. However, the lack of correlation evident with other variables suggests that type I errors are not tied tightly to farmer characteristics or access to information. Instead, these errors may be largely unavoidable from the perspective of the farmer (and may, therefore, warrant a policy or regulatory response).

The specific seed variety was only asked in the household survey for seed that was reported as improved, and so the rate of correct varietal identification can only be estimated for those seeds which are true positive (Table A2 in the online Appendix). In this group, 24% of observations are correctly reported by farmers. This rate is higher for seed that was purchased this year (27%), as compared with seed that was not (6%), and this could reflect the genetic drift or contamination that occurs during seed recycling (Morris *et al.*, 1999), or farmers' faulty memory of long-ago purchases. We wondered whether farmers might more accurately report the seed variety for those varieties that were released long ago and are therefore better known in Tanzania. However, there is no evident correlation between the year of seed variety release and the rate at which seed varieties were correctly reported (Figure A3 in the online Appendix). Although it is possible that type II errors might stem from the seed varieties being released earlier (and therefore classified as 'local' in the minds of farmers, as they have been part of the local agricultural landscape for longer), the average years since release is around 14 years for both false negative and true positive seed, with no statistically significant difference in the average values.

Table 4 displays the characteristics of maize observations across the four categories. The columns on the right display the results of a Tukey test for the equality of mean values across different columns. A Tukey test is preferred to a *t*-test to account for the number of subgroups being compared, although it should be noted that it is more conservative than a standard two-sample *t*-test. The average area under maize ranges from 0.52 to 0.63 hectares (ha) across categories. It is noteworthy that costs do not differ significantly between true positive and false positive seed. Misrepresented seed is being sold for the same average price (roughly 5,400 TSh/kg) as genuinely improved seed. In terms of seeding rate, local seed tends to be sown at a higher seeding density than improved seed (roughly 35 kg/ha, compared with 27 kg/ha), and seed that is falsely reported as being improved is sown at the same rate as true positive seed, while false negative seed (reported as local but DNA-identified as improved) is sown at roughly the same rate as true negative seed. This suggests that, if the optimal seeding rate varies across seed type, farmers' misperceptions of seed type may be driving them to apply inputs in a suboptimal manner.

Farmers are more likely to apply fertiliser to false positive seed than true negative seed (at 32% vs. 18%). Fertiliser is also applied with greater intensity on true-positive seed, as compared with the false negative seed (roughly 36 kg/ha versus 19 kg/ha, on average). It, therefore, seems that farmers apply more fertiliser when they perceive – correctly or incorrectly – that they have sown an improved variety, and this again suggests that farmers' self-report errors steer them to use inputs suboptimally. Interestingly, there is a significant difference in the rate of organic manure application to true negative and false negative seed (at 11% vs. 26%). This is the only evidence suggesting that farmers who falsely report improved seed as 'local' may actually harbour

Table 4
Maize seed identification, seed characteristics, and input use

	(1)		(2)		(3)		(4)		Tests						
	True negative (TN)	SD	False negative (FN)	Mean	SD	False positive (FP)	Mean	SD	True positive (TP)	Mean	SD	TN = FN 1 = 2	TP = FP 4 = 3	TN = FN 1 = 3	TP = FN 4 = 2
Area under crop (ha, field size/ number of crops)	0.52	0.56	0.57	0.57	0.53	0.57	0.40	0.63	0.94						
Years since improved seed variety was released	N/A	-	14.4	9.0	N/A	-	14.3	8.5	-						
Seed cost (TSh/kg)	51.0	237	394	1,156	4,570	2,666	4,927	2,368	***						****
Seed cost (TSh/kg) if $\neq 0$	Few obs.	-	2,024	1,920	5,492	1,854	5,401	1,892	-						****
Seed rate (kg/ha under crop)	36.7	21.8	33.2	20.3	24.8	14.9	28.1	14.5	***						***
1 = Use inorganic fertiliser	0.18	0.39	0.19	0.39	0.32	0.47	0.24	0.43	*						*
Fertiliser rate (kg/ha)	19.4	48.7	19.3	52.2	38.2	65.3	35.9	74.9							*
Fertiliser rate (kg/ha) if $\neq 0$	107.3	61.1	104.2	77.5	119.5	60.0	147.2	81.4	*						*
1 = Use organic manure	0.11	0.32	0.26	0.44	0.27	0.45	0.34	0.47							
Manure rate (kg/ha)	140.8	440.4	278.2	562.8	288.2	566.1	377.1	624.7							
Manure rate (kg/ha) if $\neq 0$	Few obs.	-	1,073.2	608.6	1,059.5	601.7	1,119.5	571.7	-						
Labour rate (days/ha)	126.3	106.1	112.2	92.0	103.9	80.2	118.1	89.7							
Observations	116	108	125				472								

Note: TSh = Tanzanian shillings.

