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Estimating the Direct and Indirect Effects of Improved Seed Adoption on Yields: Evidence from DNA-Fingerprinting, Crop cuts, and Self-Reporting in Ethiopia

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Abstract

Farmer adoption of improved crop varieties can potentially increase yields and enhance household welfare in the developing world. However, the presence of measurement errors in household surveys poses a serious challenge to estimating the true returns to adopting improved varieties. This article analyzed the impacts of three sources of measurement error caused by farmers' misperceptions of the varieties they planted, the area they planted, and the quantities they harvested, on maize yields and input use, using the 2018/19 Ethiopia Socio-economic Survey. These data included DNA-fingerprinting of seed, GPS plot size information, and crop cuts that we compared to farmers' self-reported estimates of these measures. Doing so allowed us to determine the degree of measurement error in the estimates of improved maize adoption. Results indicated that the measurement error in self-reported adoption of improved maize varieties attenuated their estimated yield gains by 12 percentage points on average. Furthermore, we used the relationship between self-reported and DNA-fingerprinted adoption to disaggregate how much of the yield gains from improved seeds was due to better seed genetics and how much was due to increased effort by the farmers who planted them. We found that improved seed genetics accounted for a 22 percentage point yield increase over traditional seed, and observable effort through increased input use accounted for a 15 percentage point gain for improved varieties on average. Understanding these effects has important implications for justifying the continued funding of development of improved seed varieties and their dissemination to smallholder farmers.

Key words: DNA-fingerprinting; Crop cut; Improved maize varieties; Measurement error; Effort effect; Seed effect; Technology adoption; Ethiopia; Sub-Saharan Africa.

Increasing farmer adoption of improved crop varieties can potentially raise agricultural productivity and reduce poverty in the developing world. As such, estimating the yield impacts of using improved varieties has been an important topic of research in many disciplines, including economics, for decades. Findings from agronomic field trials, conducted under specific researcher-managed conditions, generally found that improved crop varieties generated high yields (Geleti *et al.*, 2011; Legesse *et al.*, 2011). However, studies that estimated returns under actual smallholder farmer conditions often found that improved crop varieties generated yields that were not different from those of traditional varieties, and/or that yields of improved crop varieties were much lower on farmers' plots than they were in agronomic trials (Lobell, Cassman and Field, 2009; Abate *et al.*, 2018; Michler *et al.*, 2019; Khonje *et al.*, 2022). These yield gaps have been explained through differences between the trial and smallholder farmers' plots. For example, differences in soil quality and planting density, and complementary inputs such as labor and fertilizer (Bulte *et al.*, 2014; Bulte, di Falco and Lensink, 2020; Laajaj *et al.*, 2020). These findings raise questions about whether or not improved varieties are actually effective at increasing yields in the limited resource environments that typically characterize smallholder agriculture.

That being said, it is also possible that the empirical yield gaps for improved varieties between agronomic trials and smallholder fields were the result of measurement error caused by farmers incorrectly stating whether or not they used improved seed varieties, that also influenced potential misallocation of other yield-enhancing inputs. Until recently, researchers had to rely on farmers to self-report their use of improved crop varieties to determine the adoption and impacts (e.g., Conley and Udry, 2010; Suri, 2011; Amare, Asfaw and Shiferaw, 2012; Khonje et al., 2015; Zeng et al., 2017; Jaleta et al., 2018; Michler et al., 2019; Manda et al., 2020). The presence of error in self-reported variables potentially makes the smallholder data unreliable for estimating accurately the returns to adoption of improved crops.

The problem of measurement error in adoption of improved varieties could be compounded by subjective misperceptions of self-reported land area and self-reported quantities harvested. Recently, several studies compared these self-reported estimates with more precise measures of area cultivated that were calculated using Global Positioning System (GPS), and more precise measures of quantities harvested calculated via crop cuts. These studies found that misperceptions by farmers of both the denominator (land area) and the numerator (quantity harvested) introduced two potential sources of biases in the measurement of yields. For example, Carletto, Savastano and Zezza (2013), Carletto, Gourlay and Winters (2015), and Dillon et al. (2019) all showed that GPS devices provided more precise measurements of land area compared to farmers' self-reporting. Furthermore, Desiere and Jolliffe (2018), Abay et al. (2019), Gourlay, Kilic and Lobell (2019), Kosmowski et al. (2021), and Yacoubou Djima and Kilic (2021) showed that using crop cuts instead of self-reported quantities harvested reduced bias in the measurements of yields. These findings suggest that the past studies that did not have access to error-free methods of data collection in the field may have overestimated or underestimated yields. However, measurement error is not only present in yield calculations as showed through previous studies. It is likely present in technology adoption data related to improved seed varieties as well (Kosmowski *et al.*, 2020). To our knowledge, the effect of measurement error in yields and in improved seed adoption has yet to be studied. Understanding the combined magnitude of these possible sources of error is important for accurately estimating returns to adoption of improved seed varieties.

With this in mind, the objectives of the present study are to: i) estimate the impacts of improved seed adoption on maize yields, and determine how sensitive such estimations are to the measurement error in adoption of improved seeds and yields data; and ii) separate out the genetic effect of the improved seeds (*seed effect* in further text) on yields from the observable and unobservable effort effects, that we define as the behavioral response of farmers to their perception whether or not the seed they planted was improved (e.g., by adjusting the use of complementary inputs). We addressed these objectives using the most recent wave of the Ethiopia Socio-economic Survey (ESS) from 2018/19. The ESS is a unique dataset that incorporated both error-prone and error-free measurements of improved maize seed adoption and yields. The error-prone measurements included in the ESS were: self-reported adoption of maize varieties (traditional or improved), self-reported land area planted with maize, and self-reported quantities of maize harvest. The corresponding error-free measurements included in the ESS dataset were: DNA-fingerprinting information for the same seed for which a farmer self-reported adoption status, GPS area of the same plot for which a farmer self-reported the land area, and crop cut information for the same plot for which a farmer self-reported quantities harvested. We classified maize as being improved if it was hybrid or open pollinated variety with greater than 95% germplasm purity, regardless of germplasm origin.

These data provided us with two measurements of seed adoption and we created three measurements of yields with varying levels of error. First, self-reported yields were generated from self-reported harvest and self-reported land area and were deemed as having the highest level of error. Second, substituting self-reported land area with measurements obtained from GPS devices we corrected the measurement error in the denominator. Hence, we perceived yields generated from self-reported harvest and GPS land area as having medium level of error. Third, yields generated from crop cut information had the lowest level of error.

Our main contribution is that we estimate the magnitude and direction of bias in both dependent and independent variables, by dealing with measurement errors in maize adoption data on the right side and yields on the left side of the regression. That is, we use the relationship between DNA-fingerprinted adoption and crop cut yields as benchmark to understand how much bias is introduced to the estimates by farmers self-reporting their seed varieties, quantities harvested, and land area. This main contribution could therefore be broken down into two. Namely, we analyze the extent to which measurement error in yield variables alters the estimates of returns to improved maize adoption. Several recent studies on the inverse relationship between land size and productivity showed that the measurement error in yields caused the returns to land to be significantly mis-estimated (Desiere and Jolliffe, 2018; Abay *et al.*, 2019; Gourlay, Kilic and Lobell, 2019). We expand this literature by estimating how much bias is introduced through the measurement error in yield variables to the estimates of returns to improved seed varieties.

Next, we determine how much bias is introduced to the estimates of the impact of improved maize varieties on yields, through the measurement error in self-reported adoption data. Relying on the self-reported data, previous studies established that there was a positive relationship between the use of improved maize varieties and yields and household welfare (Bezu *et al.*, 2014; Zeng *et al.*, 2015; Abdoulaye, Wossen and Awotide, 2018; Darko *et al.*, 2018). However, these studies may have mismeasured the effects of adoption of improved varieties due to bias in self-reported adoption data, as shown by Wossen et al. (2019) and Wineman et al. (2020). Both of these studies compared the effects of self-reported and DNA-fingerprinted adoption of improved maize varieties on yields and found that the measurement error from self-reported adoption produced biased estimates. However, Wossen et al. (2019) generated their yield outcome variable using self-reported harvest and GPS land area, while Wineman et al. (2020) generated the yields from self-reported harvest and self-reported land area. We add to this literature by dealing with measurement error on both sides of the regression with our data on DNA-fingerprinting and crop cuts.

Our second contribution is that we disentangle the seed effect on yields from the effort effect. Our data allows us to separately identify and estimate these effects because we know the relationship between self-reported adoption (farmers' perceptions) and DNA-fingerprinting (actual adoption). Previous studies have found that farmers' use of inputs, or their perceptions on the use, guided their decisions about investing effort in crop production where the effort can be observed (e.g., labor and other plot inputs) and unobserved in agricultural datasets (Beaman *et al.*, 2013; Bulte *et al.*, 2014; Wineman *et al.*, 2020; Abay, Bevis and Barrett, 2021; Wossen, Abay and Abdoulaye, 2022). For example, Beaman et al. (2013) found that distributing fertilizer to farmers led to crowding in of herbicide and hired labor in Mali. We add to this literature by separating out how much of the estimated yield gain from adopting improved maize seeds was due to the improved genetics of the seed and how much was due to farmers' perceptions that the seed was traditional or improved, expressed through their observable and unobservable effort.

