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IITA's genebank, cowpea diversity on farms, and farmers' welfare in Nigeria

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Abstract

Background: Cowpea or black-eyed pea (*Vigna unguiculata* L.) is one of the preferred food crops in Nigeria, as expressed in land area and production. The popularity of the crop is in part related to the successful development and adoption of improved cowpea varieties. Although the genebank of the International Institute of Tropical Agriculture (IITA) has contributed to cowpea conservation and improvement efforts by breeding programs internationally and in Nigeria, few studies have attempted to link the genebank to the management of cowpea genetic resources (CGRs) on farms. This study explores the linkage between IITA's genebank and cowpea variety diversity on farms and other measures of farmers' welfare in Nigeria.

Methods: A multistage stratified sampling was used to select the sample households. A cross-sectional household survey was conducted to collect data from 1524 cowpea-producing households. In addition, "Helium", a multi-platform pedigree visualization tool with phenotype display was used to gather information about improved cowpea breeding lines and their pedigrees. For data analysis, ecological indices of spatial diversity were employed, and a conditional recursive mixed-process model and a multinomial endogenous treatment effect model were developed.

Results: We found that growing an improved variety with genebank ancestry is not significantly associated with lower spatial diversity among cowpea varieties. While they may introduce new traits through ancestry, improved varieties do not displace other cowpea varieties or landraces. We also found that genebank ancestry is positively and significantly associated with cowpea yield and farmers' welfare.

Conclusions: These findings show additional benefits from IITA's genebank in Nigeria and that adoption of improved varieties with genebank ancestry does not contribute to the erosion of CGRs on smallholder farms in Nigeria. Policymakers and practitioners should consider these findings when analyzing the benefits of conserving crop genetic diversity in genebanks and on farms.

Keywords: Genebank, On-farm cowpea diversity, Farmers' welfare, Nigeria

Background

Cowpea or black-eyed pea (*Vigna unguiculata* L.) is a food legume that provides food and fodder as well as improving soil fertility and contributes to the sustainability of food production in marginal areas of the dry

tropics (Singh 1997). It is one of the preferred food crops in Nigeria, in terms of land area and production. For instance, land areas of cowpea were estimated at 0.117 million ha in 1981 and rose to 3.2 million ha and 4.3 million ha in 2012 and 2019, respectively (FAO 2020). The North West and North East regions of Nigeria are the most productive, including Borno, Bauchi, Gombe, Jigawa, Kaduna, Kano, Katsina, Kebbi, Sokoto, and Zamfara States, which represent 75% of the total cowpea production in Nigeria (Manda et al.

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2019). Likewise, the national production of cowpea has increased by 165% from 1980 to 1990 and by 50% from 2009 to 2019 (FAO 2020; Singh 2005; See also in the Additional file 1: Fig. S1).

Rising land area and production of cowpea are partially related to cowpea conservation and improvement efforts at the International Institute of Tropical Agriculture (IITA) as well as the adoption of improved cowpea varieties in Nigeria (Ogundapo et al. 2020). Research on cowpea conservation and improvement was initiated at IITA in 1970, and over 50 countries, including Nigeria, have identified and released improved cowpea varieties from IITA for general cultivation (Singh 1997). Some recent studies have indicated that IITA's genebank houses over 17,000 accessions of cowpea (Genebank Platform 2020), which have been used for the development of over 800 improved cowpea cultivars, including lines and varieties. A substantial number of the released improved cowpea varieties have been adopted by Nigerian farmers (IITA 2013; Ogundapo 2016).

Although the genebank of IITA has contributed to cowpea conservation and improvement efforts by breeding programs worldwide and in Nigeria, few studies have attempted to link the genebank to on-farm management of cowpea genetic resources (CGRs). This may be explained by the fact that the primary role of IITA's genebank is the maintenance of crop diversity outside its natural environment. Linking IITA's genebank to on-farm management of crop genetic resources is important because it can reveal benefits from conservation of genetic materials under *ex situ* conditions in the context of scarce funding (Wale et al. 2011).

To our knowledge, only two studies have tried to investigate the impact on farms of the cowpea collection held in IITA's genebank or released from IITA. Ogundapo et al. (2020) used a combination of DNA fingerprinting and an economic surplus model to demonstrate the outcomes of CGR conservation and improvement efforts on smallholder farms in Kano State, Nigeria. The authors found increased productivity of low-income cowpea farmers who adopted improved cowpea varieties and increased net present value for cowpea germplasm conservation. They estimated that productivity changes lifted 487,219 persons out of poverty between 1980 and 2015. Manda et al. (2019) rigorously estimated the poverty impacts of crop genetic improvement on the income and poverty of farmers in Nigeria using an endogenous switching regression model and nationally representative data. Their results indicated that adoption of improved cowpea varieties raised per capita household income and asset ownership, also reducing income and asset poverty. However, the second study did not capture the link between the IITA genebank and its potential

contribution to the development of cultivated cowpea varieties in Nigeria.

We built on these two studies and utilized the same data as Manda et al. (2019) to explore the linkage to the genebank and to the variety diversity on farms and other measures of farmers' welfare. Our objective was twofold. First, we established the link between the IITA's genebank and the development of improved cowpea varieties. We related this link to measures of on-farm diversity of cowpea varieties in Nigeria. Second, we examined the impact of IITA's genebank on cowpea yield and farmers' welfare in Nigeria through the adoption of improved varieties.

Our study contributes to the empirical literature on the valuation of genebanks, especially those based in Africa. Smale and Jamora (2020) reviewed earlier work on genebank valuation and assembled a set of current empirical studies that document some of the values associated with the international genebanks coordinated by the CGIAR (formerly the Consultative Group on International Agricultural Research). Two recent studies attempted to value international genebanks in Africa. Sellitti et al. (2020) analyzed the contribution of the genebank of the International Center for Tropical Agriculture (CIAT) to the development of iron-biofortified bean varieties and impacts among farming households in Rwanda. Their study showed the role of CIAT's genebank in the improvement of bean varieties and in generating benefits for farmers. Kitonga et al. (2020) explored the benefits of using the two most popular fodder tree species among smallholder farmers, sourced from the genebank of the World Agroforestry (ICRAF). The authors traced the benefits of ICRAF's genebank germplasm distributions to smallholder farmers. However, neither of these studies related their results specifically to *in situ*, on-farm conservation. On-farm agrobiodiversity has both potential private benefits to smallholder farmers and public benefits to the world's producers and consumers. We contribute to previous literature by testing the linkage from the genebank to spatial diversity of varieties grown on farms, and ultimately to the welfare of smallholder farmers. We present the case of the IITA's genebank and cowpea production in Nigeria as an example.