Tukey test for equality of mean values.

For clarity of presentation, only the most relevant cross-category comparisons are shown, and the level of statistical significance is denoted: *** $P < 0.01$, ** $P < 0.05$, * $P < 0.1$.

Table 5
Maize seed identification and yields

	Yield (kg/ha)		Tests*	P
	Mean	SD		
True negative (TN)	1,596.5	1,411.7	TN = FN	0.462
False negative (FN, type II error)	1,291.9	1,197.6	TP = FP	0.000
False positive (FP, type I error)	1,621.4	1,375.8	TN = FP	1.000
True positive (TP)	2,309.1	1,704.7	TP = FN	0.000
True classification				
Local	1,609.4	1,390.3	Improved = local	0.000
Improved	2,119.6	1,669.3		
Self-reported classification				
Local	1,449.6	1,318.8	Improved = local	0.000
Improved	2,164.5	1,664.1		

Note: In top panel, this is a Tukey test for equality of mean values. For clarity of presentation, only the most relevant cross-category comparisons are shown. In bottom panels, this is a *t*-test for equality of mean values.

uncertainty or suspect it is not truly local, and this is revealed in their choices around manure application.

We now consider whether average maize yields differ across the four categories. Note that 72% of fields are intercropped, and maize yield measures are therefore constructed as pure stand equivalents after accounting for the space taken up by other crops in the field.⁶ The average yields presented in Table 5 reveal that, as expected, the highest average yield is realised with true positive maize seed, at 2,309 kg/ha. False positive yields were considerably lower, on average than true positive seeds (Mean difference = 691 kg/ha; $P = 0.000$). This is also not surprising, though one imagines that farmers might be disappointed with these results and opt to dis-adopt improved seed (even if they had not, in actuality, been growing improved maize). Note that type I errors might be of greatest interest to policymakers concerned about the integrity of seed markets.

The false negative seeds are perhaps the most mysterious, exhibiting the lowest average yields (at 1,291 kg/ha) even though the seed type was truly improved. Our results are not consistent with the pattern observed for cassava in Nigeria (Wossen *et al.*, 2019), where the estimated yield advantage of improved varieties is larger when using DNA-referenced crop types than when using farmer reports. (Note, however, that we might expect these patterns to differ across crops that are differentially sensitive to management choices, or across crops that reproduce by seed versus vegetative propagation.) In Tanzania, it instead seems that the average yield gap between local and improved varieties is smaller when referring to the DNA-referenced seed types, dropping by 203 kg/ha. Perhaps, holding other factors constant, the higher yields of improved seed are observed mostly when fertiliser is applied at the rate intended for

⁶Specifically, the denominator in the maize yield measure is the farmer-estimated field size, divided by the number of crops that are cultivated together on the field. The numerator is the farmer-reported quantity of maize harvested from the field.

improved seed (Table 4), as these are considered complementary technologies (Wainaina *et al.*, 2016). It is also possible that false negative seeds were previously considered by farmers to be improved, though the seed vigour had been degraded so thoroughly over generations of recycling that farmers no longer perceive them as 'improved'. In other words, the lack of correlation across farmer-reported and DNA-identified seed type for these seeds may reflect a divergence between the farmers' definition of 'improved' and what DNA fingerprinting technology can detect. This possibility will be discussed further in section 7.

It should be emphasised that we rely on the farmers' estimates of the numerator (quantity harvested) and denominator (area cropped) to construct a measure of crop yield. Several authors have recently found that farmers are systematic in their misestimation of these numbers, with the areas of small fields being over-estimated and the areas of large fields being under-estimated, and/or the quantity harvested being over-reported for small fields and under-reported for large fields (Carletto *et al.*, 2015; Desiere and Jolliffe, 2018). Although yield mismeasurement may be correlated with the four categories of seed type (true negative, false negative, true positive and false positive), we do not have expectations regarding the direction of bias we might expect in either the numerator or denominator across these categories. Furthermore, Abay *et al.* (2019) find that correcting for misestimation in either the yield ratio's numerator or denominator (only) can intensify bias in the yield measure, while ignoring mismeasurement in both variables is preferable. It should also be noted that, because yields are constructed as pure stand equivalents, this may affect our results if some seed categories are more likely to be intercropped than others (Wineman *et al.*, 2019). A robustness check is provided in section 5 that focuses only on monocropped maize plots.