Data, descriptive statistics, and sources of measurement error

Household- and production-level data come from the Ethiopia Socio-economic Survey conducted in 2018/19 growing season (CSA, 2020). The ESS was collaborative work between the World Bank Living Standards Measurement Study – Integrated Surveys of Agriculture project (LSMS-ISA) and the Central Statistics Agency of Ethiopia (CSA). The survey included 7,527 households from 565 enumeration areas across 11 regions, and it collected data using four questionnaires: post-planting, post-harvest, household, and community. From this sample, 447 maize-growing households from 5 regions (Tigray, Amhara, Oromia, SNNPR, Harar, and Dire Dawa) were randomly selected for data collection with advanced techniques in an effort to increase data accuracy. First, the arable land area was measured using GPS devices. Second, trained enumerators performed crop cutting of maize from a 4×4 meters quadrant that was randomly laid over a plot. Dry weight of the harvest from each quadrant was used to generate yield measurements. Third, dried crop cuts were also used to collect maize samples for DNA-fingerprinting. DNA-fingerprinting was carried out to determine if a farmer adopted an improved maize variety or not, and it implied examining the level of purity and variety by matching sample's genetic material to the closest genetic match from the reference library for Ethiopia (Kosmowski *et al.*, 2020). We excluded 12 households from the initial sample of 447 maize-growing households because they did not fill out the household questionnaire. This reduced our working sample to 435 households that planted maize on 491 plots.

Land area

Our data provided two measures of land area with unequal degrees of error: plot area under maize as estimated by farmers and land measurements obtained using GPS devices. The area estimated by farmers, that is self-reported land area, is subject to two types of error. The first error is associated with the use of land units where the farmers may use local, non-standard, units to express their land area for which conversion factors to standard units are not known. Or, in the case of both standard and non-standard units, the farmers may have different perceptions about how much land area is contained in a unit (e.g., farmers could have a different idea how much one *timad* of land is). Second, farmers may be uncertain of the number of units they actually cultivate or may round the number of land units for simplicity. Considering these two types of measurement errors in self-reported land area, we excluded bottom and top 5% of data as well as observations for which we could not obtain conversion factors from non-standard to standard land units. Our final sample consists of 376 households that grew maize on 419 plots.[1]

The GPS measure of land area is considered a more consistent and accurate measure compared to farmers' estimations, although it may have a certain degree of inaccuracy. Enumerators were trained on how to conduct land measurements using GPS devices and area was always reported in standard units such as meters squared.

Table 1 shows that 96% of farmers did not report land area accurately. Taking GPS land area as a benchmark, farmers overreported their land under maize on 55% of plots and underreported the land area on 41% of plots. The self-reported and GPS land area were in agreement for only 4% of the sample (17 plots). However, even though farmers were more likely to overreport their land under maize cultivation, the magnitude of underreporting was almost twice as large as that of overreporting (|–0.146| > 0.078).

Harvest

Similarly to land area, our data allowed us to generate two different variables for harvest. Harvest was completed on 93.8% of plots by the time the post-harvest survey was conducted in February and March 2019, and these farmers were asked to report their maize harvest for the entire plot. For the remaining 6.2% of plots where the harvest had not been completed, the farmers were asked how much harvest they expected to have from each plot. We used the reported and expected harvest to generate self-reported harvest variable. The second harvest variable was generated using harvest from crop cut and GPS land area, where we extrapolated harvest from the sub-plot selected for crop cut to the entire plot. We acknowledge that, even though sub-plots for crop cut were

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[1] 335 households grew maize on 1 plot, 39 households grew maize on 2 plots, and 2 households grew maize on 3 plots.

randomly laid over the maize plot, generating harvest variable in this way may also contain a certain degree of error due to assumption that yields were uniform on the entire plot. However, this measure of harvest remains less prone to error compared to self-reporting.

Comparing the self-reported harvest to harvest generated from crop cut and GPS land area in table 1, we can see that 53% of farmers overreported and 47% of farmers underreported their harvest where the absolute value of underreporting was higher than the value of overreporting (|–176| > 76).

Yields

Having two different variables for land area, self-reported harvest, and information from crop cuts, we were able to generate three yield variables with varying levels of measurement error. The first variable, self-reported yields ($yield^{SR}$), was generated using self-reported land area and self-reported harvest, and it is expected to have the highest level of error due to measurement error contained in both land and harvest variables. The second yield variable ($yield^{GPS}$) was generated using GPS land area and self-reported harvest. The GPS land area is intended to correct for measurement error in farmers' self-reporting of land planted with maize, and as such $yield^{GPS}$ should have less error compared to $yield^{SR}$. The third variable for yields was generated from crop cuts ($yield^{CC}$). We used $yield^{CC}$ as benchmark since it does not rely on farmers' estimates of harvest and land area and as such is a more accurate measurement of yields (Lobell *et al.*, 2020; Kosmowski *et al.*, 2021). We accounted for intercropping on 23% of plots in all three yield variables.

We note that, when accounted for skewness in yield data, these three measures of yields were indeed different (table 1, panel D). On average, self-reported yields were 15% lower than GPS yields (approximately 70 kg/acre) and 22% lower than crop cut yields (approximately 107 kg/acre) on average (p-values < 0.01 for both). The GPS yields were 7% lower than crop cut yields on average (approximately 37 kg/acre), but this difference was not statistically significant at the 10 percent level. These findings imply that, at least descriptively, using GPS land area in the denominator could potentially reduce the measurement error in self-reported yields without the use of crop cuts.

Table 1. Summary at the plot level: land area, harvest, and yields

Variable	Mean	Standard Deviation	N
Panel A: Percentages			
% Underreporting land area (SR < GPS)	41		173
% Overreporting land area (SR > GPS)	55		229
% Accurate land area (SR = GPS)	4		17
% Underreporting harvest (SR < CC)	47		196
% Overreporting harvest (SR > CC)	53		223
% Accurate harvest (SR = CC)	0		0
Panel B: Land area (acres)			
Self-reported land (SR)	0.21	0.171	419
GPS land	0.228	0.261	419
If underreporting (SR < GPS)	–0.146	0.191	173
If overreporting (SR > GPS)	0.078	0.093	229
Panel C: Harvest (kg)			
Self-reported harvest (SR)	156	212	419
Crop cut harvest (CC)	198	344	419
If underreporting (SR < CC)	–176	288	196
If overreporting (SR > CC)	76	93	223
Panel D: log Yield			
$\log \text{yield}^{\text{SR}}$	6.08	1.44	419
$\log \text{yield}^{\text{GPS}}$	6.23	1.26	419
$\log \text{yield}^{\text{CC}}$	6.3	0.77	419
t-test for difference in means			
$\log \text{yield}^{\text{SR}} = \log \text{yield}^{\text{GPS}}$	–0.15***		419
$\log \text{yield}^{\text{SR}} = \log \text{yield}^{\text{CC}}$	–0.22***		419
$\log \text{yield}^{\text{GPS}} = \log \text{yield}^{\text{CC}}$	–0.07		419

Significance for difference in means: *** p<0.01, ** p<0.05, * p<0.1

Improved seed adoption

As part of the post-planting survey, households were asked to identify the seed used in 2018/19 growing season on each maize plot as traditional or improved variety. A random sub-sample of all maize plots was selected for crop cut and for collecting maize samples that were then DNA-fingerprinted after the post-harvest survey. DNA-fingerprinting information enabled us to classify seeds as a traditional or improved variety based on seed germplasm purity level, and as such it is an objective measure of improved seed adoption. The variable indicating purity percentage of each maize sample came from data associated with the Kosmowski et al. (2020) report, and was matched with the main dataset using household and plot identifiers. All DNA-fingerprinted seed samples were matched with 16 different seeds from maize seed reference library.

In our data all maize samples had germplasm purity above 70% (appendix figure A.1), however we defined seed to be an improved variety if its purity was 95% or above and not improved otherwise, regardless of the germplasm origin and if the seed was a hybrid or an open pollinated variety.[2] We used a high threshold of 95% to be able to capture the effects of improved seed varieties more accurately, due to potential changes in genetic composition and production potential when maize is recycled (Morris, Risopoulos and Beck, 1999; Morris *et al.*, 2003; Pixley and Banziger, 2004). Appendix table A.1 shows information about the improved maize seed varieties used among households in the sample.

Comparing the self-reported to DNA-fingerprinted adoption status with 95% germplasm purity threshold, we were able to identify four mutually exclusive categories of adoption: i) true positive (TP): when a household reported using an improved variety and DNA-fingerprinting confirmed the seed was an improved variety; ii) true negative (TN): when a household reported using a traditional variety that was also confirmed through DNA-fingerprinting; iii) false positive (FP): when a household reported planting an improved variety but DNA-fingerprinting showed the seed used was not an improved variety; and iv) false negative (FN): when a household reported using a traditional variety but DNA-fingerprinting showed that the seed was an improved variety. With this categorization, approximately 73% of the sample reported correct adoption status (27% TP and 46% TN) while 10% and 17% of plots fell into FP and FN categories, respectively (table 2). The FP and FN categories represent measurement error in adoption of improved maize seed varieties.

