ESTIMATING THE PRODUCTIVITY IMPACTS OF TECHNOLOGY ADOPTION IN THE PRESENCE OF MISCLASSIFICATION

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This article examines the impact that misreporting adoption status has on the identification and estimation of causal effects on productivity. In particular, by comparing measurement error-ridden self-reported adoption data with measurement-error-free DNA-fingerprinted adoption data, we investigate the extent to which such errors bias the causal effects of adoption on productivity. Taking DNA-fingerprinted adoption data as a benchmark, we find 25% "false negatives" and 10% "false positives" in farmers' responses. Our results show that misreporting of adoption status is not exogenous to household characteristics, and produces a bias of about 22 percentage points in the productivity impact of adoption. Ignoring inherent behavioral adjustments of farmers based on perceived adoption status has a bias of 13 percentage points. The results of this article underscore the crucial role that correct measurement of adoption plays in designing policy interventions that address constraints to technology adoption in agriculture.

Key words: Adoption, cassava, DNA-fingerprinting, impact, misclassification, Nigeria.

JEL codes: C5, C81, C83, O12, O33.

Accurate measurement of adoption status is crucial for estimating the productivity impacts of adoption. In most adoption studies, data from household surveys are used to measure adoption rates with the assumption that farmers' self-reported data correctly reflect their true adoption status (e.g., Shiferaw et al. 2014; Zeng et al. 2015). However, self-reported adoption status is possibly misclassified, and failure to account for such misclassification may result in biased estimates with implications for policy.[1] In adoption studies, misclassification occurs when farmers wrongly report treatment status, that is, report being adopters when they are non-adopters ("false positives") or report being non-adopters when they are adopters ("false negatives"). This misclassification may occur due to seed market imperfections (e.g., seed adulteration by dealers), lack of awareness and technical information on the characteristics of improved varieties (Kosmowski et al. 2016; Maredia et al. 2016), seed recycling and poorly-regulated extension and variety naming systems (Ilukor et al. 2017).

Irrespective of the source of misreporting of adoption status, causal identification in the presence of misclassification is nontrivial.[2]

[1] In this article, productivity is defined as output/ha. Therefore, productivity and yield are used interchangeably.
[2] Note that measurement error in a binary variable is necessarily negatively correlated with the underlying true value of the variable, and is thus non-classical.

A relatively small but growing body of literature (Aigner 1973; Frazis and Loewenstein 2003; Mahajan 2006; Lewbel 2007; Hu and Schennach 2008; Meyer, Mok, and Sullivan 2009; Battistin and Sianesi 2011; Kreider et al. 2012; Almada, McCarthy, and Tchernis 2016; Gundersen, Kreider, and Pepper 2017) has suggested a variety of causal identification strategies in the presence of misclassification. The identification strategies in the above-mentioned studies are mostly proposed for nonparametric and semiparametric approaches with strong distributional assumptions. For example, both Aigner (1973) and Lewbel (2007) assumed exogenous treatment status and misclassification. Brachet (2008) derived a procedure for estimating treatment effects assuming an endogenous treatment status and exogenous misclassification. Therefore, the identification strategies proposed in the above-mentioned studies cannot be extended to the case of endogenous misclassification. Misclassification in reporting adoption status is potentially endogenous since farmers who misreport adoption status are more likely to be different from those who do not misreport in both observed and unobserved characteristics that affect productivity. There could thus be significant biases associated with endogenous misreporting for a potentially endogenous treatment variable. To our knowledge, only Nguimkeu, Denteh, and Tchernis (2017) considered the consequences of endogenous misreporting for a potentially endogenous treatment variable by exploiting the partial observability model of Poirier (1980).[3] Results from Nguimkeu, Denteh, and Tchernis (2017) suggest that endogenous misreporting in a potentially endogenous treatment variable may have not only attenuation bias but also sign-reversal effects. Considering such biases is therefore critical in the impact evaluation literature as both the size and the direction of estimated effects are key indicators for policy makers to improve program implementation or to evaluate the cost effectiveness of alternative interventions.

This article uses a unique data set that combines self-reported and DNA-fingerprinted adoption data to assess the bias in the estimated treatment effects when the treatment indicator is endogenous and endogenously misclassified. The true adoption status based on DNA-fingerprinted data is free from misclassification but is still endogenous due to self-selection into treatment (existence of observed and unobserved heterogeneities between adopters and non-adopters). As such, the usual instrumental variable (IV) procedure that takes into account the binary nature of the adoption variable will provide consistent estimates. However, when using self-reported adoption status from the household survey, IV estimates can be biased due to endogenous misclassification. Therefore, in addition to correcting for endogeneity bias stemming from unobserved heterogeneity between adopters and non-adopters (which is an omitted variable bias), accounting for endogeneity bias generated by the non-classical measurement errors is necessary for consistency. The difference in the size and direction of parameter estimates between the true adoption status (measured by DNA-fingerprinted adoption data) and the surrogate adoption status (measured from the household survey) should therefore determine the size and the sign of misclassification bias.

To the best of our knowledge, this is the first study to tackle the issue of misclassification in adoption studies. Focusing on the adoption of improved cassava varieties in Nigeria, this article offers the following contributions. First, it provides empirical evidence on misclassification rates from household surveys, including household-level correlates of misclassification. Second, it provides a reliable estimate for a highly policy-relevant parameter, namely the return from adoption in the presence of endogenous adoption status and misclassification. Third, the results of this article can provide an alternative insight into some of the discrepancies between the results of randomized control trials (RCTs) and observational data in the development economics literature since a well-designed RCT is free from misclassification. Fourth, the article also offers an alternative explanation for the seemingly paradoxical low adoption rate but high returns to agricultural research in Africa (Duflo, Kremer, and Robinson 2008; Suri 2011), focusing on the incidence of false negatives in farmers' responses from household surveys. The rest of the article is organized as follows. The next section provides an overview of the data and the empirical econometric strategy. The empirical results are

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[3] Nguimkeu, Denteh, and Tchernis (2017) considered only "false negative" cases.
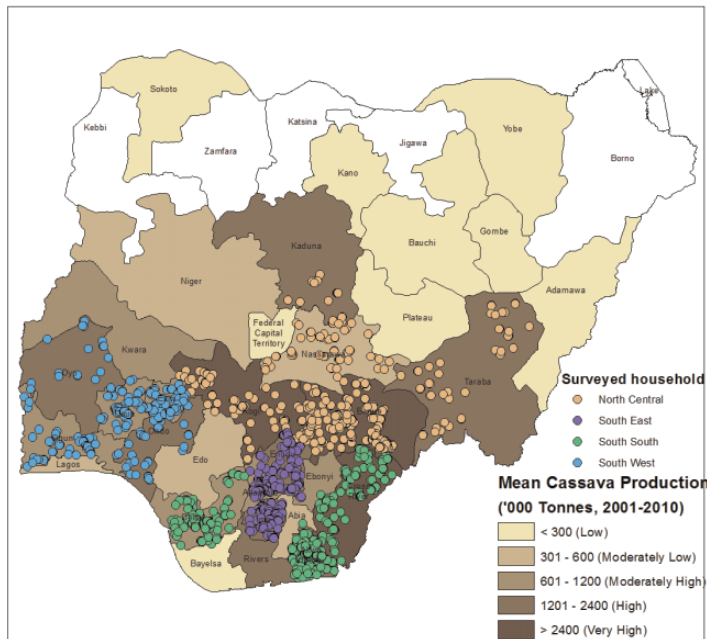
Figure 1. Map of the study area

presented and discussed in the following section, while the last section concludes with policy implications and provides some open questions for further research.