Yield functions intended to discern the correlates of crop yield often control for seed type on the right-hand side of the equation. We now use equation (2) to explore whether the coefficient on improved seed status changes when this status is alternately sourced from respondents or genetic analysis. Results, shown in Table 6, indicate that the coefficient on improved seed is smaller when using DNA results. Thus, the use of farmer-reported improved seed is associated with an increase in maize yield of 530 kg/ha (column (1)). When self-report errors are corrected in column (2), the use of improved seed is associated with an increase of 292 kg/ha. Recall that false negative seeds produce the lowest yields, on average (Table 5), and tend to receive inputs at levels that are indistinguishable from true negative seeds (Table 4), except for the likelihood of applying organic manure. These cases are now classified as improved in column (2), and the difference between the coefficient on improved status in columns (1) and (2) is statistically significant at the 5% level ($P = 0.030$).

In Table 7, we evaluate the stability of our key conclusion to different model specifications. When right-hand side variables are iteratively added, related to crop management (input intensities), field characteristics and household socio-economic characteristics, we consistently find that the coefficient on improved seed when using farmer reports is greater than when using DNA results, with the difference ranging from 184 to 314 kg/ha across these model specifications.

Equation (3) is now used to determine whether each category of seed (e.g. true positive, false positive) results in a statistically distinguishable yield, once input intensities are included as controls. Note that, if yield differences are attributed entirely to the category-specific management patterns revealed in Table 4, we would expect the coefficient on false positive seed to be insignificant, and the coefficients on true positive

Table 6
Yield functions with farmer-reported and DNA-determined improved seed status (OLS)

	Yield (kg/ha)	
	(1)	(2)
1 = Improved (farmer reports)	530.02 ^{***} (0.00)	
1 = Improved (DNA results)		292.42 ^{***} (0.00)
Area (ha under crop)	-173.27 [*] (0.07)	-184.89 [*] (0.06)
Seed kg/ha	22.72 ^{***} (0.00)	19.59 ^{***} (0.00)
Fertiliser kg/ha	2.54 ^{***} (0.00)	3.17 ^{***} (0.00)
Manure kg/ha	0.28 ^{**} (0.01)	0.30 ^{**} (0.01)
Labour days/ha	2.07 ^{***} (0.00)	2.15 ^{***} (0.00)
1 = Soil quality is good	-61.13 (0.51)	-69.16 (0.45)
1 = Plot is flat	147.73 (0.13)	129.91 (0.18)
1 = Field is intercropped	71.58 (0.50)	76.76 (0.46)
1 = Pre-harvest crop loss	-676.59 ^{***} (0.00)	-698.34 ^{***} (0.00)
1 = Female field manager	-446.30 ^{***} (0.00)	-437.25 ^{***} (0.00)
Age of field manager	-5.66 (0.15)	-6.84 [*] (0.10)
1 = Field manager completed primary school	144.35 (0.15)	137.67 (0.21)
HH members	37.26 ^{**} (0.02)	43.33 ^{**} (0.01)
Value of household assets (log, shillings)	110.43 ^{***} (0.00)	116.85 ^{***} (0.00)
Distance to nearest hybrid maize seed seller (km)	-3.49 (0.69)	-7.11 (0.45)
1 = HH reached by extension services	-12.70 (0.92)	13.68 (0.92)
1 = HH is member of farmer group	-162.04 (0.37)	-157.63 (0.38)
1 = Kilimanjaro region	508.45 ^{***} (0.00)	448.20 ^{***} (0.00)
1 = Manyara region	1,398.34 ^{***} (0.00)	1,425.59 ^{***} (0.00)
Constant	-1,658.64 ^{***} (0.00)	-1,430.90 ^{***} (0.00)
Observations	821	821
R ²	0.388	0.376

Table 6
(Continued)