Table 2. Self-reported and DNA-fingerprinted improved maize adoption from 419 plots (%)

		Self-reported	
		Adopter	Non-adopter
DNA-fingerprinted	Adopter	26.73	16.95
	Non-adopter	10.26	46.06

True Positive (TP) = Self-reported Adopter + DNA-fingerprinted Adopter
False Positive (FP) = Self-reported Adopter + DNA-fingerprinted Non-adopter
False Negative (FN) = Self-reported Non-adopter + DNA-fingerprinted Adopter
True Negative (TN) = Self-reported Non-adopter + DNA-fingerprinted Non-adopter

Estimation strategy

Estimation strategy: DNA-fingerprinted adoption

The first step of our analysis estimated how different measures of seed adoption correlated with yield measurements that contained different levels of measurement error. As discussed in the paper, varietal identification using DNA-fingerprinting will produce the most accurate measure of

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[2] Due to a relatively small sample size, we classify both hybrid and OPV seed varieties as improved and did not separately estimate their effects. If grouping hybrid and OPV varieties as improved had any impact on the results, it would have been to attenuate the estimated effects of DNA-fingerprinting because hybrid yields are normally higher than OPV yields.

whether or not a farmer adopted an improved seed variety. As such, we estimated the relationship between DNA-fingerprinted adoption of improved maize varieties and our yield variables using the following linear model:

$$\log Yield_{ip}^{k} = \alpha_0 + \alpha_1 A_{ip}^{DNA} + \boldsymbol{\gamma}'\boldsymbol{H} + \boldsymbol{\beta}'\boldsymbol{E} + \boldsymbol{\delta}'\boldsymbol{P} + \boldsymbol{\rho}'\boldsymbol{I} + \boldsymbol{\theta}'\boldsymbol{L} + \varepsilon_i \qquad (1)$$

where we separately ran each measure of $Yield$, denoted by $k = \{crop\ cut\ (CC), self-reported\ (SR), GPS\}$, for household i's plot p. The regressor of interest was $A^{DNA} = 1$ if household i used an improved maize variety with seed germplasm purity of 95% or above on plot p according to DNA-fingerprinting, and $= 0$ otherwise. We used the coefficient estimates of $\hat{\alpha}_1$ from the regression of error-free $Yield^{CC}$ on error-free A^{DNA} as benchmark coefficient estimate in our analysis of the impacts of adoption of improved maize varieties on yields.[3] The vectors $\boldsymbol{H}$, $\boldsymbol{E}$, and $\boldsymbol{P}$ included control variables for the household (gender, age of household head, indicator if the household head could read and write, marital status, household size, assets index, and ownership of livestock), access (access to extension and advisory services), and plot (owned plot, good soil quality, plot had steep slope) characteristics, respectively. We also included vectors $\boldsymbol{I}$ and $\boldsymbol{L}$ for plot inputs (indicators for the use of chemical and organic fertilizer, indicator if the plot was irrigated, indicators for erosion prevention and pure stand, and log GPS land area planted with maize) and labor inputs (log planting and log harvest labor days from all sources). We included region fixed effects and clustered standard errors at the household level.[4]

The DNA-fingerprinted measurement of adoption was the most robust option in our analysis with the least amount of measurement error, however the group of DNA-fingerprinted adopters (i.e., $A^{DNA} = 1$) was comprised of TP and FN adopters. The FN adopters also represented one component of the measurement error as they did not believe that they planted improved varieties, but DNA fingerprinting revealed that they did (table 2). As we have already discussed, lower yields for improved varieties in studies that relied on farmers-assessed varietal adoption could have been the cause and consequence of FN adoption. Therefore, using a linear model we looked at the relationship between the two subgroups of DNA adopters and yield outcomes as follows:

$$\log Yield_{ip}^{k} = \alpha_0 + \alpha_1 A_{ip}^{TP} + \boldsymbol{\gamma}'\boldsymbol{H} + \boldsymbol{\beta}'\boldsymbol{E} + \boldsymbol{\delta}'\boldsymbol{P} + \boldsymbol{\rho}'\boldsymbol{I} + \boldsymbol{\theta}'\boldsymbol{L} + \varepsilon_i \qquad (2)$$

$$\log Yield_{ip}^{k} = \alpha_0 + \alpha_1 A_{ip}^{FN} + \boldsymbol{\gamma}'\boldsymbol{H} + \boldsymbol{\beta}'\boldsymbol{E} + \boldsymbol{\delta}'\boldsymbol{P} + \boldsymbol{\rho}'\boldsymbol{I} + \boldsymbol{\theta}'\boldsymbol{L} + \varepsilon_i \qquad (3)$$

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[3] Given that most of our regressions from specifications (1)-(7) were of the log-indicator design, we interpreted the coefficient estimates as percentages for simplicity. The percentages obtained in this way were accurate for coefficient estimates of smaller magnitude, however in very few instances in our paper the coefficient estimates were of greater magnitude and our percentages represented underestimation of the effects. The coefficient estimates on dummy variables of greater magnitudes could be transformed to exact percentages using the $\left(e^{\hat{\alpha}} - 1\right) * 100$ calculation (Wooldridge, 2015).

[4] We were unable to estimate these models using household fixed effects because only 41 out of 376 households (11%) in our dataset planted maize on more than one plot.

In these specifications we simply broke down DNA adopters into two groups. First subgroup $A^{TP} = 1$ for TP adoption and $= 0$ for DNA-fingerprinted non-adopters, omitting FN adopters from the analysis. Second subgroup $A^{FN} = 1$ when FN adoption was reported and $= 0$ for DNA-fingerprinted non-adopters, thus excluding TP subgroup from the analysis. As such, in coding these variables we did not use the entire sample. The remainder of variables were the same as in equation (1).

Estimation strategy: Self-reported adoption

To gain additional insights on how misperceptions about variety adoption biased returns to improved maize seeds, we estimated several additional linear models that regressed yields on self-reported adoption of improved seeds:

$$\log Yield_{ip}^{k} = \alpha_0 + \alpha_1 A_{ip}^{SR} + \boldsymbol{\gamma}'\boldsymbol{H} + \boldsymbol{\beta}'\boldsymbol{E} + \boldsymbol{\delta}'\boldsymbol{P} + \boldsymbol{\rho}'\boldsymbol{I} + \boldsymbol{\theta}'\boldsymbol{L} + \varepsilon_i \tag{4}$$

where the measure of improved seed adoption $A^{SR} = 1$ if household i self-reported planting an improved maize variety on plot p and $= 0$ otherwise. All other variables were the same as in equation (1).

As mentioned above, the estimates in (4) could be biased when self-reported adoption is used in the analysis. The bias could be in either direction because the measurement error consisted of two different adoption categories: 10% of our sample reported FP and 17% of sample reported FN adoption. These measures of adoption can be added to the model and their coefficients can indicate the significance of controlling for measurement error in self-reported adoption data.

$$\log Yield_{ip}^{k} = \alpha_0 + \alpha_1 A_{ip}^{SR} + \alpha_2 M_{ip}^{FP} + \alpha_3 M_{ip}^{FN} + \boldsymbol{\gamma}'\boldsymbol{H} + \boldsymbol{\beta}'\boldsymbol{E} + \boldsymbol{\delta}'\boldsymbol{P} + \boldsymbol{\rho}'\boldsymbol{I} + \boldsymbol{\theta}'\boldsymbol{L} + \varepsilon_i \tag{5}$$

Here, M^{FP} represented false positive component of the measurement error and M^{FN} represented false negative component of the measurement error. These variables were coded using the entire sample, and we modeled M^{FP} $(M^{FN}) = 1$ when a household reported FP (FN) adoption, and M^{FP} $(M^{FN}) = 0$ otherwise. Note that false negative adoption A^{FN} in equation (3) was modeled differently from M^{FN} in equation (5), as the latter equation used the entire sample while former did not. To determine the extent and direction of bias in self-reported adoption we ran the χ^2 test for the equality between coefficient estimates $\hat{\alpha}_1$ from equation (4) that did not account for measurement error, and $\hat{\alpha}_1$ from equation (5) that controlled for measurement error. Similarly, to understand if it was possible to correct the measurement error in self-reported adoption by including M^{FP} and M^{FN} in the analysis, we conducted the χ^2 test for the equality between coefficient estimates $\hat{\alpha}_1$ from equation (1) where the regressor of interest was A^{DNA} and $\hat{\alpha}_1$ from equation (5) that controlled for measurement error. The coefficient estimates $\hat{\alpha}_2$ and $\hat{\alpha}_3$ in equation (5) tested for the source of bias (i.e., whether it was driven by FP or FN adopters). All other variables remained as explained for equation (1).

In addition, we ran specifications (1)-(5) with and without vectors of other plot inputs and labor ($\boldsymbol{I}$ and $\boldsymbol{L}$) since the use of complementary inputs was likely correlated with farmers' perceptions of seed (discussed below). Therefore, we performed χ^2 test for equality of coefficients estimates between specifications with and without vectors $\boldsymbol{I}$ and $\boldsymbol{L}$, for each regressor of interest (i.e., A^{DNA}, A^{SR}, M^{FP}, and M^{FN}) in equations (1)-(5), as a robustness check on the consistency of the coefficient estimates.

Separating the seed effect from the effort effect of improved varieties.