Data Sources and Empirical Strategy

Data Sources

This study is based on the 2015/16 cassava monitoring survey (CMS) in Nigeria. The CMS is a nationally representative sample of 2,500 cassava producers in Nigeria. Figure 1 shows a map of the survey villages and the distribution of the sample households. A multistage stratified sampling design was employed to select the sample households. First, the list of Enumeration Areas (EAs) for conducting national census in Nigeria was obtained from the National Population Commission (NPC). The list of EAs by Local Government Areas (LGA) was obtained for the 16 states that together account for more than 80% of the total production of cassava in Nigeria. These states were grouped into four geopolitical zones: south-west, south-south, south-east, and north.

From each region, 125 EAs were selected using the probability proportional to size (PPS) sampling approach. Finally, from each

EA, random samples of five cassava-growing households were selected for interview. This provided a sample size of 625 households per region and a total of 2,500 farming households. From each surveyed household, information was collected on self-reported treatment status (adoption of improved cassava varieties) at the variety- and plot-level, as many of the households owned more than one plot of cassava and grew different varieties in different plots. From each identified variety in the farm plot, samples of cassava leaves were collected for DNA-fingerprinting analysis. In addition to treatment status, data were collected on socio-economic characteristics of the households, as well as other outcomes of interest such as production. The DNA-fingerprinting process is one of the novel aspects of our data. To date, several varietal identification methods for tracking the adoption of improved varieties have been employed but most have inherent uncertainty levels. Compared to other conventional varietal identification methods, the DNA-fingerprinting technique offers a reliable method to accurately identify varieties grown by farmers, thereby allowing a credible measurement of adoption status. In particular, in the presence of input market imperfections (when the formal seed system is non-existent or imperfect), misclassification can be

pervasive as farmers mostly rely on informal seed sources. Unlike phenotype-based methods, DNA-based varietal identification is independent of environmental conditions or stage of plant growth (Rabbi et al. 2015; Maredia et al. 2016).[4]

Estimation Strategy

We first present our causal identification strategy. We then show how the misclassification of treatment status affects the true impacts on outcome variables. Let Y_i be the outcome variable of interest, that is, productivity. Assuming that productivity is linearly affected by the k-vector of exogenous controls $\mathbf{x}_i$ and the true binary treatment indicator T_i^*, we have the following relationship:

$$(1) \qquad Y_i = \beta T_i^* + \boldsymbol{\alpha} \mathbf{x}_i' + \epsilon_i.$$

Similarly, true adoption status is modelled by

$$(2) \qquad T_i^* = 1[\boldsymbol{\gamma} \mathbf{z}_i' + v_i \geq 0]$$

where $\mathbf{z}_i$ is a vector of determinants of adoption including the exclusion restrictions and $1[\cdot]$ is an indicator function whose value is 1 if the statement inside the brackets is true, and 0 otherwise. Note that while the treatment variable T_i^* does not suffer from misclassification, it is endogenous because of sample selection so that ordinary least squares (OLS) estimates of equation (1) would be biased. Selection bias may occur because farmers who choose to adopt improved cassava varieties may share some common unobserved characteristics, such as better farming skills and management abilities, which are clearly correlated with productivity (i.e., $\operatorname{cov}(T_i^*, \epsilon_i) \neq 0$). An IV regression approach that takes the binary nature of the endogenous treatment variable into account will, therefore, correct such biases and provide consistent estimates in the presence of unobserved heterogeneity between adopters and non-adopters. This means that if treatment status T_i^* is measured using DNA-fingerprinting, β can be consistently estimated using an IV estimation strategy. The

challenge for identification is therefore to find a variable that directly affects adoption decision but not productivity (exclusion restriction). In this article, we use the self-reported adoption status of neighbors and friends as an identifying instrument (Krishnan and Patnam 2013).

However, in most applications where measurement error-free data (such as DNA-fingerprinted adoption data) are not available, T_i^* is not observable to the researcher. Therefore, only a surrogate T_i, the farmer's self-reported treatment status (which is potentially a misclassified version of the true treatment status T_i^*) is observed. In the presence of such misclassification, the researcher can only estimate the following operational relationship,

$$(3) \qquad Y_i = \beta T_i + \boldsymbol{\alpha} \mathbf{x}_i' + (\epsilon_i - \beta u_i)$$

where

$$(4) \qquad T_i = T_i^* + u_i.$$

The measurement error u_i takes on values $(-1, 1)$ in the presence of misclassification and a value of zero otherwise. In most applications (e.g., with a continuous regressor), the measurement error (u_i) is considered to be classical and hence $\operatorname{cov}(T_i^*, u_i) = 0$. However, in our case the measurement error is non-classical as it is negatively correlated with the underlying true value of the treatment status, that is, $\operatorname{cov}(T_i^*, u_i) < 0$. Moreover, the self-reported treatment T_i is also endogenous (i.e., $\operatorname{cov}(T_i, \epsilon_i) \neq 0$) both because it inherits the endogeneity of the true treatment T_i^*, and because the associated misclassification is potentially endogenous, that is, $\operatorname{cov}(\epsilon_i, u_i) \neq 0$. Hence, neither the OLS nor the above-mentioned IV strategy would produce consistent estimates in this case. To see this, consider a simpler model without the covariates $\mathbf{x}_i$, that is,

$$(5) \qquad Y_i = \beta T_i^* + \epsilon_i$$

so that, as explained above, the operational model is given by

$$(6) \qquad Y_i = \beta T_i + \epsilon_i - \beta u_i.$$

Then, the asymptotic bias of the OLS estimator of the treatment effect β is given by

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[4] A detail description of the DNA-fingerprinting process is presented in the online supplementary material.