	Yield (kg/ha)	
	(1)	(2)
Difference (β (Improved, farmer report) – β (Improved, DNA results))	237.60	
$P > \chi^2[(\beta$ (Improved, farmer report) = β (Improved, DNA results))]	0.030	

Note: *P*-values in parentheses; standard errors clustered at village level; ****P* < 0.01, ***P* < 0.05, **P* < 0.1.

and false negative seed to be indistinguishable. The results in Table 8 show that the only category that produces significantly higher yields than the base group of true negative seed is true positive, and this pattern remains consistent as additional controls are added across columns (1)–(4). The coefficient on false positive seed is positive but not statistically significant (with true negative as the base group), indicating that the farmers' incorrect perception of this seed type is not a determinant of yield; rather, the seed's real type (local) determines the yield. The coefficients on false and true positive are statistically significantly different ($P = 0.000$), and this points to productivity losses that can be attributed to seed type misidentification. At the same time, the coefficient on false negative seed is negative but not significant, which indicates that type II errors may not present a significant loss to farmers that had expected to produce local maize. However, the coefficients on false negative and true positive seed are always statistically significantly different ($P = 0.000$). The negative coefficient on false negative seed suggests that these are systematically lower performing than true positive seed.

In a final exercise, we estimate the gain in maize production that would be realised if farmers perfectly knew the seed type they had planted. For all observations, we use the coefficients from equation (3) (i.e. those generated in column (4) of Table 8) to predict maize yields, bounded below by a value of zero. When these predicted yields are multiplied by the maize area and summed, the total predicted maize quantity produced in our sample is 901,284 kg. We then adjust the yields of false positive observations to simulate the yields expected had the farmers instead planted improved (true positive) seed. All other management decisions are held constant, as we believe the farmers made their management decisions with the perception that they had, indeed, been using improved seed. Now, the total predicted maize quantity produced is 934,297 kg, an increase of 3.7%. (Note that, specifically for the false positive subsample, this represents a 23.8% increase in quantity produced.) Next, we further adjust the yields of false negative observations to simulate the yields expected had the farmers instead planted local (true negative) seed. All other management decisions are again held constant. This brings the total predicted maize quantity produced to 946,788 kg, representing an increase of 5.0%. This simulated improvement in production could be used, in conjunction with nationally representative data on maize production, to estimate the breakeven value of a policy or program that better ensures farmers know what seed type they have acquired and planted. Note, however, that we have not accounted for the further adoption of improved seeds we might expect if

Table 7
Yield functions with different controls (OLS)

	Yield (kg/ha)			
	(1)	(2)	(3)	(4)
1 = Improved (farmer reports)	620.50*** (0.00)		676.26*** (0.00)	
1 = Improved (DNA results)		436.55*** (0.00)		362.54*** (0.00)
Controls				
Region fixed effects	Y	Y	Y	Y
Inputs			Y	Y
Field characteristics				
Household socio-economic characteristics				
Observations	821	821	821	821
Difference β (Improved, farmer report) = β (Improved, DNA results)	183.95		313.73	
$P > \chi^2[\beta$ (Improved, farmer report) = β (Improved, DNA results)]	0.138		0.005	
	Yield (kg/ha)			
	(5)	(6)	(7)	(8)
1 = Improved (farmer reports)	647.91*** (0.00)		530.02*** (0.00)	
1 = Improved (DNA results)		358.74*** (0.00)		292.42*** (0.00)
Controls				
Region fixed effects	Y	Y	Y	Y
Inputs	Y	Y	Y	Y
Field characteristics	Y	Y	Y	Y
Household socio-economic characteristics			Y	Y
Observations	821	821	821	821
Difference β (Improved, farmer report) = β (Improved, DNA results)	289.17		237.60	
$P > \chi^2[\beta$ (Improved, farmer report) = β (Improved, DNA results)]	0.011		0.030	

farmers correctly gauged the returns to the adoption of newly purchased true positive seed.