Material and methods

Description of the study area and data sources

The study was conducted in the framework of the Tropical Legumes III project and the Genebank Impacts project. The Tropical Legumes III project is an international initiative supported by the Bill & Melinda Gates Foundation and implemented by ICRISAT, CIAT, IITA and national agriculture research system partners from Africa and India (Varshney et al. 2019). Data were collected through a household survey conducted

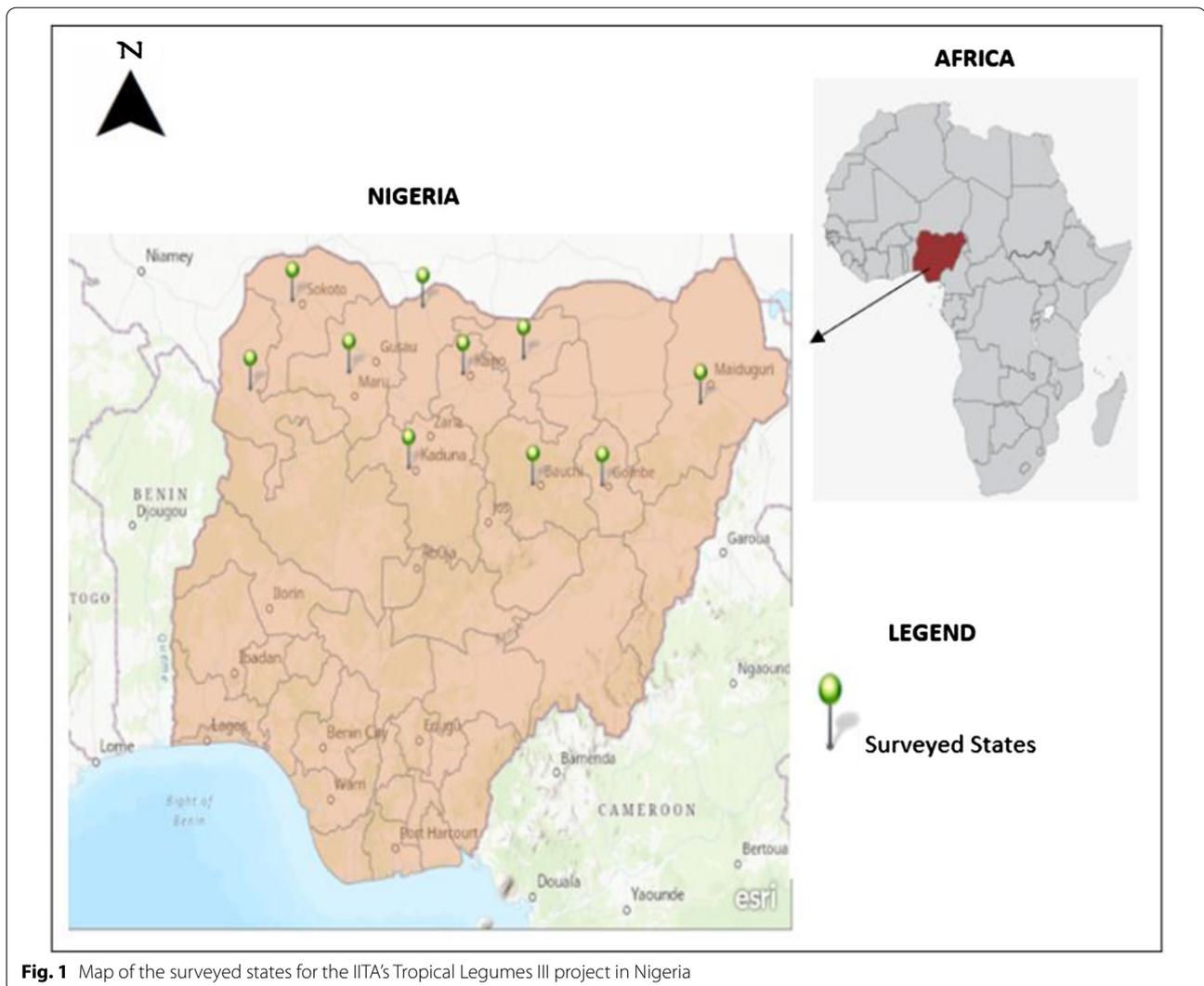


Fig. 1 Map of the surveyed states for the IITA's Tropical Legumes III project in Nigeria

in Northern Nigeria in 2017 and used by Manda et al. (2019). The survey was conducted in ten states (Borno, Bauchi, Gombe, Jigawa, Kaduna, Kano, Katsina, Kebbi, Sokoto, and Zamfara), which represent about 75% of the total cowpea production in Nigeria (Manda et al. 2019). Figure 1 shows the location of the states selected for the household survey. Enumerators collected information from 1524 cowpea-producing households. A multistage stratified sampling was used to select the surveyed households, based on a sampling frame of local government areas and villages, and households, provided by the National Population Commission and the extension agents from the Agricultural Development Program, respectively. The survey was administered electronically using “Surveybe” and covered household composition and characteristics; knowledge of improved crop varieties; input use and crop

production, including cowpea varieties grown and area allocated to each; adoption of improved cowpea varieties; crop utilization and household food security; marketing of crops; household assets; livestock production and marketing; sources of income; access to credit; household expenditure; social capital; and networking.

The quality of data was checked electronically. The data were uploaded in an electronic format immediately after collection. Supervisors were able to automatically record each interview's start time, end time and GPS location, validating the interview and comparing its time and GPS location to that of other interviews during which a supervisor was present. Considering that some areas where data were collected had limited electricity connectivity, each enumerator was given a battery pack to ensure that the tablets had the power to complete the interviews without problems.

Table 1 List and description of variables used in regression models

Variable	Definition
Dependent variables	
d^f	Menhinick richness index for cowpea varieties grown
d^e	Shannon evenness index for cowpea varieties grown
d^d	Berger-Parker dominance index for cowpea varieties grown
d^c	Herfindahl–Hirschman concentration index for cowpea varieties grown
Anc	= 1 if the cowpea variety grown has a genebank ancestor and 0 otherwise
Yield	Cowpea yield in kilograms (kg/ha)
Consumption	Quantity of cowpea used for home food consumption, in kilograms (kg)
Sale	Quantity of cowpea grain sold, in kilograms (kg)
Independent variables	
Household characteristics	
Age	Age of the household head in years
Sex	= 1 if the household head is male and 0 otherwise
Education	Education of the household head in years
Household size	Number of household members
Experience	= 1 if the household has experience growing an improved cowpea variety and 0 otherwise
Need credit	= 1 if the household head needs credit and 0 otherwise
Pedigree information	
Anc	= 1 if the cowpea variety grown has a genebank ancestor and 0 otherwise
NumAnc	The number of genebank ancestors in the pedigree of the cowpea variety grown
Farm characteristics	
Size	Farm size in ha, using GPS
Slope	Number of plots that are perceived as flat
Soil fertility	Number of plots that are perceived as poor
Distance to field	Distance to field from residence, in minutes
Market characteristics	
Distance to seed dealer	Distance to the nearest seed dealer in minutes
Distance to village market	Distance to the village (local) market in minutes
Distance to district market	Distance to the district (main) market in minutes
Geographical zone	
North East	= 1 if the household falls within the North East zone and 0 for the North West zone

The second source of data was the genebank of IITA, supported by the Genebank Impacts project. We gathered information about improved cowpea breeding lines and their pedigrees through key expert consultations and reports from IITA's cowpea breeding program (Singh 1997). We also consulted the database (or information management system) of the cowpea program of IITA and “Helium”, a multi-platform pedigree visualization tool with phenotype display (Shaw et al. 2014).

Description of variables

Our choice of variables is motivated by the case of the farm household model in which production and consumption decisions cannot be separated because of missing markets, leading to endogenous decision prices (de Janvry et al. 1991). Benin et al. (2004) adapted the model to analyze the determinants of crop diversity as an

outcome of cropland allocation by Ethiopian smallholders. Other empirical examples are found in Smale (2006). In this approach, diversity “outcomes” are not an explicit choice but a result of optimizing choices over goods consumed from production or purchase given the constraints imposed by farm physical conditions and labor availability, market features, and the household-specific characteristics that influence transactions costs. Definitions of the variables used for our analysis are presented in Table 1.