(7) $\text{plim } \hat{\beta}_{OLS} - \beta = \dfrac{\text{cov}(T_i, Y_i)}{\text{var}(T_i)} - \beta$

$= \dfrac{\text{cov}(T_i, \epsilon_i) - \beta\text{cov}(T_i, u_i)}{\text{var}(T_i)}$

$= \dfrac{\sigma_{T^*\epsilon} + \sigma_{u\epsilon} - \beta\sigma_{T^*u} - \beta\sigma_u^2}{\sigma_{T^*}^2 + 2\sigma_{T^*u} + \sigma_u^2} \neq 0.$

Likewise, when $\text{cov}(T_i^*, \epsilon_i) \neq 0$ and $\text{cov}(\epsilon_i, u_i) \neq 0$, parameter estimates will still be inconsistent, even if the above mentioned IV strategy is used (Aigner 1973; Hausman, Abrevaya, and Scott-Morton 1998; Black, Berger, and Scott 2000; Frazis and Loewenstein 2003; Mahajan 2006; Lewbel 2007; Brachet 2008; Hu and Schennach 2008; Nguimkeu, Denteh, and Tchernis 2017). Specifically, assume that z_i is a valid instrument for the true treatment T_i^*, and that it is appropriately excluded from the outcome equation. Then, the probability limit of the IV estimator is given by[5]

(8) $\text{plim } \hat{\beta}_{IV} = \dfrac{\text{cov}(E[T_i|z_i], Y_i)}{\text{var}(E[T_i|z_i])}$

$= \beta \dfrac{\text{cov}(E[T_i|z_i], T_i^*)}{\text{var}(E[T_i|z_i])}$

$= \beta \dfrac{\text{cov}(E[T_i|z_i], F_v(\gamma \mathbf{z}_i'))}{\text{var}(E[T_i|z_i])}$

where $E[T_i|z_i]$ is the predicted value of T_i in the first-stage regression, $F_v(.)$ is the cdf of v, and $F_v(\gamma \mathbf{z}_i')$ is the conditional expectation of T_i^* implied by equation (2). Denote by $q_0(z_i) = \text{Pr}[u_i = 1|vz_i]$ and $q_1(z_i) = \text{Pr}[u_i = -1|vz_i]$ the probabilities of "false positives" and "false negatives", respectively. Then, we have $E[T_i|z_i] = q_0(z_i) + [1 - q_0(z_i) - q_1(z_i)]F_v(\gamma \mathbf{z}_i')$.

Hence,

(9) $\text{plim } \hat{\beta}_{IV} =$

$\beta \dfrac{\text{cov}(q_0(z_i) + [1 - q_0(z_i) - q_1(z_i)]F_v(\gamma \mathbf{z}_i'), F_v(\gamma \mathbf{z}_i'))}{\text{var}(q_0(z_i) + [1 - q_0(z_i) - q_1(z_i)]F_v(\gamma \mathbf{z}_i'))}$

$\neq \beta.$

That is, $\hat{\beta}_{IV}$ is inconsistent (unless there is no misclassification), and we cannot sign the bias in general. However, in the special case where the misclassification probabilities are constant, the above equation reduces to

(10) $\text{plim } \hat{\beta}_{IV} = \dfrac{\beta}{1 - q_0 - q_1} > \beta$

which leads to an expansion bias in IV as found in Black, Berger, and Scott (2000) and Brachet (2008). While previous studies have attempted to address the bias associated with the measurement error focusing on partial identification using non-parametric approaches (see Mahajan 2006; Lewbel 2007; Hu and Schennach 2008), the focus of this article is to provide point estimates using validation data.[6] Note that with validation data, we have $q_0(z) = q_1(z) = 0$ and the IV estimator is consistent, that is, $\text{plim } \hat{\beta}_{IV} = \beta$.

Descriptive Statistics

This section presents our main outcome indicator (cassava yield) and the socio-economic and plot-level variables used in the regression analysis. Note that yield (output/ha) was calculated as the ratio of total output to GPS-measured plot size. In our setting, GPS measures were taken for all cassava plots from all surveyed households. However, our production data were based on self-reported values and hence they may potentially suffer from measurement errors. Estimating the production of cassava from a given plot is notoriously difficult due to continuous harvesting and a lack of harvest record-keeping by farmers. Taking this measurement issue into account, we collected production data in two rounds. The first was conducted in July/August 2015 and the second occurred in February/March 2016. In the first round, we collected data on the quantity of cassava already harvested in a specific plot as well as the expected quantity to be harvested in the future. In the second round, we collected

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[5] See the online supplementary material for a detailed derivation of the inconsistency of the IV method with misclassified data.

[6] Most of the identification strategies proposed in the literature assume that misreporting probabilities are independent of covariates, conditional on treatment status (Aigner 1973; Hausman, Abrevaya, and Scott-Morton 1998; Black, Berger, and Scott 2000; Kane, Rouse, and Staiger 1999; Frazis and Loewenstein 2003). Others, such as Mahajan (2006), Lewbel (2007), and Hu and Schennach (2008) assume that the misclassified binary variable is exogenous. In general, all the identification strategies proposed so far focus on partial identification by providing nonparametric bounds (both upper and lower). Nguimkeu, Denteh, and Tchernis (2017) suggested a two-step procedure in the presence of endogenous misreporting for a potentially endogenous treatment variable. In particular, they suggest to obtain the predicted probabilities of true participation (T_i^*) using Poirier's (1980) partial observability model and use it in the outcome equation as a measure of treatment. These authors' approach, however, only solves for one-way misreporting (e.g., false negatives only).

Table 1. Cassava Yield by Adoption Status (t/ha)

	Full Sample (N = 5,295)	Self-reported Adoption Status			DNA-fingerprinted Adoption Status		
		Adopters (N = 2,883)	Non-adopters (N = 2,412)	Diff	Adopters (N = 3,645)	Non-adopters (N = 1,650)	Diff
Cassava yield	14.7	15.7	13.4	2.3***	16.2	11.4	4.8***

Table 2. Descriptive Statistics of Socio-Economic Characteristics Based on Self-Reported Adoption Status

	Full Sample (N = 5,295)	Adopters (N = 2,883)	Non-adopters (N = 2,412)	Mean Diff.
Household size (number of members)	4.60	4.84	4.31	0.53***
Education (years of schooling)	8.70	9.04	8.28	0.76***
Age (measured in years)	51.64	51.00	52.41	−1.41***
Sex (1= male, 0= otherwise)	0.89	0.91	0.87	0.04***
Livestock ownership (TLU)	0.91	0.99	0.81	0.18***
Access to extension (1= yes, 0= no)	0.36	0.46	0.25	0.21***
Access to credit (1= yes, 0= no)	0.45	0.50	0.39	0.11***
Mobile phone ownership (1=yes, 0 =no)	0.97	0.98	0.95	0.03***
Membership in credit and saving associations (1=yes, 0=no)	0.34	0.37	0.31	0.06***
Membership in cooperatives (1=yes, 0=no)	0.25	0.30	0.20	0.1***
Membership in cassava growers' association (1=yes, 0=no)	0.21	0.27	0.14	0.13***
Plot with good soil fertility (1=good, 0= otherwise)	0.74	0.78	0.69	0.09***
Plot with medium soil fertility (1=medium, 0 =otherwise)	0.24	0.20	0.29	−0.09***
Plot with poor soil fertility (1=poor, 0= otherwise)	0.02	0.02	0.03	−0.01
Plot managed by men (1=yes, 0=no)	0.36	0.42	0.30	0.12***
Plot managed by women (1=yes, 0=no)	0.49	0.47	0.51	−0.04***
Plot managed jointly (1=yes, 0=no)	0.15	0.11	0.19	−0.08***
Plot is intercropped (1=yes, 0 =no)	0.55	0.55	0.56	−0.01
Labor use (MD/ha)	74.9	84.5	63.5	21
Fertilizer use (1=yes, 0=no)	0.33	0.30	0.37	−0.07***
Herbicide use (1=yes, 0=no)	0.47	0.54	0.38	0.16***
Pesticide use (1=yes, 0=no)	0.09	0.11	0.07	0.04***
Friend is adopter (1=yes, 0=no)	0.50	0.59	0.39	0.20***
Neighbor is adopter (1=yes, 0=no)	0.44	0.68	0.15	0.53***

production values that had been harvested since the first round. Production data were collected using local measurement units since non-standard production units are used by the majority.[7] Table 1 presents cassava yield levels differentiated by self-reported and DNA-fingerprinted adoption status.