6. Robustness Checks

We have confirmed that the patterns found in section 5 are robust to different decisions made regarding the construction of variables, the delineation of the sample and the use of weights. All results are available from the authors upon request. First, noting that instances of complete crop wipe-out may skew a yield analysis, we confirmed

Table 8
Yield functions with categories for correct identification of improved/local status (OLS)

	Yield (kg/ha)			
	(1)	(2)	(3)	(4)
Seed category (Base group = True negative)				
1 = False negative	-279.67*	-223.69	-210.64	-211.07
	(0.07)	(0.13)	(0.16)	(0.17)
1 = False positive	11.36	203.58	183.96	109.72
	(0.95)	(0.22)	(0.26)	(0.47)
1 = True positive	620.12***	670.18***	648.92***	519.79***
	(0.00)	(0.00)	(0.00)	(0.00)
Controls				
Region fixed effects	Y	Y	Y	Y
Inputs		Y	Y	Y
Field characteristics			Y	Y
Household socio-economic characteristics				Y
Observations	821	821	821	821
R^2	0.177	0.318	0.354	0.396
$P > \chi^2[\beta(\text{FP}) = \beta(\text{TP})]$	0.000	0.000	0.000	0.000
$P > \chi^2[\beta(\text{FN}) = \beta(\text{TP})]$	0.000	0.000	0.000	0.000

Note: P -values in parentheses; standard errors clustered at village level; *** $P < 0.01$, ** $P < 0.05$, * $P < 0.1$.

that results are consistent when the 17 observations of zero crop harvest are removed from the sample. To ensure that especially large yield values did not influence our results, we also repeated the analysis using the inverse hyperbolic sine transformation of yield. Again, our conclusions did not change with this alternative specification. We also confirmed that our regression results are consistent when different levels of geographic fixed effects are applied, including for the 9 districts and 78 villages in the sample. Yield regression results (similar to the analysis of Table 7) are presented in Table A3 in the online Appendix. The coefficients are quite consistent with our main results. However, when household characteristics are added as the final set of controls in a model with village fixed effects, the improved seed coefficients across models that rely on farmer reports versus DNA-derived categories are not statistically significantly different ($P = 0.185$), although the magnitude of this difference is similar to that computed with district or region fixed effects.

In our main analysis, when a farmer reported a seed type as being improved and recycled (saved from one's harvest), it was classified as being improved (farmer-reported). However, it is debatable whether this ought to be regarded as improved, as the yield of recycled seed is expected to be lower than first-generation seed, rendering the status of such seed somewhat ambiguous. In a robustness check, we repeated the analysis of section 5 with a new definition of 'improved (farmer-reported)', in which recycled seed is always treated as *not* improved. Results are quite consistent with this new variable construction. However, in a yield function based on equation (3), the gap between the coefficients on improved seed (using self-reports and DNA-derived classifications) increases from 238 kg/ha (in Table 7) to 316 kg/ha.

Our analyses of yield may be influenced by decisions around how to measure crop yield on fields that are intercropped. Specifically, for intercropped fields, we assumed that all crops share the field equally to isolate the area under maize. In a robustness check, we repeated the yield analyses with a focus only on the 231 observations that are monocropped and find patterns that are consistent with our main analysis. Specifically, true positive yields are greatest (mean = 1,853 kg/ha) while false negative yields are lowest (1,118 kg/ha), and though average true negative yields are statistically indistinguishable from false positive yields, average false negative yields are lower than true positive yields in a statistically significant manner.

As the sampled maize fields are not representative, our intention in this study is not to make claims regarding the population of maize farms in the study site. However, we have also repeated the analysis of section 5 using inverse probability weights (IPWs), adjusting the population weights to account for the likelihood of a primary field being sampled (Table A4 in the online Appendix) (Wooldridge, 2002). This is roughly intended to represent the population of primary maize fields. The results of this parallel analysis are very similar to section 5. However, we now see statistically significant differences between true positive and false negative seed in terms of application rates of both organic manure and inorganic fertiliser. This reinforces our impression that farm management decisions are influenced by perceptions about the seed type.

7. Conclusions and Policy Implications

In this paper, we draw from an agricultural household survey in Tanzania and use DNA fingerprinting as a benchmark against which the accuracy of farmer reports of maize varietal identification is evaluated. We quantify the rate of type I and type II errors in the identification of improved seed type and consider some potential explanations in the form of informal seed sources, as well as potential consequences in the form of input allocations made under faulty assumptions of seed type. We also consider how standard approaches to analysing household survey data may produce results that differ, depending on how local/improved seed status is captured.