Following Magurran (2004) and Smale (2006), we measured the varietal diversity of cowpeas on farms by adapting ecological indices of spatial diversity: the Menhinick index, the Shannon index, the Berger-Parker index, and the Herfindahl index. The choice of these indices was motivated by their use in the existing literature reported above and the fact that they represent various

diversity dimensions and fit the information collected (cowpea varieties grown and percentage of area under cowpea varieties grown).

As explained by Magurran (2004), the Menhinick index d^r is a richness index that represents the number of distinct plant populations (varieties or crops) in a defined geographical area, such as a region, community, or in our case, a farm. The applied economics literature cited above adapts this concept using crop or variety area planted by farmers as a proxy for plant populations. Thus, the Menhinick index was computed as follows:

$$d^r = S/\sqrt{A}, \quad (1)$$

where S is the number of cowpea varieties and A is the total cowpea area on a farm.

The Shannon index d^e is an evenness (or heterogeneity) measure, which takes the relative abundance of the plant populations into account and is defined as:

$$d^e = -\sum_{i=1}^n p_i \ln p_i \dots p_i \geq 0. \quad (2)$$

In our case, p_i is the cowpea area share planted to variety i .

The Berger-Parker index d^d expresses the inverse of the degree to which the most abundant plant population dominates the geographical area. We computed the Berger-Parker index as follows:

$$d^d = 1/\max(p_i), \quad (3)$$

where $\max(p_i)$ is the maximum cowpea area share planted to any of the farmer's cowpea varieties.

The Herfindahl index, d^c , is derived from the better known Herfindahl–Hirschman index of concentration that is widely applied in economic analysis of industrial organizations. As applied here, it expresses specialization and tells us whether a single variety occupies most of the planted area. We calculated the Herfindahl index as follows:

$$d^c = \sum_{i=1}^n p_i^2, \quad (4)$$

where p_i is cowpea area share occupied by variety i .

We accounted for the impact of genebank ancestry using “Anc”, a binary variable that measures the adoption of an improved cowpea variety that has a genebank ancestor. Anc takes the value 1 if the farmer is cultivating an improved cowpea variety that has a genebank ancestor and 0 otherwise. This variable helped establish the link between the genebank and improved cowpea varieties grown by farmers.

We also considered cowpea yield. Yield is obtained by dividing the total cowpea harvested on a farm by the farm size, expressed in kg/ha. Two variables were used for measuring farmers' welfare: consumption and sale. Consumption is a nutrition indicator, which refers to the quantity of cowpea used for home food consumption by the household, expressed in kg. Sale is a market (or revenue) indicator, referring to the quantity of cowpea grain sold by the household, expressed in kg.

The other variables that were used for our econometric analysis were vectors of independent variables that represent household characteristics (age of the household head, sex of the household head, education of the household head, household size, household's need of credit, and household's experience growing an improved cowpea variety), pedigree information (whether the household is growing a cowpea variety that has a genebank ancestor), farm characteristics (size, number of plots that are perceived as flat, number of plots that are perceived as poor, and distance to field from residence), market characteristics (distance to the nearest seed dealer, distance to the village market and distance to the district market), and geographical zone (North West and North East).

Methods of data analysis

We used both descriptive and econometric analyses to analyze the data. Primary data from the household survey and secondary data from the genebank of IITA were analyzed using measures of central tendency (means), dispersion (standard deviations), and frequency (percentages). We also used parametric and non-parametric tests (t-test, Fisher test, and Chi-squared test) to compare these measures between populations and regions.

To measure the impact of IITA's genebank on the on-farm diversity of cowpea varieties, we applied a system of two equations. The system helps capture: (1) farmers' decisions to grow a cowpea variety that has a genebank ancestor, and (2) the impact of growing this variety on the spatial diversity of cowpea varieties. We hypothesized that growing an improved cowpea variety that has a genebank ancestor generates benefits from the decision, such as the introduction of new traits or attributes through diverse ancestry.¹ If the farmer favors the improved variety with genebank ancestry over others, growing it may lead to abandonment or a reduction in area allocated to

¹ This is confirmed by the general strategy for cowpea breeding at IITA, which combines multiple disease and insect resistance and broad adaptability to meet the varied requirements of different countries and regions, including Nigeria (Singh 1997; Singh et al. 1997). For instance, the IT90K-277-2 (Sasakawa), which is an improved cowpea variety grown by Nigerian farmers, combines disease (Brown Blotch and Anthracnose) and insect (Aphid) resistance and intercropping characteristics (Singh 1997; Singh et al. 1997).

other cowpea varieties—reducing the spatial diversity of cowpea varieties. The model was formulated for the *i*th farmer as follows:

$$G_i^* = \alpha X_i + e_i \tag{5}$$

$$I_i^* = \beta G_i + \gamma Z_i + u_i \tag{6}$$

Equation 5 describes a farmer’s decision to grow a cowpea variety with genebank ancestry. The farmer *i* compares the expected utility from growing an improved cowpea variety with genebank ancestry, $U_{genebank}$, with the expected utility from growing other cowpea varieties, U_{others} . She grows an improved cowpea variety with genebank ancestry if $G_i^* = U_{genebank} - U_{others} > 0$. G_i^* is a latent variable that captures the expected benefits from the decision and is determined by a set of exogenous variables X_i and the error term e_i . The farmer’s observed decision is a binary variable:

$$G_i = \begin{cases} 1 & \text{if } G_i^* > 0 \\ 0 & \text{otherwise} \end{cases} \tag{7}$$

Equation 6 describes the impact of growing a cowpea variety with genebank ancestry on the spatial diversity of cowpea varieties. I_i^* is an unobservable variable that captures farmer’s diversification strategy, which is determined by the decision to grow a cowpea variety with genebank ancestry and a set of exogenous variables Z_i and the error term u_i . However, on farms, this diversification strategy may be approached by an index I_i , which has the minimum value \underline{I} and the maximum value \bar{I} :

$$I_i = \begin{cases} \underline{I} & \text{if } I_i^* \leq \underline{I} \\ I_i^* & \text{if } \underline{I} < I_i^* < \bar{I} \\ \bar{I} & \text{if } I_i^* \geq \bar{I} \end{cases} \tag{8}$$

We used the conditional recursive mixed-process (CMP) framework (Roodman 2011) to estimate the parameters of the two-equation system. The use of the CMP approach was motivated by the following reasons. First, our system is a multiequation mixed model (the two equations have different forms of dependent variables), with Eqs. 5 and 6 being probit/logit and tobit models, respectively. Second, our system may be perceived as recursive, in the sense that we have clearly defined stages. Stage 1 (Eq. 5), the probit/logit model, captured a farmer’s decision to grow a cowpea variety that had a genebank ancestor, whereas Stage 2 (Eq. 6), the tobit model, captured the effect of a farmer’s decision on spatial diversity of cowpea varieties. The system of equations was estimated using a maximum likelihood (ML)

approach² (Roodman 2011). As our recursive system is fully observed, meaning that the endogenous variable G_i^* appears on the right-hand side as observed, the CMP framework provided consistent estimates (Roodman 2011).

