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
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 IITAs 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 IITAs 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...
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.
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

Table 1  List and description of variables used in regression models

| Variable | Definition |
|----------|------------|
| Dependent variables | |
| $d_r$ | 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 |
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 \( d^c \) 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:

\[
d^c = S/\sqrt{A},
\]

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

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

\[
d^e = -\sum_{i=1}^{n} p_i \ln p_i, \ldots p_i \geq 0.
\]

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:

\[
d^d = 1/\max(p_i),
\]

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

The Herfindahl index, \( d^h \), 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:

\[
d^h = \sum_{i=1}^{n} p_i^2,
\]

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 grain sold 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

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\(^1\)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:

$$G_i^* = \alpha X_i + e_i$$ (5)

$$I_i^* = \beta G_i + \gamma Z_i + u_i$$ (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:

$$G_i = \begin{cases} 1 & \text{if } G_i^* > 0 \\ 0 & \text{otherwise} \end{cases}$$ (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 $I$ and the maximum value $T$:

$$I_i = \begin{cases} I & \text{if } I_i^* \leq I \\ I_i^* & \text{if } I < I_i^* < T \\ T & \text{if } I_i^* \geq T \end{cases}$$ (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) approach (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 crop: (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. 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

$$EV_{ij}^* = z_i \alpha_j + \delta_i I_{ij} + \eta_{ij}$$ (9)

where $z_i$ is a vector of exogenous covariates with associated parameters $\alpha_j$, and $\eta_{ij}$ 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 $\delta_j$.

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

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

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 $d_i$ refer to binary variables representing the observed cowpea variety choice (observed treatment choice) and $d_i = (d_{i0}, d_{i1}, d_{i2})$. Also let $l_i = (l_{i0}, l_{i1}, l_{i2})$. 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:

$$
Pr(d_i|z_i, l_i) = \frac{\exp(z_i^\prime \alpha_j + \delta_j l_i)}{1 + \sum_{k=1}^2 \exp(z_i^\prime \alpha_k + \delta_k l_i)}
$$

(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:

$$
E(y_i|d_i, x_i, l_i) = x_i^\prime \beta + \sum_{j=1}^2 \gamma_j d_{ij} + \sum_{j=1}^2 \lambda_j l_{ij}
$$

(11)

where $x_i$ is a set of exogenous covariates with associated parameter vectors $\beta$, and $\gamma_j$ denoting the treatment effects relative to the control. $\lambda_j$ 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 continuous 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.

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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.
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 the cowpea varieties grown in 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

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**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.

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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.
cowpea varieties grown, indicates that some improved cowpea varieties\textsuperscript{11} (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.

\textbf{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.

\begin{table}[h]
\centering
\caption{Repartition of households over main cowpea varieties grown}
\begin{tabular}{lllll}
\hline
Cowpea varieties & \multicolumn{2}{c}{North West} & \multicolumn{2}{c}{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 \\
\hline
Improved cowpea varieties & & & & \\
IT99K-216-24-2/Kwan kwaso & 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 & 1.7176 & 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 \\
\hline
\end{tabular}
\end{table}

\textsuperscript{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.
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 characteristics 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. 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, IT89K-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). IT89K-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 IT89K-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.

### 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 |
| IT89K-288/Sampea-11 | Yes | 13 | 7 | 2009 |
| IT99K-216-24-2 (Kwankwaso) | Yes | 22 | 7 | Not yet released |
| IT89K-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.
recursive mixed-process model (Eqs. 5 and 6), using an ML estimation approach. 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 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

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

| Explanatory variable | First specification | Anc | Richness index (d) | Anc |
|----------------------|---------------------|-----|-------------------|-----|
| Endogenous variable  |                     |     |                   |     |
| Anc                  | 0.293 (0.357)       |     |                   |     |
| Household characteristics |             |     |                   |     |
| Age                  |                     |     |                   |     |
| Sex                  |                     |     |                   |     |
| Education            |                     |     |                   |     |
| Education²           |                     |     |                   |     |
| Household size       | −0.017* (0.010)     |     |                   |     |
| Need credit          | −1.57** (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 |                 |     |                   |     |
| Distance to village market |               |     |                   |     |
| Distance to district market |             |     |                   |     |
| Geographical zone    |                     |     |                   |     |
| North East           | −0.443*** (0.099)   | −0.253*** (0.071) |
| Constant             | 2.444*** (0.187)    | −0.951*** (0.293) |
| Prob > chi²          | 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.

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

| Explanatory variable | Second specification | Anc | Inverse dominance index (d) | Anc |
|----------------------|----------------------|-----|-----------------------------|-----|
| Endogenous variable  |                      |     |                             |     |
| Anc                  | 2.270*** (0.110)     |     |                             |     |
| Household characteristics |             |     |                             |     |
| Age                  |                     |     |                             |     |
| Sex                  |                     |     |                             |     |
| Education            |                     |     |                             |     |
| Education²           |                     |     |                             |     |
| 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 |                 |     |                             |     |
| Distance to village market |               |     |                             |     |
| Distance to district market |             |     |                             |     |
| Geographical zone    |                      |     |                             |     |
| North East           | 0.078 (0.101)        | −0.195*** (0.067) |
| Constant             | 1.914*** (0.109)     | −0.525*** (0.202) |
| Prob > chi²          | 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.
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. 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, 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, 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 farm from the residence, or has plots not far from the village/district market is likely to have higher cowpea yields.

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

| Explanatory variable | Third specification |
|----------------------|---------------------|
|                      | Concentration index (d²) | 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) |
|                       | Education² | − | −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) |
|                       | Constant | 0.232*** (0.013) | −0.245*** (0.071) |
|                       | Prob > chi² | 0.000 | −0.927*** (0.285) |
|                       | 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.

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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: \(e^{1.090} - 1\) × 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 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%, 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.

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.

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

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 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; ICARDA: International Center for Agricultural Research in Dry Areas; ICRAF: World Agroforestry; ICRISAT: International Crops Research Institute for the Semi-Arid Tropics; IITA: International Institute of Tropical Agriculture; IAR: Institute of Agricultural Research; IAR&T: Institute of Agricultural Research and Training; ICARDA: International Center for Agricultural Research in Dry Areas; 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

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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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