The second question we sought to answer in this analysis was, if DNA-fingerprinting and crop cut yield estimates revealed that improved maize varieties had higher yields than traditional varieties, how much of the yield increase was due to the seed effect and how much was due to the effort effect (both observable and unobservable effort) from farmers? Fortunately, comparing yields among the four adoption categories, TP, FP, FN, and TN allowed us to answer this question. As such, to separate the actual seed effect and effort effect, we had to compare each group of farmers (TP, FP, and FN) with TN farmers *only*, since DNA-fingerprinting matched TN farmers' perceptions that seed was not improved, and therefore TN did not include effort or seed effects. We defined the variable $Effort = 1$ when FP $= 1$, because this group of farmers used traditional seed based on DNA-fingerprinting but perceived their seed as improved. Similarly, we generated the variable $Seed = 1$ when FN $= 1$, as these farmers used improved seed based on DNA-fingerprinting but perceived it as traditional. And lastly, we defined the variable $Effort\&Seed = 1$ when TP $= 1$, since these farmers planted improved seed according to DNA-fingerprinting and perceived it as such. All three variables were coded as 0 when TN $= 1$. We ran three separate regressions using linear specification, one for each effect variable as discussed above.

$$\log Yield_{ip}^{CC} = \alpha_0 + \alpha_1 O_{ip}^{l} + \boldsymbol{\gamma}'\boldsymbol{H} + \boldsymbol{\beta}'\boldsymbol{E} + \boldsymbol{\delta}'\boldsymbol{P} + \boldsymbol{\rho}'\boldsymbol{I} + \boldsymbol{\theta}'\boldsymbol{L} + \varepsilon_i \qquad (6)$$

Here variable O represented the effect $l = \{Effort, Seed, Effort\&Seed\}$. The dependent variable was log of yields from crop cut, since this measure was the most likely to be correctly measured, and all other variables remained the same as in equation (1). We included region fixed effects and clustered at the household level.

In order to estimate and test the seed effect and the effort effect (both observable effort and unobservable effort) we ran the three models in equation (6) with and without the vector of other plot inputs and labor ($\boldsymbol{I}$ and $\boldsymbol{L}$). Doing so controlled for the observable effort effect that could be attributed to changes in complementary labor and other input use. We ran χ^2 tests for equality of coefficient estimates from equation (6) with and without these vectors, for each regressor of interest (i.e., $Effort$, $Seed$, $Effort\&Seed$). In addition, we used the χ^2 test to estimate the difference between two different regressors of interest from different specifications.

Understanding behavioral changes that create the effort effect

Finally, if our analysis were to find evidence of an effort effect, we wanted to understand how farmers adjusted production intensity to their perception of seed, that is what, if any, components observable in our data were captured through the effort effects from equation (6). To do so we estimated the following function at the plot level:

$$I_{ip}^{j} = \alpha_0 + \alpha_1 TP + \alpha_2 FN + \alpha_3 FP + \boldsymbol{\gamma}'\boldsymbol{H} + \boldsymbol{\beta}'\boldsymbol{E} + \boldsymbol{\delta}'\boldsymbol{P} + u_i \tag{7}$$

where I was production input j used on household i's plot p, and TP, FN, and FP were indicator variables for the categories of improved maize seed adoption identified for plot p. The TN was used as base category. We ran this model separately for each production input j which use may have been affected by farmers' perception of maize seed. These inputs included i) use of chemical fertilizer (yes = 1), ii) use of organic fertilizer (yes = 1), iii) log GPS land planted with maize, iv) log planting labor days from all sources of labor (household, hired, and exchange labor), and v) log harvest labor days from all sources of labor. For each specification, we ran multiple F-tests for equality of coefficient estimates $\hat{\alpha}_1$, $\hat{\alpha}_2$, and $\hat{\alpha}_3$, to uncover potential differences in the use of inputs by the TP, FN, and FP groups of farmers. The vectors $\boldsymbol{H}$, $\boldsymbol{E}$, and $\boldsymbol{P}$ remained as described previously for equation (1). We included region fixed effects and clustered standard errors at the household level. We address the issues of potential endogeneity in Appendix B.

Results

The effect of measurement errors in yields

Table 3a presents the results from the estimation of equation (1), showing results of crop cut yields ($Yield^{CC}$) on DNA adoption. In table 3a and in subsequent tables, the coefficient estimates became increasingly robust moving from column 1 to column 5 as additional controls were added. Estimates of column 5 were the most robust and they indicated that on average DNA-fingerprinted adoption of improved maize varieties was associated with 22% increase in yields compared to DNA-fingerprinted non-adopters on average. The χ^2 tests at the bottom of table 3a showed that coefficient estimates were very consistent as additional controls were added to the model. The only significant difference in coefficient estimates was between column 5 and column 1, when other plot inputs and labor were controlled for and when they were not. This lends some initial evidence to the role that observable effort may have played in affecting improved seed adoption, which is discussed in detail below.

The results in table 3a can be compared to the first row of results in appendix tables A.2 and A.3 where self-reported and GPS yields were regressed on DNA-fingerprinted adoption, respectively. The results from these appendix tables showed that improved maize adoption through DNA-fingerprinting did not have a statistically significant effect on self-reported and GPS yields. This was likely due to insufficient correction of measurement error in these two outcome variables, since correcting the measurement error in the denominator of yields (i.e., using GPS land area instead of self-reported land area) was not enough to generate unbiased estimates of adoption of improved seed varieties. Our results suggest that using self-reported and GPS yields led to underestimation of the effects of improved seed adoption, since the coefficient estimates were not statistically different from zero. None of the other coefficient estimates for different adoption categories were statistically different from zero in appendix tables A.2 and A.3, that used self-reported yields and GPS yields as dependent variables, respectively. Therefore, we focus the rest of the results discussion on the models where crop cut yield was the dependent variable.

The effect of improved seed adoption on yields: DNA-fingerprinting versus self-reporting

Tables 3b and 3c present the estimated effects of other categories of improved seed adoption on crop cut yields, as modelled in equations (2) and (3). The columns 1-10 represent the results with and without vectors of household, access, plot, other plot inputs, and labor variables.

When we disaggregated DNA-fingerprinted adopters in two subgroups in table 3b (true positive TP and false negative FN adopters), the most robust results for A^{TP} in column 5 and A^{FN} in column 10 indicated that the positive association between the two subgroups and crop cut yields remained almost unchanged. The A^{TP} subgroup of DNA-fingerprinted adopters was associated with approximately 22% increase in yields and the A^{FN} subgroup was associated with an increase in yields of around 21% on average, compared to DNA-fingerprinted non-adopters. Therefore, A^{TP} and A^{FN} both carried the effect of adoption that was consistent with the most robust estimation for A^{DNA} in table 3a column 5. All coefficient estimates across table 3b were very stable and consistent as seen by the lack of statistical significance in seven out of the eight χ^2 tests at the bottom of table 3b. In fact, as in table 3a, the only statistically different coefficient estimates came from comparisons between column 5 and column 1 for A^{TP}, when labor and other plot inputs were controlled for and when they were not.

Table 3c shows the estimates of self-reported adoption of improved maize seeds, A^{SR}, on crop cut maize yields, corresponding to equations (4) and (5). It is interesting to note that the most robust specification presented in column 5, that included the full set of controls, showed that adoption of improved maize varieties based on farmers' self-reporting did not have a statistically significant impact on yields. However, when we used the DNA-fingerprinted adoption data in combination with the self-reported adoption data to identify and control for two components of measurement error in column 10 (false-positive error M^{FP} and false negative error M^{FN}), the coefficient estimate on self-reported adoption A^{SR} became associated with approximately 26% increase in crop cut yields. Thus, not controlling for measurement error in farmers' self-reported adoption status led to underestimating the effects of adoption, even when using crop-cut yield estimates. In our results, the false negative component of measurement error M^{FN} was correlated with around 28% increase in yields, while false positive component of measurement error M^{FP} remained non-significant in column 10.

The difference between coefficient estimates of self-reported adoption A^{SR} from table 3c in columns 5 and 10 represented the bias in self-reported adoption when measurement error was not accounted for in the analysis. The false negative measurement error M^{FN} was the source of statistically significant downward bias of approximately 12 percentage points, as indicated by the χ^2 test in row 5) of column 10 at the bottom of table 3c. The false negative measurement error M^{FN} in column 10 picked up the effect of a farmer unknowingly planting an improved maize seed variety with germplasm purity of 95% or above. This form of measurement error seemed to have been the main factor biasing the estimates of self-reported adoption in column 5.

The difference of 3 percentage points between the coefficient estimates of DNA-fingerprinted adoption A^{DNA} in column 5 in table 3a and self-reported adoption A^{SR} with measurement error added to the analysis in table 3c column 10 was not statistically significant, as seen in row 6) of column 10 at the bottom of table 3c. This result suggests that the measurement error in self-reported adoption was the reason that coefficient estimates in column 5 of table 3c were biased compared to DNA-fingerprinted adoption.

Table 3a. Yield function for $\log \mathrm{Yield}^{\mathrm{CC}}$ with $\mathrm{A}^{\mathrm{DNA}}$ improved seed adoption

Variables	(1) $\log \mathrm{Yield}^{\mathrm{CC}}$	(2) $\log \mathrm{Yield}^{\mathrm{CC}}$	(3) $\log \mathrm{Yield}^{\mathrm{CC}}$	(4) $\log \mathrm{Yield}^{\mathrm{CC}}$	(5) $\log \mathrm{Yield}^{\mathrm{CC}}$
$\mathrm{A}^{\mathrm{DNA}}$	0.290***	0.244***	0.232***	0.218***	0.222***
	(0.080)	(0.078)	(0.080)	(0.081)	(0.081)
Household (H)	Yes	–	Yes	Yes	Yes
Access (E)	Yes	–	–	Yes	Yes
Plot (P)	Yes	–	–	–	Yes
Inputs (I)	–	Yes	Yes	Yes	Yes
Labor (L)	–	Yes	Yes	Yes	Yes
Region FE	Yes	Yes	Yes	Yes	Yes
Constant	5.875***	5.214***	5.182***	5.151***	5.112***
	(0.277)	(0.213)	(0.316)	(0.320)	(0.335)
Observations	419	419	419	419	419
R-squared	0.156	0.240	0.249	0.256	0.258
χ^2test for equality of coefficient estimates					
$\hat{\alpha}\mathrm{A}^{\mathrm{DNA}}_{(5)} - \hat{\alpha}\mathrm{A}^{\mathrm{DNA}}_{(i)} = 0$	–0.068**	–0.022	–0.01	0.004	–

Columns 1-5 = Equation (1). Robust standard errors in parentheses. Clustered at household level. *** p<0.01, ** p<0.05, * p<0.1.