To measure the impact of IITA’s genebank on Nigerian farmers’ welfare, we applied a multinomial endogenous treatment effect model. The multinomial endogenous treatment effect model helps analyze the effects of an endogenous multinomial treatment (when exactly one treatment is chosen from a set of more than two choices) on a specific outcome (Deb and Trivedi 2006a, b). In settings with potential selection on unobservable characteristics and a treatment variable that has more than two categories, both the multinomial endogenous treatment effect model and the multinomial endogenous switching regression model may be used to measure a treatment effect. Our choice of the multinomial endogenous treatment model was motivated by our interest in the average treatment effect and testing the significance of selection effects.

We assumed that farmers were growing one of the three types of cowpea varieties as the main crop³: (1) an (improved) cowpea variety that has a genebank ancestor, (2) an (improved) cowpea variety that does not have a genebank ancestor, and (3) a cowpea landrace. We hypothesized that each of the three types of cowpea varieties has a different impact on farmers’ welfare, the improved cowpea variety with genebank ancestor having the highest impact on farmers’ welfare.⁴ The farmer *i* selects one of the three types of cowpea varieties mentioned above. Following Deb and Trivedi (2006a), let EV_{ij}^* denotes the indirect utility that farmer *i* would obtain by selecting the *j*th cowpea variety type (the *j*th treatment), $j = 0, 1, 2$ and

$$EV_{ij}^* = z_i' \alpha_j + \delta_j I_{ij} + \eta_{ij} \tag{9}$$

where z_i is a vector of exogenous covariates with associated parameters α_j , and η_{ij} are independently and identically distributed error terms. I_{ij} are unobserved characteristics common to farmer *i*’s cowpea variety choice (treatment choice) and outcome, with associated parameters δ_j .

² Please note that Stata’s ML approach in the CMP framework is fundamentally an ML seemingly unrelated regression (SUR) estimation program (Roodman 2011).

³ This is confirmed by the dataset in which farmers are growing a specific cowpea variety as the main crop.

⁴ This hypothesis is motivated by the fact that the improved cowpea variety with genebank ancestor combines multiple disease and insect resistance and broad adaptability to meet the varied requirements of the region, which may have a higher impact on yield, home food consumption, and sale.

Let $j = 0$ denote the control group, farmers who are growing a cowpea landrace, and $EV_{i0}^* = 0$. While EV_{ij}^* was not observed, we observed farmer i 's cowpea variety choice (treatment choice). Let d_j refer to binary variables representing the observed cowpea variety choice (observed treatment choice) and $\mathbf{d}_i = (d_{i0}, d_{i1}, d_{i2})$. Also let $\mathbf{l}_i = (l_{i0}, l_{i1}, l_{i2})$. Then the probability of growing a specific type of cowpea variety (the probability of treatment) can be represented with a mixed multinomial logit structure (MMNL)⁵:

$$Pr(\mathbf{d}_i | \mathbf{z}_i, \mathbf{l}_i) = \frac{\exp(\mathbf{z}_i' \boldsymbol{\alpha}_j + \delta_j l_{ij})}{1 + \sum_{k=1}^2 \exp(\mathbf{z}_i' \boldsymbol{\alpha}_k + \delta_k l_{ik})} \quad (10)$$

The second stage of the model assessed the impact of growing a specific type of cowpea variety on three outcome variables: (1) cowpea yield, (2) cowpea consumption, and (3) cowpea sale. The expected outcome equation for farmer i was formulated as follows:

$$E(y_i | \mathbf{d}_i, \mathbf{x}_i, \mathbf{l}_i) = \mathbf{x}_i' \boldsymbol{\beta} + \sum_{j=1}^2 \gamma_j d_{ij} + \sum_{j=1}^2 \lambda_j l_{ij} \quad (11)$$

where \mathbf{x}_i is a set of exogenous covariates with associated parameter vectors $\boldsymbol{\beta}$, and γ_j denoting the treatment effects relative to the control. λ_j shows the impacts of unobserved characteristics (common to farmer i 's cowpea variety choice and outcome) on the outcome. We also assumed that the outcome variables were continuous⁶ and followed a normal (Gaussian) probability distribution.⁷ The model was estimated using a maximum simulated likelihood (MSL) approach. Provided that the number of draws is sufficiently large, the maximization of the simulated log-likelihood is equivalent to maximizing the log-likelihood (Deb and Trivedi 2006a). Regarding the identification of the model, in principle, the parameters of the model are identified even if the regressors in the treatment equation are identical to those used in the outcome equation (Deb and Trivedi 2006a). However, in practice, we followed Deb and Trivedi's (2006a) recommendation, which consists of using exclusion restrictions (or instruments) through the inclusion of regressors in the treatment equations that do not enter the outcome equation. We used the geographical zone as the exclusion restriction (or instrument), in the sense that it affected

the treatments (growing an improved cowpea variety with genebank ancestry and growing an improved cowpea variety without genebank ancestry) significantly and had no partial effect on the outcomes.⁸

Results

Descriptive statistics

Our analysis was based on the surveyed households and the characteristics of their household heads. Table 2 presents a summary of descriptive statistics of independent variables. We found significant differences between the North East and North West regions, where the survey was conducted. For socioeconomic characteristics, we found that household heads from the North West regions were older and needed less credit compared with households from the North East region. In addition, in the North West region, fewer women (4%) were heads of cowpea-producing households than in the North East region (10%). However, the two regions were similar in terms of the level of education of the household head. On average, household heads of both regions had 5 years of education.

Regarding the pedigree information of cowpea varieties grown by farmers, we found that more households from the North West region were growing improved cowpea varieties that had a genebank ancestor. In the North West region, 44% of households were growing improved cowpea varieties that had a genebank ancestor, compared with 36% in the North East region. In addition, on average, the improved cowpea varieties grown in the North West region had more genebank ancestors (12) than those grown in the North East region (8). Finally, regarding farm and market characteristics, farms were larger and had lands with more variation in elevation in the North East region, but households living in this region were farther away from village and district markets.

Spatial diversity of cowpea varieties on farms

The first research objective consisted of measuring the spatial diversity of cowpea varieties on farms, and testing their association with genebank ancestry in the pedigrees of improved cowpea varieties. The survey on the 1524 cowpea-producing households was able to identify and name 16 improved cowpea varieties and 6 cowpea landraces grown by farmers. Other improved cowpea varieties and cowpea landraces grown by farmers were also identified. The other improved cowpea varieties had been developed by the Institute of Agricultural Research (IAR), affiliated to the Ahmadu Bello University

⁵ Please note that the MMNL structure is an assumption. Other multinomial probability distributions could also be considered.

⁶ Please note that in other contexts the outcome variable may be a count variable. In this case, the negative binomial-2 density could be a good choice.

⁷ Using $\ln(\cdot)$ helps have normal distributions of outcome variables.

⁸ We establish the admissibility of the exclusion restriction (or instrument) by performing a simple test, which shows that the geographical zone affects the treatments significantly, whereas it does not affect the outcomes.