We found significantly higher yields among adopters, irrespective of the way adoption status was measured. However, the yield difference between adopters and non-adopters

is higher when DNA-fingerprinted data are used. This observed difference in cassava yield between adopters and non-adopters is only indicative of correlations and cannot be used to make causal inferences regarding the impacts of adoption on cassava yields without controlling for other confounding factors. Table 2 presents descriptive statistics for socio-economic and plot-level variables. For the sake of convenience, we present mean differences based on self-reported adoption status. Household characteristics such as age, household size, education, and membership in different social groups, as well as wealth indicators such as livestock ownership

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[7] Implications of using the self-reported production value is discussed in the conclusions.

measured in terms of tropical livestock units (TLU) are included to control for possible heterogeneities between adopters and non-adopters. We hypothesize that these household characteristics affect farmers' adoption decisions as well as their productivity levels. We found statistically significant differences between adopters and non-adopters for most of the control variables. In general, adopters tend to be younger, more educated, and wealthier (have more livestock). Moreover, adopters have better access to extension and credit.

We also included plot-level variables and input use to control for plot-level heterogeneity. Our plot-level controls are mainly for soil fertility, input use, and agronomic practices. For example, application of chemical fertilizers is quite low (chemical fertilizer was applied only in about 33% of the plots). In about 55% of the plots, cassava is intercropped with other crops.[8] Even though cassava can be grown in fragile soils, our survey results suggest that farmers tend to plant the crop in fertile soils. For instance, in about 74% of the cassava plots, farmers reported that the fertility level of the soil was good.

Results

Extent of Misclassification

In our survey, we identified more than 114 cassava varieties. Of these, about 42% were improved and the remaining were landraces. Table 3 reports misclassification in treatment status (both "false positives" and "false negatives") by comparing adoption data from the household survey with DNA-fingerprinted data.

Because adoption rates from DNA-fingerprinted data are error-free, we used them as a benchmark to calculate misclassification rates from the household survey. Our results show that both false positives and false negatives are prevalent. However, the incidence of false negatives is significantly higher. This result is consistent with other studies that documented the presence of persistent false negatives in the U.S. food stamp

Table 3. Misclassification Rate of Adoption Status at the Plot Level

	HH Surveys	
DNA	Adopter	Non-adopter
Adopter	43.7	25.2
Non-adopter	10.7	20.4

program (Bollinger and David 1997; Marquis and Moore 2010; Almada, McCarthy, and Tchernis 2016). As shown in table 3, 25% of the responses are false negatives and 10% are false positives.[9] This implies that in about 25% of the plots farmers identified improved varieties as landraces and in about 10% they identified landraces as improved varieties. Our data also show a high correlation between misclassification and the underlying features of the cassava seed system. According to our survey, more than 70% of the adopters obtain planting materials through informal local exchange and most of them were not able to identify the varieties they grow by name. For example, the most popular improved variety, "TMS30572", has an adoption rate of 17.5% (based on DNA-fingerprinting). From our survey, we found 237 different names for this variety. However, despite its popularity, only one farmer could identify it by its official release name. In most of the villages, this variety is called *Agric*. However, there are about 43 other varieties that are also called *Agric* by farmers. Of these 43 varieties, 15 are improved and 28 are landraces. This suggests that a lack of proper variety naming, as well as weak dissemination efforts play a role in the observed high misclassification rates of improved varieties. Overall, the above results suggest that adoption data from household surveys cannot be relied upon in estimating the productivity effects of adoption.

Determinants of Correct Classification

In this section we examine whether misclassification is exogenous to household characteristics. This assumption has been commonly used as an important criterion for parameter identification in several studies (Aigner 1973; Black, Berger, and Scott 2000; Frazis

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[8] Note that farmers also practice relay cropping. In Nigeria, cassava is mostly relay cropped following maize. The maize is often harvested before the cassava develops canopy. Note that in some plots farmers mix improved varieties with local varieties. Thus, some of the adopters are "partial adopters".

[9] Given this result, the conditional probability of false negatives becomes 36%, calculated as $25/(25+47)$ and the conditional probability of false negatives becomes 34.4%, calculated as $10.7/(10.7+20.4)$.

and Loewenstein 2003; Brachet 2008). In particular, the analysis is intended to understand household-level correlates of correct identification of improved cassava varieties. We address this question using the following operational Probit specification,

$$(11) \quad Y_{ip} = \boldsymbol{\beta} \mathbf{x}_i' + v_i$$

where Y_{ip}, is an indicator of classification by household i at plot p. For each plot, Y_{ip} takes a value of one if farmers correctly identify the improved varieties they grow, and zero otherwise. To add further insights, we also estimated the determinants of false positives and false negatives separately using the above specification. For false negative cases, the dependent variable takes a value of one if a farmer wrongly identifies an improved variety as landrace in a specific plot, and zero otherwise. Similarly, for false positive cases, the dependent variable takes a value of one if a farmer wrongly identifies a landrace as improved variety in a specific plot, and zero otherwise. Results are reported in table 4. Our findings indicate that correct identification of improved varieties is correlated with a range of household characteristics. In particular, three sources of heterogeneity largely explain the probability of correct identification of improved varieties. These include the level of education, access to information (such as mobile phone ownership, access to extension and membership to associations), and location.

Farmers with access to more structured sources of information (mobile phone ownership, access to extension, and formal and informal associations) and with a better educational level are more likely to identify the improved varieties they grow in their plots. We also found that farmers in northern, south-western, and south-south Nigeria are more likely to identify correctly the varieties they grow compared to those in the southeast. Mobile phone ownership, access to extension and membership in associations are negatively correlated with the probability of false negative responses. In addition, we find that more educated households are less likely to identify landraces as improved varieties.