Table 3b. Yield function for $\log \text{Yield}^{\text{CC}}$ with true positive adoption (A^{TP}) and false negative adoption (A^{FN})

Variables	(1) $\log \text{Yield}^{\text{CC}}$	(2) $\log \text{Yield}^{\text{CC}}$	(3) $\log \text{Yield}^{\text{CC}}$	(4) $\log \text{Yield}^{\text{CC}}$	(5) $\log \text{Yield}^{\text{CC}}$	(6) $\log \text{Yield}^{\text{CC}}$	(7) $\log \text{Yield}^{\text{CC}}$	(8) $\log \text{Yield}^{\text{CC}}$	(9) $\log \text{Yield}^{\text{CC}}$	(10) $\log \text{Yield}^{\text{CC}}$
A^{TP}	0.338***	0.257**	0.230**	0.213*	0.221*					
	(0.107)	(0.105)	(0.110)	(0.115)	(0.115)					
A^{FN}						0.197*	0.214**	0.216**	0.217**	0.207**
						(0.103)	(0.099)	(0.099)	(0.098)	(0.099)
Household (H)	Yes	–	Yes	Yes	Yes	Yes	–	Yes	Yes	Yes
Access (E)	Yes	–	–	Yes	Yes	Yes	–	–	Yes	Yes
Plot (P)	Yes	–	–	–	Yes	Yes	–	–	–	Yes
Inputs (I)	–	Yes	Yes	Yes	Yes	–	Yes	Yes	Yes	Yes
Labor (L)	–	Yes	Yes	Yes	Yes	–	Yes	Yes	Yes	Yes
Region FE	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Constant	6.090***	5.247***	5.375***	5.333***	5.306***	6.049***	5.353***	5.520***	5.510***	5.430***
	(0.330)	(0.264)	(0.390)	(0.404)	(0.422)	(0.278)	(0.235)	(0.332)	(0.334)	(0.343)
Observations	348	348	348	348	348	307	307	307	307	307
R-squared	0.161	0.264	0.274	0.277	0.278	0.136	0.192	0.212	0.227	0.230
χ^2test for equality of coefficient estimates *{row 1) = column (5) – column (i)}* *{row 2) = column (10) – column (i)}*										
1) $\widehat{\alpha}\text{A}^{\text{TP}}_{(5)} - \widehat{\alpha}\text{A}^{\text{TP}}_{(\text{i})} = 0$	–0.117**	–0.036	–0.009	0.008	–					
2) $\widehat{\alpha}\text{A}^{\text{FN}}_{(10)} - \widehat{\alpha}\text{A}^{\text{FN}}_{(\text{i})} = 0$						0.01	–0.007	–0.009	–0.01	–

Columns 1-5 = Equation (2); Columns 6-10 = Equation (3). Robust standard errors in parentheses. Clustered at household level. *** p<0.01, ** p<0.05, * p<0.1.
True Positive (TP) = Self-reported Adopter + DNA-fingerprinted Adopter; False Negative (FN) = Self-reported Non-adopter + DNA-fingerprinted Adopter.

Table 3c. Yield function for $\log \text{Yield}^{\text{CC}}$ with self-reported adoption (A^{SR}) without and with measurement errors M^{FP} and M^{FN}

Variables	(1) $\log \text{Yield}^{\text{CC}}$	(2) $\log \text{Yield}^{\text{CC}}$	(3) $\log \text{Yield}^{\text{CC}}$	(4) $\log \text{Yield}^{\text{CC}}$	(5) $\log \text{Yield}^{\text{CC}}$	(6) $\log \text{Yield}^{\text{CC}}$	(7) $\log \text{Yield}^{\text{CC}}$	(8) $\log \text{Yield}^{\text{CC}}$	(9) $\log \text{Yield}^{\text{CC}}$	(10) $\log \text{Yield}^{\text{CC}}$
A^{SR}	0.294***	0.167*	0.156*	0.126	0.134	0.408***	0.300***	0.282**	0.245**	0.255**
	(0.088)	(0.092)	(0.093)	(0.097)	(0.098)	(0.106)	(0.108)	(0.112)	(0.117)	(0.118)
M^{FP}						–0.053	–0.111	–0.098	–0.076	–0.084
						(0.134)	(0.125)	(0.130)	(0.130)	(0.129)
M^{FN}						0.317***	0.283***	0.275***	0.278***	0.276***
						(0.103)	(0.101)	(0.101)	(0.101)	(0.101)
Household (H)	Yes	–	Yes	Yes	Yes	Yes	–	Yes	Yes	Yes
Access (E)	Yes	–	–	Yes	Yes	Yes	–	–	Yes	Yes
Plot (P)	Yes	–	–	–	Yes	Yes	–	–	–	Yes
Inputs (I)	–	Yes	Yes	Yes	Yes	–	Yes	Yes	Yes	Yes
Labor (L)	–	Yes	Yes	Yes	Yes	–	Yes	Yes	Yes	Yes
Region FE	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Constant	5.793***	5.291***	5.185***	5.155***	5.112***	5.800***	5.242***	5.188***	5.149***	5.114***
	(0.274)	(0.222)	(0.324)	(0.329)	(0.342)	(0.278)	(0.220)	(0.318)	(0.323)	(0.336)
Observations	419	419	419	419	419	419	419	419	419	419
R-squared	0.155	0.228	0.238	0.245	0.247	0.174	0.245	0.253	0.260	0.262
χ^2test for equality of coefficient estimates										
{row 1) = column (5) – column (i)}										
{rows 2), 3), 4) = column (10) – column (i)}										
{row 5) = column (10) – column (5)}										
{row 6) = column (10) – column (5) in table 3a}										
1) $\hat{\alpha}\text{A}^{\text{SR}}_{(5)} - \hat{\alpha}\text{A}^{\text{SR}}_{(\text{i})} = 0$	–0.16	–0.033	–0.022	0.008	–					
2) $\hat{\alpha}\text{A}^{\text{SR}}_{(10)} - \hat{\alpha}\text{A}^{\text{SR}}_{(\text{i})} = 0$						–0.153***	–0.045	–0.027	0.01	–
3) $\hat{\alpha}\text{M}^{\text{FP}}_{(10)} - \hat{\alpha}\text{M}^{\text{FP}}_{(\text{i})} = 0$						0.137	0.195	0.182	0.16	–
4) $\hat{\alpha}\text{M}^{\text{FN}}_{(10)} - \hat{\alpha}\text{M}^{\text{FN}}_{(\text{i})} = 0$						–0.041	–0.007	0.001	–0.002	–
5) $\hat{\alpha}\text{A}^{\text{SR}}_{(10)} - \hat{\alpha}\text{A}^{\text{SR}}_{(5)} = 0$										0.121**
6) $\hat{\alpha}\text{A}^{\text{SR}}_{(10)} - \hat{\alpha}\text{A}^{\text{DNA}}_{(5)} = 0$										0.033

Columns 1-5 = Equation (4); Columns 6-10 = Equation (5). Robust standard errors in parentheses. Clustered at household level. *** p<0.01, ** p<0.05, * p<0.1.
False Positive (FP) = Self-reported Adopter + DNA-fingerprinted Non-adopter; False Negative (FN) = Self-reported Non-adopter + DNA-fingerprinted Adopter.

The effects of seed and effort on yields

The results in tables 3a, 3b, and 3c hinted at the seed effect and effort effect influencing the returns to improved maize adoption. For example, the coefficient estimates on the returns to DNA-fingerprinted improved maize seed adoption decreased significantly across columns in table 3a, when labor and other plot inputs were included in the model. This was likely due to the relationship between the use of improved seeds and other complementary production inputs, as farmers who thought they had adopted improved seed may have also used more labor and fertilizer, which contributed to higher yields.

The results in table 4 show the estimates from model presented in equation (6) that estimated the seed effect and the effort effect associated with farmers' beliefs about the varieties they adopted. Column 1 of table 4 shows the magnitude of the total effort effect (observable + unobservable) for traditional varieties. This was captured by comparing FP to TN groups of farmers. Results indicated that the extra effort exerted by FP farmers who thought they were adopting an improved variety but were not according to DNA-fingerprinting had a 26% increase in yields on average. This effect disappeared when we included vectors of labor and other plot input variables in column 2, indicating that we were able to (mostly) control for the observable effort effect with our set of complementary input variables on the right side of the regression. Column 2 also tells us that the seed used by FP farmers was not significantly different from the seed used by TN farmers in terms of yield gains, on average. Moreover, when traditional varieties were planted, the observable effort effect can be verified through the χ^2 test of the difference in coefficient estimates between columns 1 and 2 in row 1) at the bottom of table 4. These coefficients were not different indicating that there was no statistically significant benefit to increased use of complementary inputs when farmers planted traditional varieties.