Table 2 Descriptive statistics for independent (control) variables

Variable	All	North West	North East
Household characteristics			
Age***	43.759 (12.369)	44.823 (12.292)	41.758 (12.277)
Sex (0/1)***	0.941 (0.236)	0.961 (0.194)	0.904 (0.295)
Education	5.248 (5.931)	5.304 (5.920)	5.142 (5.955)
Household size***	8.292 (4.511)	8.558 (4.786)	7.793 (3.897)
Experience (0/1)***	0.957 (0.203)	0.942 (0.234)	0.985 (0.121)
Need credit (0/1)***	0.514 (0.500)	0.480 (0.500)	0.577 (0.495)
Pedigree information			
Anc (0/1)***	0.409 (0.492)	0.436 (0.496)	0.358 (0.480)
NumAnc***	10.708 (17.538)	11.907 (18.134)	8.395 (16.104)
Farm characteristics			
Size***	1.938 (2.377)	1.736 (2.101)	2.317 (2.787)
Slope***	1.241 (1.002)	1.303 (1.011)	1.124 (0.975)
Soil fertility	0.072 (0.328)	0.069 (0.339)	0.077 (0.306)
Distance to field*	26.215 (27.820)	25.551 (25.161)	27.464 (32.224)
Market characteristics			
Distance to seed dealer	68.952 (142.333)	67.058 (167.225)	72.498 (76.381)
Distance to village market***	42.510 (61.023)	39.424 (60.115)	48.290 (62.334)
Distance to district market***	85.898 (85.329)	79.670 (75.739)	97.563 (99.903)

Means are reported with standard deviations in parentheses. The range for categorical variables is provided. (0/1) indicates a dummy variable equals to one if the response is yes, and 0 otherwise. The t-test and Chi-squared test were used to compare means and proportions between regions, respectively. ***, **, *: differences in means or proportions are statistically significant at 1, 5, or 10% significance level, respectively

(Nigeria), and the Institute of Agricultural Research and Training (IAR&T), affiliated to the Obafemi Awolowo University (Nigeria).

On average, each household dedicated 2 plots to cowpea growing, which covered an area of 1.938 ha per farm. The distribution of cowpea variety types on these plots was as follows: 62.34% of these plots were dedicated to cowpea landraces, 37.19% were dedicated to improved cowpea varieties that have a genebank ancestor, and 0.47% were dedicated to other improved cowpea varieties.⁹ In addition, 41.29% of households were growing at least one improved cowpea variety as the main crop,¹⁰ whereas 40.91% were growing at least one improved cowpea variety that has a genebank ancestor as the main crop. Finally, 68.50% of households were growing at least one cowpea landrace as the main crop.

Table 3 presents descriptive statistics for spatial diversity indices of cowpea varieties grown in the North East and North West regions of Nigeria. The average value of the Menhinick index (2.896) was higher in the North West region (two-sample two-sided t-test: $p=0.000$),

than in the North East region (2.204), suggesting greater richness of cowpea varieties on farms in the North West region, when standardized by area. For instance, Table 4, which shows the repartition of households over main

Table 3 Descriptive statistics for indices of the spatial diversity of the cowpea varieties grown in Nigeria

Index	Mean	SD	Minimum	Maximum
Total				
Menhinick index	2.656	1.838	0.442	31.623
Shannon index	0.344	0.041	0	0.693
Berger-Parker index	2.833	1.414	1	25
Herfindahl index	0.169	0.123	0.002	1
North West region				
Menhinick index	2.896	2.051	0.515	31.623
Shannon index	0.343	0.045	0	0.693
Berger-Parker index	2.856	1.349	1	10
Herfindahl index	0.169	0.128	0.01	1
North East region				
Menhinick index	2.204	1.230	0.442	9.129
Shannon index	0.345	0.034	0	0.368
Berger-Parker index	2.788	1.530	1	25
Herfindahl index	0.170	0.112	0.002	1

Means, standard deviations (SD), minimums and maximums are reported for each diversity index, and broken down by regions

⁹ According to the household survey questionnaire, a field is a piece of land physically separated from others and a plot is a subunit of a field. Some farmers may be intercropping on a plot. Only nine households (0.58%) were growing more than one cowpea variety per plot.

¹⁰ Main crop refers to the crop that occupies the largest share of farm area.

Table 4 Repartition of households over main cowpea varieties grown

Cowpea varieties	North West		North East	
	Total area planted (in ha) as main cowpea variety	Number of households growing it as main cowpea variety	Total area planted (in ha) as main cowpea variety	Number of households growing it as main cowpea variety
Improved cowpea varieties				
IT99K-216-24-2/Kwankwaso	33.544	110	18.777	27
IT90K-277-2/Sasakawa	26.363	62	12.732	18
IT89KD-288/Sampea-11	32.724	92	39.210	45
IT97K-499-35/Sampea-10	10.041	25	3.062	5
IAR48/Sampea 7	2.538	4	3.326	3
IT89KD-391/Sampea 12	4.224	9	4.656	6
IT99K-573-1-1/Sampea-14	18.191	45	9.605	13
IT98K-573-2-1/Sampea 15	5.746	22	2.209	6
IT93K-452-1/Sampea 8	2.543	6	1.304	3
IT98K-131-2	2.068	6	0.118	1
IT98K-491-4	13.355	30	13.064	26
IT07K-318-33/Sampea 17	0.605	1	0.429	1
IT07K-292-10/Sampea 16	4.596	16	2.99	7
IT98K-205-8	5.8	18	1.532	3
UAM09-1055-6	21.104	64	18.960	32
UAM09-1046-6-1	2.923	5	0	0
Cowpea landraces				
Silver (Local)	8.282	16	15.08	25
Portiskum (Local)	27.431	36	25.252	33
Kananado Brown (Local)	3.130	13	16.951	22
Kananado White/Dan Bokolo	94.548	175	67.997	103
Gwalam	24.205	60	17.176	56
Bosadp	8.461	24	13.783	30
Other improved cowpea varieties	2.657	10	0	0
Other cowpea landraces	213.654	358	131.773	162

cowpea varieties grown, indicates that some improved cowpea varieties¹¹ (UAM09-1046-6-1 and other improved cowpea varieties) were not grown as main cowpea varieties by households from the North East region, whereas 15 households were growing them as main cowpea varieties in the North West region.

The average value of the Shannon index (0.343) in the North West region was not statistically different from that in the North East region (0.345) (two-sample two-sided t-test: $p=0.275$), indicating that cowpea varieties grown are equally abundant in both regions.

Finally, in terms of inverse dominance, we found that the difference between the average values of the Berger-Parker index in the North East region and the North West region was not statistically significant (two-sample two-sided t-test: $p=0.417$). While Kananado White/Dan Bokolo was the most widely grown cowpea variety in both regions, farmers cultivated other varieties too.

IITA's contribution to the ancestry of improved cowpea varieties grown by farmers

Before investigating the impact of IITA's genebank on varietal diversity of cowpeas on farms, we provide some results on the link between IITA's genebank and improved cowpea varieties grown in Nigeria. Research on cowpea improvement was initiated at IITA in 1970 and over 50 countries, including Nigeria, have identified and released improved cowpea varieties from IITA

¹¹ A possible explanation is that some of these varieties have not been released officially. Few farmers may have had access to the seeds through evaluation trials.