Effect of Adoption on Productivity

OLS estimation results. In this section, we present OLS results using both household survey

and DNA-fingerprinted adoption data. Results are presented in table 5. The first column presents results based on farmers' self-reported adoption status, whereas the second column presents the results based on DNA-fingerprinted data. Both models are estimated at the plot level to account for plot-level heterogeneities between adopters and non-adopters. Parameter estimates on the adoption of improved cassava varieties are 0.353 based on self-reported adoption status and 0.467 based on DNA-fingerprinted adoption status. This result suggests a yield advantage of 42% to 60% for improved cassava varieties over landraces.[10] As such, misclassification results in an attenuation bias as the productivity impacts of adoption is 18 percentage points higher when using DNA-fingerprinted adoption data compared to self-reported adoption data.

This result is consistent with the findings of previous studies (Aigner 1973; Hausman, Abrevaya, and Scott-Morton 1998; Kane, Rouse, and Staiger 1999; Black, Berger, and Scott 2000; Frazis and Loewenstein 2003; Mahajan 2006; Lewbel 2007; Hu and Schennach 2008; Nguimkeu, Denteh, and Tchernis 2017). In the absence of misclassification, parameter estimates of the two models should be the same. Therefore, the large discrepancy between the two results suggests that measurement error is consequential. OLS estimates could still be biased due to the endogeneity of the adoption decision.[11] The next subsection presents IV estimation results.

IV estimation results. We first present the determinants of adoption (first-stage results for our IV estimation) and then the determinants of productivity (second-stage results for our IV regression). First-stage results using household survey data and DNA-fingerprinted data are presented in table 6. Note that the importance of estimating the first stage using the two data sources may be doubted as classical measurement error in the dependent variable does not bias parameter estimates. However, in our case, the measurement error is necessarily non-classical since our dependent variable is binary, and

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[10] Note that effects are calculated as 100[exp(coef.) - 1] since the dependent variable is expressed in logarithm.

[11] The R-squared in the outcome regressions are quite low. This is not surprising given the cross-sectional nature of the data, and it is not an issue either, given that the joint F-statistic is highly significant.

Table 4. Probit Model Estimates of the Determinants of Varietal Identification

	Correct Classification	False Negatives	False Positives
Household size	0.024*	−0.022	−0.011
	(0.014)	(0.017)	(0.022)
Education	0.016**	−0.008	−0.022***
	(0.006)	(0.008)	(0.008)
Age	−0.013	0.013	0.017
	(0.013)	(0.016)	(0.017)
Age^2	0.000	−0.000	−0.000
	(0.000)	(0.000)	(0.000)
Sex	−0.060	−0.090	0.188
	(0.128)	(0.150)	(0.192)
Livestock ownership (TLU)	0.032*	−0.018	−0.056**
	(0.019)	(0.021)	(0.024)
Mobile phone ownership	0.479***	−0.575***	−0.052
	(0.146)	(0.169)	(0.263)
Access to extension	0.156**	−0.162**	−0.022
	(0.066)	(0.075)	(0.101)
Access to credit	0.046	−0.080	−0.045
	(0.070)	(0.086)	(0.100)
Membership in credit and saving associations	0.082	−0.086	0.040
	(0.067)	(0.081)	(0.116)
Membership in cooperatives	0.128*	−0.178**	−0.136
	(0.071)	(0.088)	(0.111)
Membership in cassava growers' associations	0.163**	−0.249**	0.062
	(0.081)	(0.101)	(0.113)
Plot intercropped	0.083	−0.058	−0.082
	(0.051)	(0.059)	(0.072)
Plot with good soil fertility	0.007	0.080	0.106
	(0.197)	(0.233)	(0.273)
Plot with medium soil fertility	−0.055	0.208	0.057
	(0.194)	(0.232)	(0.275)
Plot managed by men	0.152	−0.160	0.041
	(0.125)	(0.156)	(0.155)
Plot managed jointly	0.063	−0.047	0.065
	(0.113)	(0.136)	(0.149)
North	0.471***	−0.563***	−0.303*
	(0.109)	(0.120)	(0.171)
South-West	1.026***	−1.029***	−0.453***
	(0.111)	(0.115)	(0.167)
South-South	0.827***	−0.870***	−0.400**
	(0.113)	(0.116)	(0.184)
Wald $\chi^2(27)$	225***	212.5***	34.9***
Pseudo R^2	0.117	0.137	0.03
Percentage correct predictions	0.66	0.724	0.80
N	5,295	3,645	2,883

Note: Standard errors clustered at the enumeration area level are reported in parentheses. Asterisks ***, **, and * refer to significance at the 1%, 5%, and 10% levels, respectively.

thus the measurement error in adoption status cannot be independent of the true adoption status, but rather is negatively correlated with the true adoption status (Meyer and Mittag 2014). As such, parameter estimates can become biased and may even assume the wrong sign when misclassification is pervasive (Nguimkeu, Denteh, and Tchernis 2017). The results show that some socio-economic characteristics have robust effects. For example, household size has a positive and statistically significant effect on the probability of adopting improved cassava varieties irrespective of the way adoption status is measured. For education, we found a statistically significant effect when using DNA-fingerprinted data but it turned out to be insignificant when using the farmer's self-reported data. Theory

Table 5. OLS Estimates of the Determinants of Cassava Yields in Nigeria Dependent Variable: Log (Yield)

	Self-reported Adoption Data	DNA-fingerprinted Adoption Data
Improved cassava variety	0.353***	0.467***
	(0.051)	(0.052)
Other controls	Yes	Yes
Location dummies	Yes	Yes
Joint F-statistic	8.6***	11.1***
R^2	0.075	0.09
N	5,295	5,295

Note: Standard errors clustered at the enumeration area-level are reported in parentheses. Asterisks ***, **, and * refer to significance at the 1%, 5%, and 10% levels, respectively. Other controls include use of fertilizer, herbicide and pesticide, plot management, intercropping and soil fertility status, ownership of mobile phones, access to extension, access to credit, membership in a cassava growers association, membership in informal saving and credit institutions, membership in cooperatives, livestock size in TLU, age, education, household size, and sex. Location dummies are as follows: north, south-west south-east and south-south.

predicts that more educated farmers are more likely to adopt improved technologies. In this regard, measuring adoption status using DNA-fingerprinted data provides consistent estimates. In addition, access to extension and membership in cassava growers' associations are significant only when self-reported adoption data are used. However, for some of the socio-economic variables, effects differ not only in magnitude but also in direction. For instance, we found sign reversal effects for mobile phone ownership. These results underscore the fact that self-reported adoption status can lead to erroneous conclusions about the determinants of adoption and thus the measurement of adoption is very important for designing appropriate policy interventions that address constraints to adoption. Moreover, the results show that the selected instruments are relevant since they are statistically significant at a 1% level.

Second-stage results on the determinants of productivity are presented in table 7. The results suggest that the effect of adoption on productivity ranges from 60% to 81%. Note that in the first column, we did not control for the endogeneity of misclassification, only unobserved heterogeneity in adoption status was controlled for. Since the second column does not suffer from measurement error, we controlled only for the endogeneity bias caused by unobserved heterogeneities between adopters and non-adopters. Moreover, our results suggest that using an instrumental variable for the endogeneity of adoption decision does not correct for the endogeneity bias caused by endogenous misclassification. This is because parameter estimates based on self-reported adoption status are always different from those estimates based on

DNA-fingerprinted data (see table 7). Correcting such bias requires an instrument to control for the endogeneity of adoption status and an extra instrument to control for the endogeneity of misclassification.