We find that a majority (72%) of maize observations are correctly identified as local or improved, while 19% of improved seeds, and 48% of local seeds, are misidentified. These results suggest that farmers in Tanzania are slightly inclined to over-report their maize seed as being improved. This pattern is in contrast to the under-reporting observed among wheat and maize farmers in Ethiopia (Tizale *et al.*, 2015) and rice farmers in Bolivia (Labarta *et al.*, 2015). Seeds that are falsely reported as improved are more likely to have been recycled or obtained from other farmers. This may relate to the ambiguities of genetic drift when seed is recycled or cross-pollinated (Morris *et al.*, 1999; Westengen *et al.*, 2014) or the uncertainties inherent in sourcing seed through informal channels. Along these lines, seed obtained through a recent purchase is also more likely to be correctly identified at the seed variety level. The challenge for poor farmers is balancing a need for quality assurance with their budget constraints.

With regard to patterns of crop management, we find that management of improved seed that is perceived as improved (correctly) or local (incorrectly) does vary. For example, compared with correctly reported improved seed, the seeding rate is higher (on average) and the fertiliser rate is lower on improved seed that is incorrectly reported as local. At the same time, we find little evidence that farmers

differentiate their management decisions between seed that is either correctly or incorrectly reported as improved, and the same is generally true for the seed that is either correctly or incorrectly reported as local. Though these correlations do not imply a causal relationship, this evidence is suggestive that farmer (mis)perceptions may guide input decisions, and errors in farmers' awareness of their seed type may translate into suboptimal management practices.

We find some evidence that analytical results differ when relying on farmer reports versus DNA analysis to categorise seed as being improved. In particular, the measured yield benefit of improved seed use is smaller in magnitude (by 202 kg/ha) with a DNA-derived categorisation. This difference persists in econometric analysis, where application rates of inputs and field characteristics are included as controls. This suggests that the true impact of improved germplasm research is somewhat lower than would be estimated with more conventional (survey-based) methods. However, this does not tell us what the effect of crop research *would be* if farmers were more aware of their seed type. In fact, the yield benefit is greatest for true positive seed (Table 8), which suggests that agricultural research centres might maximise the return on their investments by increasing farmers' knowledge of seed type or improving quality control within the seed system.

We emphasise that our results tell a story of correlation, and further research on this topic may be able to find exogenous variation in farmers' awareness of seed type through use of an instrumental variable or a randomised experiment in which correct information on seed type is provided to some farmers before the growing season. Further research on DNA fingerprinting in this setting could also include a cost-effectiveness comparison of seed type identification through DNA analysis versus more conventional methods (e.g. farmer self-reports). Note that the cost of DNA-based identification is inclusive of the upfront costs of establishing a reference library of maize varieties. Such an analysis should extend beyond a simple comparison of the costs of data collection to account for the differential rate of correct seed type identification.

As the costs of genotyping continue to decline (Kosmowski *et al.*, 2018) and the application of DNA analysis to household surveys becomes more prevalent, it is worth highlighting several lessons learned from our experience. On a logistical note, it is important for crop samplers to visit households long enough before the harvest that the sample may be considered representative of a given population. It may also be worthwhile to sample from all maize plots, rather than only each household's primary maize plot, in order to build a sample that is representative of all maize produced in the study site. It would be advisable to provide survey respondents with a clearer explanation regarding the difference between recycled seed and seed that ought to be categorised as local (according to the survey designers). Thus, improved seed that has been recycled a certain number of times may be understandably categorised as either improved or local. In such cases, farmer reports and the results of genetic analysis might be harmonised if farmers had been provided with more precise criteria for seed classification.

For a more comprehensive exploration of patterns of improved seed adoption, it would be ideal to collect information on seed variety (i.e. local names), source, and history for seed that was reported as local; to collect more details on seed transactions, particularly with other farmers; and to track patterns of improved seed adoption and dis-adoption over time. Furthermore, to better understand the backstory behind any discrepancies between farmer reports and DNA evidence, it would have been

fascinating to discuss the laboratory results with farmers. One imagines that these conversations could shed light on what led farmers to the responses they had provided (e.g. uncertainty versus a confident misperception), and could inform survey design to more accurately capture seed type in future studies.

Supporting Information

Additional supporting information may be found online in the Supporting Information section at the end of the article.

Figure A1. Study site.

Figure A2. Rate of correct seed type reporting, by district.

Table A1. Summary statistics of key variables.

Table A2. Rate of correct varietal identification among seeds correctly identified as improved.

Figure A3. Year of seed variety release and rate of correct variety identification.

Table A3. Yield functions with different controls, including district and village fixed effects (OLS).

Table A4. Likelihood of maize field being sampled (probit model).

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