Table 5 Contribution of IITA's genebank to the ancestry of the adopted improved cowpea varieties in Nigeria

Cowpea variety	Does the cowpea variety have a genebank ancestor?	How many genebank ancestors are in the pedigree respective of number of appearances?	How many genebank ancestors are in the pedigree relative to unique counts?	Year of release
IT90K-277-2 (Sasakawa)	Yes	14	7	2005
IT89KD-288/Sampea-11	Yes	13	7	2009
IT99K-216-24-2 (Kwankwaso)	Yes	22	7	Not yet released
IT89KD-391/Sampea12	Yes	16	8	2009
IT97K-499-35/Sampea-10	Yes	55	8	2008
IT93K-452-1/Sampea8	Yes	29	13	2005
IT99K-573-1-1/Sampea-14	Yes	43	12	2011
IT99K-573-2-1/Sampea-15	Yes	43	12	2011
IT98K-131-2	Yes	33	7	Not yet released
UAM09-1046-6-1	Yes	56	8	Not yet released
UAM09-1055-6	Yes	56	8	2016
IT98K-205-8	Yes	55	9	Not yet released
IAR48 /Sampea 7	Not available	Not available	Not available	Not available
IT98K-491-4	Yes	Not available	Not available	Not Available
IT07K-318-33/Sampea 17	Yes	50	13	2015
IT07K-292-10/Sampea 16	Yes	67	14	2015

Information retrieved from the database of the cowpea program of IITA. "Unique count" refers to the number of IITA ancestors appearing in the pedigree and "number of appearances" refers to the number of times the IITA ancestors have been used in the breeding line

for general cultivation (Singh 1997). Table 5 presents the contribution of IITA's genebank to the ancestry of the improved cowpea varieties grown in Nigeria. Additional file 1: Fig. S2 also shows diagrams depicting the pedigrees of improved cowpea varieties. We found that most of the improved cowpea varieties grown by Nigerian farmers were released recently (between 2005 and 2015) and had a genebank ancestor.

Earlier breeding activities (from the 1970s to early 2000s) focused on the development of insect and multiple disease resistances, varieties characteristic by white rough seed coat, extra-early maturity (60–70 days) and late maturity (85–120 days). Photo-insensitive, dual-purpose varieties were developed, along with photosensitive early to late maturing varieties and high yielding, bush-type vegetable varieties (Singh et al. 1997; Boukar et al. 2019). The uniqueness of recently released improved cowpea varieties reflects advances in cowpea genetics, genomics, and the deployment of integrated breeding approaches (Boukar et al. 2019; Varshney et al. 2019).

On average, the pedigree of an improved cowpea variety grown by Nigerian farmers included 9 unique IITA ancestors, which have been incorporated 39 times during the breeding process. For instance, the most recently released improved cowpea variety, UAM09-1055-6, had 8 unique IITA ancestors that have been incorporated 56 times in the breeding process. The oldest improved cowpea variety, IT90K-277-2 (Sasakawa), had 7 unique IITA ancestors that have been incorporated 14 times during

the breeding process. UAM09-1055-6 is the result of a single cross between Borno Brown and IT97K-499-35. IT90K-277-2 (Sasakawa) is the result of breeding IITA's genebank accession IT87F-1777-2 with IT84S-2246-4, crossed with TVx3236.

The improved cowpea variety, IT89KD-288/Sampea-11, released in 2009 was the most widely adopted by Nigerian farmers, in terms of the main cowpea variety grown on plots (it was grown as the main cowpea variety on 7.24% of plots). IT07K-318-33/Sampea 17, released in 2015, was the least adopted by Nigerian farmers, in terms of the main cowpea variety grown on plots (it was grown on 0.08% of plots). IT89KD-288/Sampea-11 was the result of the combination between an IITA's genebank accession, IT87F-1777-2, and IT84S-2246-4, whereas IT07K-318-33/Sampea 17 was developed through the cross of IT98K-131-2 with IT95K-238-3. Additional file 1: Fig. S2 shows the IT89KD-288/Sampea-11 and IT07K-318-33/Sampea 17 pedigree trees.

Overall, we confirm the use of germplasm from the IITA genebank by scientists to develop improved cowpea varieties grown by Nigerian farmers.

IITA's genebank and spatial diversity of cowpea varieties on farms

To measure the effect of IITA's genebank on the spatial diversity of cowpea varieties on farms, we ran the

Table 6 Recursive mixed-process model estimates, first specification with the richness index

Explanatory variable	First specification	
	Richness index (d ^f)	Anc
Endogenous variable		
Anc	0.293 (0.357)	–
Household characteristics		
Age	–	– 0.001 (0.003)
Sex	–	– 0.119 (0.144)
Education	–	0.011 (0.019)
Education ²	–	– 0.001 (0.001)
Household size	– 0.017* (0.010)	–
Need credit	–	– 0.157** (0.067)
Experience	–	1.030*** (0.204)
Farm characteristics		
Size	– 0.232*** (0.019)	–
Slope	0.593*** (0.047)	–
Distance to farm	0.004** (0.002)	–
Soil fertility	–	0.379*** (0.107)
Market characteristics		
Distance to seed dealer	–	0.000 (0.000)
Distance to village market	–	0.000 (0.001)
Distance to district market	–	0.001 (0.000)
Geographical zone		
North East	– 0.443*** (0.099)	– 0.253*** (0.071)
Constant	2.444*** (0.187)	– 0.951*** (0.293)
Prob > chi ²	0.000	
N	1557	

Column 1 is a tobit regression with the richness index as dependent variable. Column 2 is a probit regression with genebank ancestry as dependent variable. Standard errors are in parentheses. ***, **, *: estimates are statistically significant at 1, 5, or 10% significance level, respectively

recursive mixed-process model (Eqs. 5 and 6), using an ML estimation approach.¹² Table 6 presents the estimates of the model, where the spatial diversity index is a richness index (the Menhinick index). Based on the results, we found that growing an improved cowpea variety that had a genebank ancestor was not significantly associated with richness—either positively or negatively.

Farm characteristics, including farm size, distance to the farm from residence, the number of plots that are perceived as flat, and the geographical zone (being part of the North West region), were important determinants of the richness of cowpea varieties on farms in Nigeria. The richness of cowpea varieties on farms was higher in the

¹² The model is estimated using the Stata command *cmp*. The same analysis was conducted for improved varieties that do not have a genebank ancestor. We found no significant effects on diversity indices.

Table 7 Recursive mixed-process model estimates, second specification with the inverse dominance index

Explanatory variable	Second specification	
	Inverse dominance index (d ^d)	Anc
Endogenous variable		
Anc	2.270*** (0.110)	–
Household characteristics		
Age	–	0.002 (0.002)
Sex	–	– 0.078 (0.098)
Education	–	– 0.01 (0.013)
Education ²	–	– 0.000 (0.001)
Household size	0.009 (0.008)	–
Need credit	–	– 0.192*** (0.048)
Experience	–	0.490*** (0.141)
Farm characteristics		
Size	0.017 (0.015)	–
Slope	– 0.139*** (0.036)	–
Distance to farm	0.001 (0.001)	–
Soil fertility	–	0.221*** (0.082)
Market characteristics		
Distance to seed dealer	–	0.000 (0.000)
Distance to village market	–	0.001*** (0.000)
Distance to district market	–	0.000 (0.000)
Geographical zone		
North East	0.078 (0.101)	– 0.195*** (0.067)
Constant	1.914*** (0.109)	– 0.525*** (0.202)
Prob > chi ²	0.000	
N	1559	

Column 1 is a tobit regression with the inverse dominance index as dependent variable. Column 2 is a probit regression with genebank ancestry as dependent variable. Standard errors are in parentheses. ***, **, *: estimates are statistically significant at 1, 5, or 10% significance level, respectively

North West region and in households with smaller sizes and farms, a higher number of flat plots, or whose members reside not far from their plots. Results also showed that farmers who either belong to the North West region, have been exposed to (or have experience of) improved cowpea varieties, or do not need credit for their farming activities were more likely to grow improved cowpea varieties that have a genebank ancestor. The result concerning experience aligns with that presented by Manda et al. (2019), who found that the number of years a farmer has been exposed to improved cowpea varieties is an important determinant of adoption.