The seed effect captured through comparing FN with TN in columns 3 and 4 showed that the enhanced seed genetics of improved varieties boosted average yields by 22-23% on average. The coefficient estimates between columns 3 and 4 did not change when labor and other plot input controls were added to the model, as seen in the insignificant χ^2 test in row 2) at the bottom of table 4. These results show that farmers in this sample were able to achieve higher yields by using improved seeds as opposed to traditional varieties, regardless of whether or not they used complementary inputs.

Column 5 of table 4 shows the joint effect of effort and seed on yields by comparing TP adoption to TN adoption. The combined effect was greater in magnitude than the effect of effort or the effect of seed individually. The combined effect was associated with 48% increase in yields compared to farmers who did not use improved seeds and additional inputs on average. Testing the difference between the joint effect of seed and effort in column 5 and individual seed effect from column 4 using the χ^2 test in row 3) at the bottom of table 4 provided the total effort effect (observable + unobservable) for improved varieties. The test results were statistically significant and indicated that there was a 26 percentage point increase in total effort on average from planting improved varieties over traditional varieties.

The coefficient estimate from column 5 attenuated significantly from 48% to 33% after we added labor and other plot inputs as control variables to regression seen in column 6 of table 4. This change indicated that farmers' observable effort, as measured by labor and other plot input use, was essential for achieving higher yields when using improved maize varieties. The significant difference of 15 percentage points between coefficient estimates from columns 5 and 6 represented the observable effort effect from labor and input reallocation when using improved varieties. The significance of the χ^2 test can be seen in row 4) at the bottom of table 4.

Finally, the difference of 11 percentage points between coefficient estimates in column 6 and column 4 represented the unobservable effort effect. This effect was not significant according to the χ^2 test in row 5) at the bottom of table 4.

Table 4. Effort and seed effects

Variables	(1) $\log \text{yield}^{\text{CC}}$	(2) $\log \text{yield}^{\text{CC}}$	(3) $\log \text{yield}^{\text{CC}}$	(4) $\log \text{yield}^{\text{CC}}$	(5) $\log \text{yield}^{\text{CC}}$	(6) $\log \text{yield}^{\text{CC}}$
O^{Effort} (FP *vs.* TN)	0.257**	0.179				
	(0.127)	(0.136)				
O^{Seed} (FN *vs.* TN)			0.233**	0.219**		
			(0.108)	(0.104)		
$O^{\text{Effort\&Seed}}$ (TP *vs.* TN)					0.479***	0.334**
					(0.116)	(0.138)
Household (H)	Yes	Yes	Yes	Yes	Yes	Yes
Access (E)	Yes	Yes	Yes	Yes	Yes	Yes
Plot (P)	Yes	Yes	Yes	Yes	Yes	Yes
Inputs (I)	–	Yes	–	Yes	–	Yes
Labor (L)	–	Yes	–	Yes	–	Yes
Region FE	Yes	Yes	Yes	Yes	Yes	Yes
Constant	6.266***	5.889***	5.913***	5.495***	6.007***	5.381***
	(0.324)	(0.407)	(0.287)	(0.339)	(0.347)	(0.449)
Observations	236	236	264	264	305	305
R-squared	0.178	0.271	0.127	0.221	0.179	0.282

χ^2 test for equality of coefficient estimates, between columns

{row 1) tests observable effort effect for traditional varieties}
{row 2) tests if the seed effect of improved varieties is affected by observable input use}
{row 3) tests total effort effect for improved varieties}
{row 4) tests observable effort effect for improved varieties}
{row 5) tests unobservable effort effect for improved varieties}

1) $\hat{\alpha}O^{l}_{(2)} - \hat{\alpha}O^{l}_{(1)} = 0$	–0.078
2) $\hat{\alpha}O^{l}_{(4)} - \hat{\alpha}O^{l}_{(3)} = 0$	–0.014
3) $\hat{\alpha}O_{(5)} - \hat{\alpha}O_{(4)} = 0$	0.26**
4) $\hat{\alpha}O^{l}_{(6)} - \hat{\alpha}O^{l}_{(5)} = 0$	–0.145**
5) $\hat{\alpha}O_{(6)} - \hat{\alpha}O_{(4)} = 0$	0.115

Results from Equation (6). Robust standard errors in parentheses. Clustered at household level. *** $p<0.01$, ** $p<0.05$, * $p<0.1$. Note: True Positive (TP) = Self-reported Adopter + DNA-fingerprinted Adopter; False Positive (FP) = Self-reported Adopter + DNA-fingerprinted Non-adopter; False Negative (FN) = Self-reported Non-adopter + DNA-fingerprinted Adopter; True Negative (TN) = Self-reported Non-adopter + DNA-fingerprinted Non-adopter.
$l = \{\text{Effort}, \text{Seed}, \text{Effort \& Seed}\}$; Effort = 1 if FP = 1; Effort = 0 if TN = 1, Seed = 1 if FN = 1; Seed = 0 if TN = 1, Effort & Seed = 1 if TP = 1; Effort & Seed = 0 if TN = 1.

Correlates of input use

In previous results we found evidence that the yields of improved seed varieties were enhanced by improved seed genetics and by farmers' increasing their observable effort (through changes in inputs) when they believed their seeds were improved. Therefore, we estimated equation (7) to understand what inputs were used differently based on their beliefs. These results are reported in table 5. We found that farmers' perceptions of seed variety were indeed reflected through the complementary inputs that they invested in maize production. Results indicated that compared to the base group of TN adopters who were correct in their belief that they were using traditional seed, TP adopters, who were correct in their belief about planting improved maize varieties, planted approximately 10% more land with maize on average. The TP farmers were also 50 percentage points more likely to use chemical fertilizer, and 15 percentage points less likely to use organic fertilizer compared to TN farmers on average. This suggested that farmers may have believed that there was a positive benefit to increasing complementary inputs like land and inorganic fertilizer along with improved seed use.

We found similar behavioral response to farmers' perception of seed in the FP group who incorrectly believed that they were using improved varieties. Farmers in this group were 46 percentage points more likely to use chemical fertilizer compared to the base group of TN adopters on average. They also spent 36% more labor days at planting and 50% more labor days at harvest compared to TN adopters on average.

Finally, it is important to point out that FN adopters, who believed they were using traditional seed but were actually using improved seed according to DNA-fingerprinting, were not significantly different across all 5 production inputs on average from TN adopters, who knew that they were using traditional varieties. This speaks to the importance of variety perception in farmers' decisions regarding the use of complementary inputs, and is consistent with the F-tests at the bottom of table 5 that compared coefficients on adoption status for each model of input use. For example, TP adopters planted significantly more land, were more likely to use chemical fertilizer and spent more labor days at planting than did FN adopters on average. Recall that the only difference between these two groups was in their perception about whether or not they planted improved seed. Furthermore, FP farmers who incorrectly believed they planted improved seeds were significantly more likely to use chemical fertilizer and spent more labor days during both planting and harvest seasons than did FN farmers who believed they were using traditional seeds but were actually using improved seeds.

Table 5. Correlates of input use with TN adoption as base category

Variables	(1) log land GPS	(2) Used chemical fertilizer (=1)	(3) Used organic fertilizer (=1)	(4) log planting labor days	(5) log harvest labor days
TP	0.099***	0.495***	–0.151**	0.226	0.158
	(0.030)	(0.059)	(0.064)	(0.141)	(0.146)
FN	0.008	0.106	–0.089	–0.068	0.088
	(0.025)	(0.068)	(0.070)	(0.158)	(0.135)
FP	0.061	0.458***	0.042	0.362**	0.501***
	(0.037)	(0.073)	(0.084)	(0.152)	(0.149)
Household (H)	Yes	Yes	Yes	Yes	Yes
Access (E)	Yes	Yes	Yes	Yes	Yes
Plot (P)	Yes	Yes	Yes	Yes	Yes
Region FE	Yes	Yes	Yes	Yes	Yes
Constant	0.124*	0.011	0.393**	2.140***	2.827***
	(0.068)	(0.151)	(0.189)	(0.384)	(0.376)
Observations	419	419	419	419	419
R-squared	0.158	0.404	0.150	0.176	0.102
F-test for equality of coefficient estimates					
Compares coefficient estimates in same specification / column					
1) $\hat{\alpha}\mathrm{TP} - \hat{\alpha}\mathrm{FN} = 0$	0.091***	0.389***	–0.062	0.294*	0.07
2) $\hat{\alpha}\mathrm{FP} - \hat{\alpha}\mathrm{FN} = 0$	0.053	0.352***	0.131	0.43**	0.413**

Results from Equation (7). Robust standard errors in parentheses. Clustered at household level. *** p<0.01, ** p<0.05, * p<0.1. Note: True Positive (TP) = Self-reported Adopter + DNA-fingerprinted Adopter; False Positive (FP) = Self-reported Adopter + DNA-fingerprinted Non-adopter; False Negative (FN) = Self-reported Non-adopter + DNA-fingerprinted Adopter; True Negative (TN) = Self-reported Non-adopter + DNA-fingerprinted Non-adopter. TN is comparison group.

Discussion and conclusion

We found that positive and statistically significant relationship between the seed adoption variables and yields existed only when we used yields generated from crop cuts as the outcome variable. Our descriptive analysis revealed that using GPS measures instead of self-reported land area could correct some error in the yield measurements, since GPS yields and crop cut yields were not different from each other on average. But the regressions analysis showed that self-reported and GPS yields in fact contained enough measurement error that we were not able to detect any effect of improved seed adoption on these two yield measurements. Therefore, in the absence of better measurements of harvest, both self-reported and GPS yields could provide biased estimates when used in the analysis of productivity. Our results are consistent with findings in Desiere and Jolliffe (2018) and Yacoubou, Djima and Kilic (2021), by showing how the measurement error in quantities harvested can substantially change results.