Another related problem, perhaps peculiar to technological interventions in the agricultural sector, is the inherent behavioral adjustment of farmers based on their own subjective self-assessment of adoption status. Using a double-blind randomized experiment for improved maize varieties in rural Tanzania, Bulte et al. (2014) showed that behavioral adjustment effects can play an important role as productivity depends not only on the improved variety itself (the effect associated with genetic gain) but also on the use of complementary inputs and agronomic practices (behavioral adjustments). For instance, conditional on all other confounding factors, a given farmer may allocate more labor and fertilizer and apply better management techniques to an improved variety compared to a traditional variety. These observed behaviors in input allocation can, in a regression framework, be fully controlled for. However, some dimensions of behavioral adjustment are unobserved and may introduce bias.[12] As such, it is difficult to distinguish whether heterogeneity in returns is caused by the technology itself or because of such unobserved behavioural adjustments. For example, false negative cases may introduce downward bias due to negative behavioural adjustment effects. Similarly, false positive cases will also introduce downward bias due

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[12] If such unobserved dimensions are time-invariant, they can also be controlled through plot fixed effects.

Table 6. Probit Model Estimates of the Determinants of Adoption

	Self-reported Adoption Data	DNA- fingerprinted Adoption Data
Household size	0.030**	0.029*
	(0.015)	(0.016)
Education	0.008	0.020***
	(0.007)	(0.007)
Age	−0.001	−0.016
	(0.016)	(0.016)
Age2	0.000	0.000
	(0.000)	(0.000)
Sex	−0.002	−0.176
	(0.141)	(0.147)
Livestock ownership (TLU)	0.011	0.051**
	(0.020)	(0.022)
Mobile phone ownership	0.404***	−0.437**
	(0.149)	(0.176)
Access to extension	0.244***	0.094
	(0.073)	(0.081)
Access to credit	0.019	−0.043
	(0.075)	(0.077)
Membership to credit and saving associations	0.096	−0.089
	(0.073)	(0.084)
Membership in cooperatives	0.098	0.009
	(0.079)	(0.079)
Membership in cassava growers' associations	0.341***	−0.037
	(0.092)	(0.092)
Plot intercropped	0.085	0.090
	(0.055)	(0.059)
Plot with good soil fertility	−0.042	−0.116
	(0.167)	(0.201)
Plot with medium soil fertility	−0.043	−0.012
	(0.169)	(0.189)
Plot managed by men	0.190	0.238*
	(0.136)	(0.124)
Plot managed jointly	0.083	0.242**
	(0.126)	(0.121)
Neighbor is adopter	1.440***	0.152**
	(0.075)	(0.069)
Friend is adopter	0.166**	1.414***
	(0.069)	(0.080)
Wald $\chi^2(27)$	636.3***	410***
Pseudo R2	0.32	0.22
Percentage correct predictions	0.79	0.75
N	5,295	5,295

Note: Standard errors clustered at the enumeration area level are reported in parentheses. Asterisks ***, **, and * refer to significance at the 1%, 5%, and 10% levels, respectively. Regional dummies were included but not reported here.

to positive behavioural adjustments. Therefore, unbiased and consistent parameter estimates on the impact of adoption can only be obtained when behavioural adjustment effects are zero. We tested for the presence of such behavioral adjustment effects by interacting adoption with correct identification (excluding false negatives and positives). In this case, the treatment variable (correct identification) takes a value of one if the farmer correctly identifies improved varieties, and zero if the farmer correctly identifies landraces (false negative/positive responses will have missing values).[13] The interaction

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[13] Another way of estimating behavioral adjustment effects is to compare "true adopters" with "false negatives" since the two groups have the same technology, which is an improved variety. In addition, effects can also be estimated by comparing "false positives" with "true non-adopters".

Table 7. IV Regression Estimates of the Determinants of Cassava Yields in Nigeria (Dependent Variable: Log (Yield))

	1 Self-reported Adoption Data	2 DNA-fingerprinted Adoption Data	3 Interaction
Improved cassava variety	0.471***	0.596***	
	(0.106)	(0.119)	
Improved cassava variety*Correct identification			0.663***
			(0.108)
Other controls	Yes	Yes	Yes
Location dummies	Yes	Yes	Yes
Joint F-statistic	6.9***	8.2***	7.98***
R^2	0.073	0.086	0.116
N	5,295	5,295	3,395

Note: Standard errors clustered at the enumeration area-level are reported in parentheses. Asterisks ***, **, and * refer to significance at the 1%, 5%, and 10% levels, respectively. Other controls include use of fertilizer, herbicide and pesticide, plot management, intercropping and soil fertility status, ownership of mobile phones, access to extension, access to credit, membership in cassava growers' association, membership in informal saving and credit institutions, membership in cooperatives, livestock size in TLU, age, education, household size, and sex. Location dummies are as follows: north, south-west south-east and south-south.

term between the correct identification and the adoption variable then captures the improved variety and behavioral adjustment effect consistently. Results reported in column 3 of table 7 suggests that when both technological effects and unobserved behavioral adjustments of farmers are considered, adoption increases productivity by about 94%. However, when such unobserved behavioral adjustments of farmers are not considered, adoption of improved varieties increases productivity by 81% (column 2, table 7). These results underscore the importance of capturing not only pure technological effects through innovative techniques of data collection such as DNA-fingerprinting but also the subsequent behavioral adjustments of farmers based on their own subjective assessment of treatment status.

Finally, we summarized the magnitude of biases due to endogeneity, misclassification and behavioral adjustment effects. We find that failure to control for misclassification of adoption status (assuming adoption is exogenous) biases productivity estimates by 18 percentage points (60% to 42% from OLS estimates in table 5), while failure to control for the endogeneity of the treatment status biases productivity estimates by about 22 percentage points (based on estimates from the DNA-fingerprinted adoption data which ranges from 81.5% in table 7 to 60% in table 5). Without the homogeneity assumption, IV estimates are only local average treatment effects (LATE) while OLS results are average treatment effects (ATEs). Bias

due to misclassification is calculated using OLS estimates while the bias due to endogeneity is calculated by comparing the naive OLS with IV coefficients. Assuming homogenous treatment effects (ATE=LATE), our results underscore that controlling for misclassification is as important as controlling for unobserved heterogeneity, at least in this case study. In fact, the bias due to misclassification can be similar to the bias due to the endogeneity of adoption decision. The magnitude of the two biases is largely an empirical question and depends on the severity of misclassification. When misclassification is minor, controlling for the endogeneity of adoption decision may become more important than controlling for misclassification. Moreover, ignoring inherent behavioral adjustments has an additional bias of 13 percentage points (94%-81%).