Table 7 presents the estimates of the model, using an inverse dominance index (the Berger-Parker index) as a spatial diversity index. The results indicate that the adoption of an improved cowpea variety that had a genebank ancestor had a positive and significant effect on the inverse dominance index. Farm characteristic, especially

Table 8 Recursive mixed-process model estimates, third specification with the concentration index

Explanatory variable	Third specification	
	Concentration index (d ⁶)	Anc
Endogenous variable		
Anc	− 0.066*** (0.025)	−
Household characteristics		
Age	−	0.000 (0.003)
Sex	−	− 0.138 (0.140)
Education	−	− 0.002 (0.019)
Education ²	−	− 0.001 (0.001)
Household size	− 0.002*** (0.001)	−
Need credit	−	− 0.189*** (0.066)
Experience	−	0.998*** (0.202)
Farm characteristics		
Size	− 0.003** (0.001)	−
Slope	− 0.007** (0.003)	−
Distance to farm	− 0.000 (0.000)	−
Soil fertility	−	0.400*** (0.105)
Market characteristics		
Distance to seed dealer	−	0.000 (0.000)
Distance to village market	−	0.000 (0.001)
Distance to district market	−	0.001 (0.000)
Geographical zone		
North East	− 0.004 (0.007)	− 0.245*** (0.071)
Constant	0.232*** (0.013)	− 0.927*** (0.285)
Prob > chi ²	0.000	
N	1559	

Column 1 is a tobit regression with the concentration index as dependent variable. Column 2 is a probit regression with genebank ancestry as dependent variable. Standard errors are in parentheses. *** ** *: estimates are statistically significant at 1, 5, or 10% significance level, respectively

the slope, was a determinant of the inverse dominance index. Farmers who had a high number of plots perceived as flat devote more area to their preferred variety. A new important determinant of growing a cowpea variety that has a genebank ancestor is soil fertility. Farmers were more likely to grow an improved cowpea variety that had a genebank ancestor when they had a higher number of plots with perceived poor soil quality. This suggests a possible association with traits conferred through diverse ancestry. These traits may be adapted to the poor soil quality conditions.

Finally, Table 8, which presents the estimates of the model, using a concentration index (the Herfindahl index) as spatial diversity index, indicates that growing an improved cowpea variety that has a genebank ancestor

has a negative and significant effect on the concentration index. In other words, growing an improved cowpea variety that had a genebank ancestor decreased the specialization in a single cowpea variety. This is consistent with the results for the Berger-Parker index.

To sum up, genebank ancestry did not contribute to more specialization or dominance of any particular cowpea variety on farms or lead to the displacement of other cowpea varieties; in fact, it was consistent with less concentration and less dominance by the main cowpea variety. The results also indicated that certain farm characteristics were more important determinants of greater richness among cowpea varieties.

IITA's genebank, cowpea yield and farmers' welfare

To investigate the effect of IITA's genebank on cowpea yield and farmers' welfare, we ran a multinomial endogenous treatment effect model, using an MSL approach.¹³ Table 9 presents the results of multinomial endogenous treatment effects model estimates of impacts on cowpea yield. We found a positive and significant treatment effect of growing an improved cowpea variety that had a genebank ancestor on cowpea yield. Growing an improved cowpea variety that had a genebank ancestor increased by 177.042% the yield of cowpea,¹⁴ compared to growing a cowpea landrace. However, the significant value (− 1.194) of the coefficient on the latent factor indicated significant selection on unobservables. In other words, farmers who were more likely to grow a cowpea variety that had a genebank ancestor relative to a cowpea landrace, based on their unobserved characteristics,¹⁵ experienced a decline in cowpea yield more often, which might upset this effect on the yield of cowpea for some of them. Other factors like household characteristics (sex of the household head and need of credit), farm characteristics (size, distance to farm from residence and soil fertility), and market characteristics (distance to village market from residence and distance to district market from residence) had significant effects on cowpea yield. For instance, a household which either has a man as head, has a small farm size, has plots not far from the residence, or has plots not far from the village/district market is likely to have higher cowpea yields.

¹³ The model is estimated using the Stata command *mtreatreg*. We used 1000 simulation draws.

¹⁴ It is computed, using the value 1.090, the estimate of the average treatment effect: $(e^{1.090} - 1) \times 100$.

¹⁵ The unobserved characteristics are common to the farmer's/household's adoption of improved cowpea varieties that have a genebank ancestor and outcomes (cowpea yields). For instance, Abdulai and Huffman (2014) show that the management and technical ability of the farmers to understand new technology may affect outcomes, including crop yields.

Table 9 Multinomial endogenous treatment effects model estimates

Explanatory variables	Outcome models		
	Ln cowpea yield	Ln cowpea consumption	Ln cowpea sale
Treatment variable			
Adoption of cowpea variety without genebank ancestry	− 1.545** (0.781)	0.186 (0.205)	− 0.578 (1.025)
Adoption of cowpea variety with genebank ancestry	1.019*** (0.395)	0.381*** (0.095)	− 0.027 (0.158)
Household characteristics			
Age	− 0.018 (0.022)	0.012 (0.010)	0.001 (0.035)
Age ²	0.000 (0.000)	− 0.000 (0.000)	− 0.000 (0.000)
Sex	0.735*** (0.238)	0.081 (0.101)	− 0.116 (0.258)
Education	0.007 (0.025)	− 0.013 (0.010)	0.017 (0.041)
Education ²	0.000 (0.002)	0.000 (0.001)	− 0.002 (0.003)
Need credit	0.385*** (0.109)	0.059 (0.045)	− 0.631*** (0.132)
Farm characteristics			
Size	− 0.172*** (0.031)	0.065*** (0.015)	− 0.000 (0.021)
Slope	0.041 (0.056)	− 0.044* (0.025)	0.105 (0.071)
Distance to farm	− 0.006*** (0.002)	0.001 (0.001)	0.003 (0.002)
Soil fertility	− 0.335** (0.151)	− 0.134** (0.067)	0.133 (0.220)
Market characteristics			
Distance to village market	− 0.003*** (0.001)	− 0.000 (0.000)	− 0.004*** (0.001)
Distance to district market	− 0.001* (0.001)	0.000 (0.000)	0.000 (0.001)
Constant	3.111*** (0.620)	0.822*** (9.264)	5.399*** (0.909)
Selection terms (λ)			
Adoption of cowpea variety without genebank ancestry	0.958** (0.480)	− 0.419*** (0.156)	0.000 (0.000)
Adoption of cowpea variety with genebank ancestry	− 1.194*** (0.457)	− 0.419*** (0.109)	− 0.000 (0.000)
Prob > chi ²	0.000	0.000	0.000
N	1442	1376	500

Columns 1, 2 and 3 are multinomial endogenous treatment effects model regressions with natural logarithms of cowpea yield, cowpea consumption and cowpea sale as outcomes, respectively. The control group is households that grow a cowpea landrace. 1000 simulation draws were used. Standard errors are in parentheses. ***, **, *: Significance at 1, 5, or 10% significance level, respectively

Table 9 also presents the results of multinomial endogenous treatment effects model estimates of impacts on cowpea consumption. We found a positive and significant treatment effect of growing an improved cowpea variety with a genebank ancestor on cowpea consumption as food by the household. Growing an improved cowpea variety that had a genebank ancestor increased household consumption of cowpea as food by 46.375%,¹⁶ compared to growing a cowpea landrace. However, the significant value (− 0.419) of the coefficient on the latent factor indicated significant selection on unobservables. In other words, farmers who were more likely to grow a cowpea variety having a genebank ancestor relative to a cowpea landrace, based on their unobserved characteristics, reduced their level of cowpea consumption as food more often, which might upset this effect on cowpea

consumption for some of them. Other factors like farm characteristics (size, slope, and soil fertility) had significant effects on cowpea consumption as food.¹⁷

Finally, Table 9 also presents the results of multinomial endogenous treatment effects model estimates of impacts on cowpea sale. We did not find a significant treatment effect of growing a cowpea variety that had a genebank ancestor on cowpea sale. However, the need for credit and the distance to village market (from residence) did have significant effects on cowpea sale. Farmers who either did not need credit for their farming activities or were not far from the village market increased their levels of cowpea sales.