Comparing the estimates of how adoption of improved maize varieties affected maize yields with both self-reported and DNA-fingerprinted adoption allowed us to estimate the extent of measurement error in self-reported adoption data. We found that most of the bias in self-reported adoption was due to the presence of false negative adopters (those who self-reported not adopting an improved maize variety, but DNA-fingerprinting showed otherwise). The magnitude of the bias in yields was 12 percentage points on average, with self-reported estimates attenuating the impact of improved seed adoption compared to DNA-fingerprinting estimates. This attenuation bias may help explain why some studies that measured the impact of improved seed adoption in farmer survey data did not find that these varieties had a significant impact on yields.

We also found that when we controlled for measurement error in self-reported adoption of improved seeds by including control variables for false positive adopters (who incorrectly believed they were adopting improved varieties) and false negative adopters, the relationship between self-reported adoption and crop cut yields became statistically significant and positive. In addition, with these controls, the coefficient estimates of self-reported adoption became statistically equivalent to the coefficient estimates in the model of DNA-fingerprinted adoption on average. The false negative group of farmers introduced a downward bias in the estimates of self-reported adoption because they were identified as non-adopters based on their own reporting. However, false negative adoption reflected yield gains from planting improved maize seeds with germplasm purity of 95% or more.

The analysis that complements DNA-fingerprinted adoption with self-reported adoption allowed us to also attribute how much gain in yields from improved seed adoption was due to the genetic seed effect of improved varieties and how much was due to the effort effect, that could be both observable through reallocation of complementary inputs like labor and unobservable effort through motivation and other factors. Our analysis revealed that 22% of the yield increase for improved maize seed was due to seed effect of the improved varieties compared to traditional varieties on average. In addition, 15 percentage points of the average gain for improved seeds was due to observable effort in the form of additional input use when farmers planted improved seeds on average. We did not find a statistically significant observable effort effect in the returns to adoption of traditional seeds. This suggests that the payoff for extra complementary inputs like labor and inorganic fertilizer were higher for improved seeds than they are for traditional seeds. Overall, these findings imply that farmers' perceptions of varietal adoption should be taken into consideration in the analysis of improved seed varieties because they influence their use of complementary inputs that affect yields.

Results from our study showed that returns to improved seed varieties were higher than those of traditional varieties, while highlighting the need for information campaigns since farmers' knowledge and perceptions play a key role in achieving higher benefits of adoption. Dissemination of improved varieties should be coupled with efforts to educate farmers how to determine the land area and quantify harvest. Ultimately, our study results provide strong evidence that performing both DNA-fingerprinting and crop cuts was important to measure accurately the impacts of adoption of improved crop varieties on yields.

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Appendix A

Table A.1. Improved maize seed variety information

Variety name	Year released	Type	Germplasm origin	Characteristics
BH-140	1988	OPV	EIAR	Early- to intermediate-maturing for mid- and lower altitudes.
BH-660	1993	Hybrid	CIMMYT/EIAR	Late-maturing for traditional growing areas with adequate rainfall.
BH-540	1995	Hybrid	EIAR	Medium-maturing for mid-altitudes.
Jabi	1995	Hybrid	Crossing by Pioneer Hi-Bred	Early-maturing.
Kuleni	1995	OPV	CIMMYT/EIAR	For highland transition areas.
Melkassa-1	2001	OPV	CIMMYT/EIAR	Extra early-maturing for low- to mid-altitude drought prone areas.
Gibe-1	2001	OPV	EIAR	For mid-altitude areas.
BH-670	2002	Hybrid	EIAR	For highland transition areas with adequate rainfall.
Melkassa-2	2004	OPV	CIMMYT/EIAR	Medium-maturing for mid-altitude drought prone areas.
Shone	2006	Hybrid	Crossing by Pioneer Hi-Bred	Drought tolerant, medium-maturing.
AMH-850	2008	Hybrid	EIAR	Early-maturing.
BH-661	2011	Hybrid	CIMMYT/EIAR	Drought-tolerant for dry and normal areas.
Limu	2012	Hybrid	Crossing by Pioneer Hi-Bred	Disease tolerant, medium-maturing, for mid-altitude with high rainfall.
Melkassa-1Q	2013	OPV	CIMMYT/EIAR	Extra early-maturing for dry and marginal areas. Quality protein maize.
Damote	2015	Hybrid	Crossing by Pioneer Hi-Bred	
AMH-852Q	2016	Hybrid	CIMMYT/EIAR	Quality protein maize.

Source: by the author with reference to (Kosmowski *et al.*, 2020).

Table A.2. Yield function for $\log \text{yield}^{\text{SR}}$ with improved seed adoption: least and most robust estimations

Variables	(1) $\log \text{Yield}^{\text{SR}}$	(2) $\log \text{Yield}^{\text{SR}}$	(3) $\log \text{Yield}^{\text{SR}}$	(4) $\log \text{Yield}^{\text{SR}}$	(5) $\log \text{Yield}^{\text{SR}}$	(6) $\log \text{Yield}^{\text{SR}}$	(7) $\log \text{Yield}^{\text{SR}}$	(8) $\log \text{Yield}^{\text{SR}}$	(9) $\log \text{Yield}^{\text{SR}}$	(10) $\log \text{Yield}^{\text{SR}}$
A^{DNA}	0.158	0.059								
	(0.175)	(0.191)								
A^{TP}			0.260	0.058						
			(0.221)	(0.266)						
A^{FN}					0.100	0.141				
					(0.204)	(0.199)				
A^{SR}							0.242	–0.006	0.277	0.024
							(0.161)	(0.203)	(0.215)	(0.269)
M^{FP}									0.053	0.041
									(0.307)	(0.309)
M^{FN}									0.172	0.129
									(0.207)	(0.205)
Household (H)	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Access	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Plot	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Inputs (I)	–	Yes	–	Yes	–	Yes	–	Yes	–	Yes
Labor (L)	–	Yes	–	Yes	–	Yes	–	Yes	–	Yes
Region FE	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Constant	5.738***	5.238***	6.362***	5.797***	5.805***	5.383***	5.684***	5.231***	5.669***	5.226***
	(0.452)	(0.511)	(0.521)	(0.582)	(0.485)	(0.573)	(0.442)	(0.507)	(0.452)	(0.512)
Observations	419	419	348	348	307	307	419	419	419	419
R-squared	0.046	0.109	0.053	0.117	0.044	0.147	0.049	0.109	0.051	0.110
$\hat{\alpha}A^{j}_{\text{IL}} - \hat{\alpha}A^{j}_{\text{full}} = 0$	0.099*	–	0.202**	–	–0.041	–	0.248**	–	0.253**	–
$\hat{\alpha}M^{\text{FP}}_{\text{IL}} - \hat{\alpha}M^{\text{FP}}_{\text{full}} = 0$									0.012	–
$\hat{\alpha}M^{\text{FN}}_{\text{IL}} - \hat{\alpha}M^{\text{FN}}_{\text{full}} = 0$									0.043	–

Columns 1 & 2 = Equation (1); Columns 3 & 4 = Equation (2); Columns 5 & 6 = Equation (3); Columns 7 & 8 = Equation (4); Columns 9 & 10 = Equation (5).
$j = \{\text{DNA}, \text{TP}, \text{FN}, \text{SR}\}$. Robust standard errors in parentheses. Clustered at household level. *** p<0.01, ** p<0.05, * p<0.1.

Table A.3. Yield function for $\log \text{yield}^{\text{GPS}}$ with improved seed adoption: least and most robust estimations

Variables	(1) $\log \text{Yield}^{\text{GPS}}$	(2) $\log \text{Yield}^{\text{GPS}}$	(3) $\log \text{Yield}^{\text{GPS}}$	(4) $\log \text{Yield}^{\text{GPS}}$	(5) $\log \text{Yield}^{\text{GPS}}$	(6) $\log \text{Yield}^{\text{GPS}}$	(7) $\log \text{Yield}^{\text{GPS}}$	(8) $\log \text{Yield}^{\text{GPS}}$	(9) $\log \text{Yield}^{\text{GPS}}$	(10) $\log \text{Yield}^{\text{GPS}}$
A^{DNA}	0.056	0.037								
	(0.150)	(0.172)								
A^{TP}			0.048	–0.002						
			(0.195)	(0.253)						
A^{FN}					0.115	0.137				
					(0.175)	(0.172)				
A^{SR}							0.062	–0.037	0.056	–0.025
							(0.143)	(0.196)	(0.189)	(0.254)
M^{FP}									0.168	0.111
									(0.272)	(0.289)
M^{FN}									0.166	0.146
									(0.178)	(0.176)
Household (H)	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Access	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Plot	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Inputs (I)	–	Yes	–	Yes	–	Yes	–	Yes	–	Yes
Labor (L)	–	Yes	–	Yes	–	Yes	–	Yes	–	Yes
Region FE	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Constant	5.992***	5.650***	6.321***	5.939***	5.940***	5.812***	5.976***	5.640***	5.935***	5.631***
	(0.415)	(0.479)	(0.474)	(0.562)	(0.436)	(0.534)	(0.411)	(0.477)	(0.420)	(0.481)
Observations	419	419	348	348	307	307	419	419	419	419
R-squared	0.046	0.099	0.050	0.104	0.049	0.135	0.046	0.099	0.049	0.101
$\widehat{\alpha}\text{A}_{\text{IL}}^{\text{j}} - \widehat{\alpha}\text{A}_{\text{full}}^{\text{j}} = 0$	0.019	–	0.070	–	–0.022	–	0.099	–	0.081	–
$\widehat{\alpha}\text{M}_{\text{IL}}^{\text{FP}} - \widehat{\alpha}\text{M}_{\text{full}}^{\text{FP}} = 0$									0.057	–
$\widehat{\alpha}\text{M}_{\text{IL}}^{\text{FN}} - \widehat{\alpha}\text{M}_{\text{full}}^{\text{FN}} = 0$									0.020	–

Columns 1 & 2 = Equation (1); Columns 3 & 4 = Equation (2); Columns 5 & 6 = Equation (3); Columns 7 & 8 = Equation (4); Columns 9 & 10 = Equation (5).
$\text{j} = \{\text{DNA}, \text{TP}, \text{FN}, \text{SR}\}$. Robust standard errors in parentheses. Clustered at household level. *** p<0.01, ** p<0.05, * p<0.1.