Robustness check. In our main analysis, we used neighbors/friends' adoption decisions as an identifying instrument. However, the exclusion restriction can be violated if farmers learn about productivity-enhancing techniques in addition to improved varieties from neighbors/friends. In our case, this is less likely to make the instrument invalid. If farmers learn about productivity-enhancing methods beyond learning about improved varieties, then this will not be a concern as our specification controls for management practice, soil quality, and input use. In addition, farmers are less likely to learn about unobservable characteristics of neighbors/friends that makes them more productive.

Table 8. Robustness Check Results

	Self-reported Adoption Data	DNA-fingerprinted Adoption Data
Lower bound	0.47	0.59
Upper bound	0.50	0.62

Nonetheless, we present an alternative robustness check based on the approach proposed by Conley, Hansen, and Rossi (2012). This approach allows bounding effects in situations where the exclusion restriction need not be precisely held (Clarke and Matta 2017). Therefore, with some assumptions, the above method allows for consistent estimation of treatment effects when unobserved heterogeneities are present and appropriate exclusion restrictions are not met strictly. Our robustness check results are reported in table 8. Lower and upper bound effects suggest that our IV estimates are consistent.

Discussion and Conclusions

It is widely recognized that improved agricultural technologies play a critical role in agricultural transformation and economic growth in developing countries. The dissemination and diffusion of improved crop varieties has been cited as the primary pathway through which technological change in the agricultural sector can bring about productivity gains (Gollin, Stephen, and Richard 2002). Understanding how and why households adopt improved varieties and their subsequent effects on productivity gains is, therefore, important to disseminate technologies that are appropriate to the conditions of smallholder farmers. This article combined a household survey and a DNA-fingerprinting-based varietal identification approach to answer the above policy-relevant questions. In particular, we used adoption status from DNA-fingerprinted data as a benchmark and examined to what extent misclassification biases parameter estimates of adoption on productivity. Furthermore, this article compared the rates of misclassification from traditional household surveys using DNA-fingerprinted adoption data as a benchmark. Such a validation exercise is particularly important for the impact evaluation literature

since most adoption studies rely on household surveys for measuring the impact of adoption on a range of outcome variables of interest. Our results show that both false positive and false negative responses are prevalent. However, the incidence of false negative is more than twice that of false positive. This suggests that traditional household surveys are more likely to underestimate adoption rates. Moreover, we show that misreporting is not exogenous to household characteristics and largely depends on the educational level of the respondents and their access to structural sources of information.

Our results show that the estimated effects of adoption on productivity in the presence of misclassification are biased. Our results further suggest that the presence of a well-functioning seed system is crucial as misclassification is more likely to be lower and hence the effect of adoption on a range of outcome variables of interest can be estimated consistently. For example, our survey shows that a formal seed market for cassava is almost non-existent in rural Nigeria, and more than 70% of the farmers rely on social networks (friends, relatives, and neighbors) for access to cassava planting material. Survey designs also need to take into account the fact that farmers rely on informal seed systems and should employ a variety of data collection techniques to validate information on adoption. These techniques include asking farmers not only about the type of varieties they grow but also about the source of the planting material. Training farmers on varietal identification using social networks and a more efficient extension delivery system may improve farmers' awareness about the varieties they grow in their plots.

In terms of impact evaluation, estimating impact using a higher level of aggregation would be less biased in the presence of misclassification. For example, defining adoption at the household level "if a farmer grows at least one improved variety" would introduce less misclassification compared to measuring adoption at the plot level "if a farmer grows improved variety in a specific plot." A plot-level/variety-level model would be more precise in the absence of misclassification as observed/unobserved plot-level heterogeneities are accounted for. However, misclassification in treatment status is likely to be more pronounced as farmers are more likely to be wrong in identifying the type of variety in some of the plots, especially when different

varieties are grown in several plots. As such, estimating adoption at the varietal/plot level probably suffers the most from misclassification. The fact that most adoption studies were conducted at the varietal/plot level raises concerns about the accuracy of parameter estimates, given the level of misclassification found in this validation study.

Despite its advantage, the use of DNA-fingerprinting has cost implications at different levels. This involves costs associated with the construction of the reference library, logistics for sample collection in the field, DNA extraction, genotyping, and data analysis for varietal identification (Kosmowski et al. 2016; Maredia et al. 2016). In this case study, the cost of DNA-fingerprinting was about $74/household (note that this cost does not include fixed costs associated with the construction of the reference library since it was constructed as part of a previous project. In addition, the cost does not capture salary-related costs accurately). In our application, the benefits associated with DNA-fingerprinting are measured by the added precision on productivity estimates. If all farmers who believe they are adopters (albeit falsely) are willing to grow improved varieties, the use of DNA-fingerprinting will bring false positive subjects on board. At the same time, the false negative subjects will adjust their behavior. Hence, the expected economic benefit/household is roughly the dollar value of the correct treatment effect estimate multiplied by the proportion of false positives, plus the dollar value of the behavioral adjustment effect estimate multiplied by the proportion of false negatives. Given our parameter estimates in tables 7 and the average price of $0.1/kg for fresh cassava roots, the benefits/household from the use of DNA-fingerprinting is about $87.5. This results in a benefit-cost ratio of about 1.17. Thus, the short-run economic gain of using DNA-fingerprinting is marginally positive. Moreover, the cost of undertaking DNA-fingerprinting is likely to be cheaper in the future due to a rapidly declining cost of genotyping (Maredia et al. 2016). Therefore, our estimates are likely to be a lower bound.

For our main empirical analysis, we relied on self-reported production values. However, estimating the production of cassava from a given plot is notoriously difficult due to continuous harvesting and lack of harvest record-keeping by farmers. The nature of the crop might therefore make self-reported production values prone to measurement error. Moreover, farmers often use local production units, and converting production values to standard units is also prone to errors (Gourlay, Kilic, and Lobell 2017). If self-reported production values are measured with errors and if such errors are systematic (if farmers that misreported adoption status also misreport production values), then this error may introduce bias. In our data, we did not find this to be the case. For example, farmers that report improved varieties as local varieties should report a lower production value in the presence of systematic bias. However, this group of farmers did not underreport their production value as they reported a significantly higher production value compared to actual non-adopters. Despite the above assertion from our data, measurement errors in self-reported production data may still be non-classical. Future research using full crop cutting could, therefore, be important to understand the effect of such measurement errors.

Supplementary material

Supplementary material is available online at *American Journal of Agricultural Economics* online.

References

Aigner, D. 1973. Regression with a Binary Independent Variable Subject to Errors of Observation. *Journal of Econometrics* 1 (1): 49–59.

Almada, L., I. McCarthy, and R. Tchernis. 2016. What Can We Learn about the Effects of the Food Stamps on Obesity in the Presence of Misreporting? *American Journal of Agricultural Economics* 98 (4): 997–1017.