In summary, growing a cowpea variety with genebank ancestry had a positive and significant impact on cowpea yield and cowpea consumption at home, but not on cowpea sale.

¹⁶ It is computed, using the value 0.381, the estimate of the average treatment effect: $(e^{0.381} - 1) \times 100$.

¹⁷ This is understandable, in the sense that, *ceteris paribus*, a bigger or more fertile farm may mean a greater use of cowpea as food.

Discussion

The evidence presented in this research indicates that Nigerian farmers are growing improved cowpea varieties that have genebank ancestors in their pedigree trees, showing the contribution of IITA's genebank to the development and release of improved cowpea varieties in Nigeria. Some recent studies confirmed that genebanks in Africa contribute to the development of improved crop varieties and the conservation and distribution of tree germplasm (Kitonga et al. 2020; Sellitti et al. 2020).

Evidence also shows that adoption of a cowpea variety with genebank ancestry does not contribute to the specialization or dominance of any particular variety, and has no significant association with richness of cowpea varieties grown. Therefore, although IITA's genebank accessions are used for the development of improved cowpea varieties that have been widely adopted by farmers in Nigeria, we see no evidence that their adoption contributes to fewer varieties grown by smallholder farmers. Other factors like household size, farm characteristics and geographical zone are more important in explaining the pattern of cowpea varieties grown on farms. Our findings are consistent with the empirical literature on the determinants of crop diversity on farms, which finds that household characteristics, farm characteristics, and geographical zone have significant effects on the diversity within crops (Smale et al. 2003; Benin et al. 2004; Bellon et al. 2020).

Regarding the decision to grow a cowpea variety that has a genebank ancestor, farmers' experience is an important determinant, meaning that the exposition to/adoption of a former agricultural technology is a predictor of the adoption of a new agricultural technology. This is in line with a recent study on the poverty impacts of improved cowpea varieties in Nigeria (Manda et al. 2019). We found that education of the household head is not a significant determinant of a farmer's decision to grow a cowpea variety that has a genebank ancestor, whereas education has been cited as an important determinant of the adoption of agricultural technologies in Africa in other studies (Alene and Manyong 2007; Foster and Rosenzweig 2010). A possible explanation is that education does not matter when geographical factors incentivize the farmer's decision to grow a cowpea variety that has a genebank ancestor. We found that the geographical zone is an important determinant of farmers' decision to grow a cowpea variety that has a genebank ancestor. This is also in line with Manda et al. (2019), who found that the adoption of improved cowpea varieties was lower in the North East region compared to the North West region, reflecting the unobservable differences in terms of the resources and weather patterns between the two regions of Nigeria. Finally, as expected, growing a cowpea

variety that has a genebank ancestor affects cowpea yield and farmers' welfare. Evidence showed a positive and significant effect on cowpea yield and cowpea consumption. Numerous studies have demonstrated that improved crop varieties or agricultural technologies have a positive and significant impact on agricultural productivity in Africa (for example, Duflo et al. 2008; Kassie et al. 2008; Pender and Gebremedhin 2007; Abdulai and Huffman 2014).

Conclusion and recommendations

Cowpea is an important food legume that provides food and fodder, improves soil fertility and contributes to the sustainability of food production in marginal areas of the dry tropics (Singh 1997). Using data from a household survey conducted in Northern Nigeria in 2017, and data from IITA's cowpea breeding program, we measured varietal diversity, linked improved cowpea varieties grown to IITA's genebank and investigated the effect of IITA's genebank on varietal diversity of cowpeas on farms. We also examined the impact of IITA's genebank on cowpea yield and farmers' welfare.

Our spatial diversity indices show that richness of cowpea varieties is higher in the North West region than the North East region (when standardized by area). The pedigree analyses confirm the use of germplasm from the IITA genebank by scientists to develop improved cowpea varieties grown by Nigerian farmers. Regarding the effect of IITA's genebank on varietal diversity of cowpeas on farms, our recursive mixed-process model indicates that genebank ancestry does not lead to the displacement of other cowpea varieties. In addition, it does not contribute to specialization or dominance of any particular variety. Finally, our multinomial endogenous treatment effect model indicates that growing a cowpea variety that has a genebank ancestor has a positive and significant impact on cowpea yield and cowpea consumption.

These findings show additional benefits from IITA's genebank, through the adoption of improved cowpea varieties that have a genebank ancestor. Benefits are threefold. First, we find no negative effects of growing improved varieties on the spatial diversity of cowpea varieties grown on farms. Second, IITA's genebank helps increase cowpea yield on farmers, showing a contribution to agricultural productivity in smallholder farms in Nigeria. Finally, IITA's genebank contributes to increased household consumption of cowpea as food, contributing to farmers' welfare in Nigeria. Policymakers and practitioners should consider these findings when analyzing the benefits of conserving crop genetic diversity in genebanks and on farms.

Several caveats are in order when considering the results. Farmers' welfare is only measured by

cowpea consumption and cowpea sale. Further empirical research could explore other welfare dimensions. For instance, in the context of climate change, reduced vulnerability to drought and reduced soil erosion could be added to farmers' welfare dimensions. Linkages between genebank ancestry and traits conferred to cowpea varieties grown on farms have not been clearly established. Understanding these linkages is needed to draw inferences about their value on farms and in varietal portfolios. Possible non-use benefits from IITA's genebank may also be found.

Abbreviations

CGR: Cowpea genetic resource; CIAT: International Center for Tropical Agriculture; CMP: Conditional recursive mixed-process; DNA: Deoxyribonucleic Acid; IAR: Institute of Agricultural Research; IAR&T: Institute of Agricultural Research and Training; ICRAF: World Agroforestry; ICRISAT: International Crops Research Institute for the Semi-Arid Tropics; IITA: International Institute of Tropical Agriculture; ML: Maximum likelihood; MMNL: Mixed multinomial logit structure; MSL: Maximum simulated likelihood.

Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s43170-022-00083-w>.

Additional file 1: Fig. S1. Land area harvested (ha) and production quantity (tons) of cowpea in Nigeria (1980–2020). **Fig. S2.** Diagrams of adopted improved cowpea varieties pedigree trees.

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Authors' contributions

A-GK contributed to the research conceptualization and design, data gathering, data analysis, writing, and editing. AO contributed to data gathering and data analysis. MS and NJ contributed to research conceptualization and design, writing, and editing. JM and MA contributed to data gathering. All authors read and approved the final manuscript.

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Availability of data and materials

The datasets used and analyzed during the current study are available from the corresponding authors on request.

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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