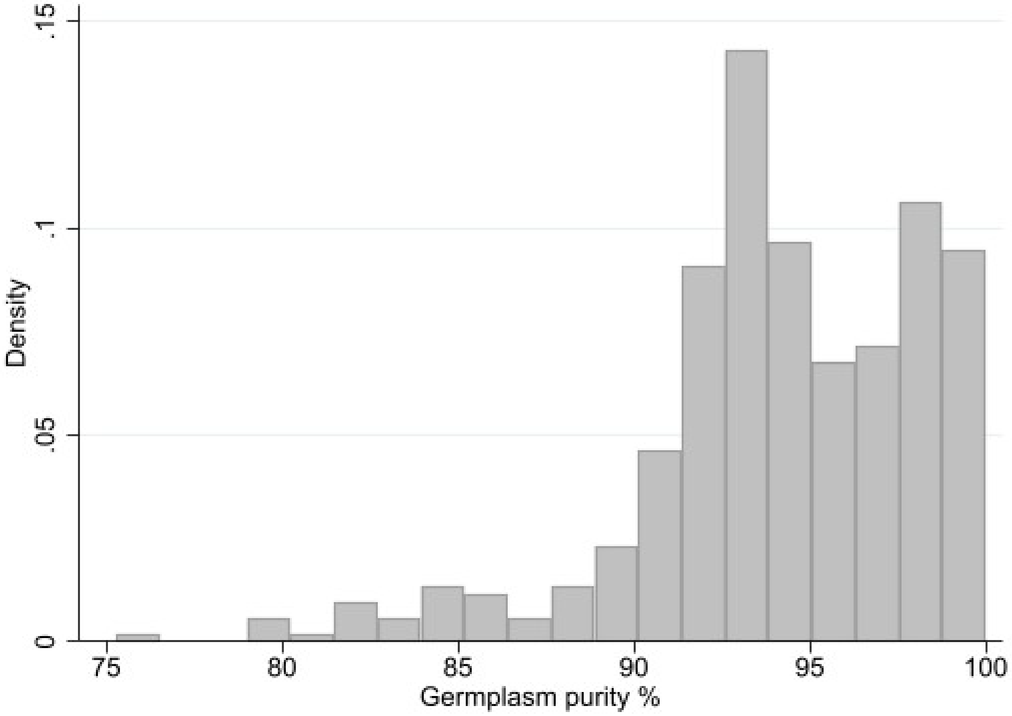

Figure A.1. Germplasm purity % distribution

Appendix B

Addressing potential endogeneity

This study focuses on potential measurement error in yield and improved seed adoption data. However, there are three other potential sources of bias that we need to address in this study. First, bias in yield estimates may stem from the standard problem of omitted variables. The decision to adopt an improved seed variety may be endogenous due to absence of random assignment of adoption status. This can occur at the household level or at the plot level. For example, at the household level if more able farmers were more likely to adopt improved seed varieties and were more likely to get higher yields, then there would be overestimation bias due to omitted household variables. Similarly, at the plot level, if farmers planted improved seeds on their most fertile plots, then we would also expect overestimation bias due to omitted plot-level variables. One potential way to deal with this type of endogeneity is to find instrumental variable (IV). However, finding a suitable IV that is exogenous itself is challenging in an observational dataset. Most IVs will likely be endogenous themselves, and an endogenous IV can bias coefficient estimates more than having no IV (Wooldridge, 2011). Fortunately, we had a rich set of controls in this dataset, so the most straightforward way to deal with this type of endogeneity was to include household, access, and plot characteristics in the vectors $\boldsymbol{H}$, $\boldsymbol{E}$, and $\boldsymbol{P}$ as described above. The variables such as assets, age, and education of the household head proxy for ability, access to extension services proxy for informational connections, and plot quality and slope proxy for soil fertility. Thus, bringing these factors out of the error term and into the model can reduce the overestimation bias we might expect in improved seed adoption.

We ran specifications (1)-(5) in our main results shown in tables 3a, 3b, and 3c with and without $\boldsymbol{H}$, $\boldsymbol{E}$, and $\boldsymbol{P}$. The results of all specifications were very consistent and as hypothesized the coefficient estimates on the different improved adoption variables attenuated as additional controls were added. This suggests that we were able to reduce omitted variable bias by adding these controls.

The second potential endogeneity issue is that correct identification of seed variety could also be endogenous, since smarter and more experienced farmers may have been more likely to correctly identify, or perceive, their seeds as of improved or traditional variety. To infer if this was the case, we ran the following linear regression:

$$C_{ip} = \tau_0 + \boldsymbol{\gamma}'\boldsymbol{H} + \omega_i \qquad \text{(B1)}$$

In this equation, $C = 1$ if a household i correctly identified seed variety on its plot p and $= 0$ otherwise. That is, variable C was assigned a value of 1 for TP and TN adoption categories, and a value of 0 in the case of FP and FN adoption. Vector $\boldsymbol{H}$ included household characteristics that may have been endogenous to proper or false identification of maize seed variety, the variables in the vector $\boldsymbol{H}$ were outlined previously for equation (1). We included region fixed effects and clustered standard errors at the household level. We found no effect of household characteristics on the correct reporting of adoption status as per appendix table B.1.

Third, less experienced farmers may have also been less accurate in their reporting of production inputs and outcomes. That is, they may have been more likely to underestimate or overestimate the land area planted with maize and quantities harvested, that could have ultimately led to underestimation or overestimation of yields. We checked for this by running three separate linear regressions as outlined in equation (B1), but with $Yield_{ip}^{diff}$ on the left-hand side. The variable $Yield_{ip}^{diff}$ was generated as a difference between yield measures. Namely, $diff = \{SR - CC,\ GPS - CC,\ SR - GPS\}$. Like in the previous estimation, we found no effect of household characteristics on underestimation and overestimation of yields according to appendix table B.2. All things considered, it seemed that household and household head characteristics did not have a major detectable effect on our main results.

Finally, despite our efforts to control for endogeneity there may have still been effects that we were not able to capture. We do not claim that our results produced from above regressions were fully causal. That being said, we had the data and models necessary to provide important new information on the main focus of the study, namely the impact of measurement error on yields and improved seed adoption in smallholder datasets.

Table B.1. Correlates of correct reporting of adoption status

Variables	Correct reporting (= 1)
HH Head is male (yes = 1)	–0.023
	(0.075)
HH Head age (years)	–0.001
	(0.002)
HH Head can read and write (yes = 1)	0.046
	(0.048)
HH Head is married (yes = 1)	–0.102
	(0.079)
HH size	0.011
	(0.013)
Assets index	–0.005
	(0.012)
Livestock (TLU)	0.003
	(0.005)
Region FE	Yes
Constant	0.800***
	(0.155)
Observations	419
R-squared	0.058

Results from Equation (8). Robust standard errors in parentheses. Clustered at household level. *** $p<0.01$, ** $p<0.05$, * $p<0.1$

Table B.2. Correlates of overestimation and underestimation of yields (kg/acre)

Variables	(1) $\text{Yield}^{\text{SR}-\text{CC}}$	(2) $\text{Yield}^{\text{GPS}-\text{CC}}$	(3) $\text{Yield}^{\text{SR}-\text{GPS}}$
HH Head is male (yes = 1)	–30.579	33.717	–64.297
	(127.571)	(133.986)	(86.279)
HH Head age (years)	1.878	3.397	–1.519
	(3.074)	(3.275)	(2.337)
HH Head can read and write (yes = 1)	–58.984	13.307	–72.291
	(101.990)	(92.451)	(79.847)
HH Head is married (yes = 1)	–21.749	–80.561	58.812
	(142.654)	(156.219)	(94.177)
HH size	17.668	7.054	10.614
	(22.415)	(21.218)	(15.373)
Assets index	–30.625	–14.798	–15.827
	(28.750)	(25.758)	(17.371)
Livestock (TLU)	–9.442	–15.817	6.374
	(9.629)	(9.747)	(7.618)
Region FE	Yes	Yes	Yes
Constant	154.628	71.438	83.190
	(259.595)	(282.735)	(222.773)
Observations	419	419	419
R-squared	0.048	0.045	0.030

Results from Equation (8). Robust standard errors in parentheses. Clustered at household level. *** p<0.01, ** p<0.05, * p<0.1