Battistin, E., and B. Sianesi. 2011. Misclassified Treatment Status and Treatment Effects: An Application to Returns to Education in the United Kingdom. *Review of Economics and Statistics* 93 (2): 495–509.

Black, D.A., M. Berger, and F. Scott. 2000. Bounding Parameter Estimates with Non-Classical Measurement Error. *Journal of American Statistical Association* 95 (451): 739–48.

Bollinger, C., and M. David. 1997. Modeling Discrete Choice with Response Error:

Food Stamp Participation. *Journal of American Statistical Association* 92 (439): 827–35.

Brachet, T. 2008. Maternal Smoking, Misclassification, and Infant Health, University of Pennsylvania. Accessed October 22, 2015. Available at: https://papers.ssrn.com/sol3/papers.cfm?abstract_id=1009781.

Bulte, E., G. Beekman, S. Di Falco, J. Hella, and P. Lei. 2014. Behavioral Responses and the Impact of New Agricultural Technologies: Evidence from a Double-Blind Field Experiment in Tanzania. *American Journal of Agricultural Economics* 96 (3): 813–30.

Clarke, D., and M. Matta. 2017. Practical Considerations for Questionable IVs. MPRA Paper 79991. Available at: https://mpra.ub.uni-muenchen.de/79991/.

Conley, T.G., C.B. Hansen, and P.E. Rossi. 2012. Plausibly Exogenous. *Review of Economics and Statistics* 94 (1): 260–72.

Duflo, E., M. Kremer, and J. Robinson. 2008. How High Are Rates of Return to Fertilizer? Evidence from Field Experiments in Kenya. *American Economic Review* 98: 482–8.

Frazis, H., and M.A. Loewenstein. 2003. Estimating Linear Regressions with Mis-Measured, Possibly Endogenous, Binary Explanatory Variables. *Journal of Econometrics* 117 (1): 151–78.

Gollin, D., P. Stephen, and R. Richard. 2002. The Role of Agriculture in Development. *American Economic Review* 92 (2): 160–4.

Gourlay, S., T. Kilic, and D. Lobell. 2017. Could the Debate be Over? Errors in Farmer-Reported Production and Their Implications for Inverse Scale—Productivity Relationship in Uganda. Paper presented at the Center for the Study of African Economies (CSAE) Conference, 20 March 2017, Oxford, UK.

Gundersen, C., B. Kreider, and J.V. Pepper. 2017. Partial Identification Methods for Evaluating Food Assistance Programs: A Case Study of the Causal Impact of SNAP on Food Security. *American Journal of Agricultural Economics* 99 (4): 875–93.

Hausman, J., J. Abrevaya, and F. Scott-Morton. 1998. Misclassification of the Dependent Variable in a Discrete-Response Setting. *Journal of Econometrics* 87 (2): 239–69.

Hu, Y., and S. Schennach. 2008. Instrumental Variable Treatment of Non-Classical Measurement Error Models. *Econometrica* 76 (1): 195–216.

Ilukor, J., T. Kilic, J. Stevenson, S. Gourlay, F. Kosmowski, A. Kilian, J. Serumaga, and G. Asea. 2017. Blowing in the Wind: The Quest for Accurate Crop Variety Identification in Field Research, with an Application to Maize in Uganda. Paper presented at the CGIAR SPIA Conference on the Impact of Agricultural Research: Rigorous Evidence for Policy, Nairobi, Kenya, July 2017.

Kane, T.J., C.E. Rouse, and D. Staiger. 1999. Estimating Returns to Schooling when Schooling is Misreported. NBER Working Paper No. 7235. Available at: http://www.nber.org/papers/w7235.

Kosmowski, F., A. Aragaw, A. Kilian, A. Ambel, J. Ilukor, B. Yigezu, and J. Stevenson. 2016. Varietal Identification in Household Surveys: Results from an Experiment Using DNA-Fingerprinting of Sweet Potato Leaves in Southern Ethiopia. World Bank Policy Research Working Paper No. 7812.

Kreider, B., J. Pepper, C. Gundersen, and D. Jolliffe. 2012. Identifying the Effects of Snap (Food Stamps) on Child Health Outcomes When Participation Is Endogenous and Misreported. *Journal of American Statistical Association* 107 (499): 958–75.

Krishnan, P., and M. Patnam. 2013. Neighbors and Extension Agents in Ethiopia: Who Matters More for Technology Adoption. *American Journal of Agricultural Economics* 96 (1): 308–27.

Lewbel, A. 2007. Estimation of Average Treatment Effects with Misclassification. *Econometrica* 75 (2): 537–51.

Mahajan, A. 2006. Identification and Estimation of Regression Models with Misclassification. *Econometrica* 74 (3): 631–65.

Maredia, M.K., B. Reyes, J. Manu-Aduening, A.A. DAnkyi, K.M. Hamazakaza, I. Rabbi, P. Kulakow, et al. 2016. Testing Alternative Methods of Varietal Identification Using DNA Fingerprinting: Results of Pilot Studies in Ghana and Zambia. MSU International Development Working Paper No. 149.

Marquis, K., and J. Moore. 2010. Measurement Errors in SIPP Program Reports. Technical Report 113. Available at: https://www2.census.gov/prod2/sipp/wp/SIPP_WP_113.pdf.

Meyer, B., and N. Mittag. 2014. Misclassification in Binary Choice Models. NBER Working Paper No. 20509. Available at: http://www.nber.org/papers/w20509.

Meyer, B., W. Mok, and J. Sullivan. 2009. The Under-reporting of Transfers in Household Surveys: Its Nature and Consequences. NBER Working Paper No. 15181. Available at: http://www.nber.org/papers/w15181.

Nguimkeu, P., A. Denteh, and R. Tchernis. 2017. On the Estimation of Treatment Effects with Endogenous Misreporting. NBER Working Paper No. 24117. Available at: http://www.nber.org/papers/w24117.pdf.

Poirier, D.J. 1980. Partial Observability in Bivariate Probit Models. *Journal of Econometrics* 12: 209–17.

Rabbi, I., P. Kulakow, J.A. Manu-Aduening, A.A. Dankyi, J.Y. Asibuo, E.Y. Parkes, T. Abdoulaye, et al. 2015. Tracking Crop Varieties Using Genotyping-by-Sequencing Markers: A Case Study Using Cassava (Manihot Esculenta Crantz). *BMC Genetics* 16 (115): 1–11.

Shiferaw, B., M. Kassie, M. Jaleta, and C. Yirga. 2014. Adoption of Improved Wheat Varieties and Impacts on Household Food Security in Ethiopia. *Food Policy* 44: 272–84.

Suri, T. 2011. Selection and Comparative Advantage in Technology Adoption. *Econometrica* 79: 159–209.

Zeng, D., J. Alwang, G.W. Norton, B. Shiferaw, M. Jaleta, and C. Yirga. 2015. Ex Post Impacts of Improved Maize Varieties on Poverty in Rural Ethiopia. *Agricultural Economics* 46 (4): 515–26.