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

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Abstract

Genebanks and *in-situ* conservation approaches have been recognized as complementary and useful to researchers, plant breeders and farmers. However, empirical evidence linking genebanks to on-farm management of crop genetic resources is limited. Using a household survey conducted in Northern Nigeria in 2016 and 2017, and data from the cowpea program of IITA, this paper investigates the impacts of IITA's genebank on the spatial diversity of cowpea varieties on farms, cowpea yield, and farmers' welfare, using a recursive mixed-process model and a multinomial endogenous treatment effect model, respectively. We find 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, these varieties do not displace other cowpea varieties or landraces. We find that genebank ancestry is positively and significantly associated with cowpea yield and farmers' welfare, showing additional benefits from IITA's genebank in Nigeria. Policymakers and practitioners should consider these findings when analyzing the benefits from conserving crop genetic diversity in genebanks and on farms.

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Contents

1 Introduction and motivation

Genebanks and *in situ* conservation approaches have been recognized as complementary (FAO 2017; Maxted et al. 1997). Genebanks are useful to researchers, plant breeders, and farmers (Koo et al. 2004; Smale and Jamora 2020), and organized in national and international networks. 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.

Empirical evidence of the value of genebanks is rather limited in Africa. Valuing genebanks in Africa is important to demonstrate value for money, in the context of scarce funding resources. In addition, in the context of Africa's vulnerability to climate change, through natural disasters and loss of agrobiodiversity (FAO 2010; FAO et al. 2015), valuing African genebanks contribute to showing their role in maintaining biodiversity and as disaster relief.

Two recent studies have attempted to value genebanks in Africa. Sellitti et al. (2020) analyzes 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. This study shows the role of CIAT's genebank in the improvement of bean varieties and in generating benefits for farmers. Kitonga et al. (2020) explore the benefits of using the two most popular fodder tree species among smallholder farmers, sourced from the genebank of the World Agroforestry (ICRAF). It contributes to tracing the benefits of ICRAF's genebank germplasm distributions to smallholder farmers. However, both studies did not relate results to *in situ* conservation and did not consider on-farm agrobiodiversity as a potential benefit to smallholder farmers.

Our study contributes to the 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 genebank of the International Institute of Tropical Agriculture (IITA) and cowpea production in Nigeria as an example.

2 Background and research objectives

Cowpea or black-eyed pea (*Vigna unguiculata* L.) is a food legume that provides food and fodder as well as improving soil fertility and contributing 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 (Figure 1; FAO 2020), the

North West and North East regions being the most productive regions, 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. 2019). Likewise, the national production of cowpea has increased by 165%, from 1980 to 1990, and 50%, from 2009 to 2019 (Figure 1; FAO 2020; Singh 2005). This increase in cowpea production is partially related to cowpea conservation and improvement efforts at IITA, and adoption of improved cowpea varieties in Nigeria (Ogundapo et al. 2020). 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, and a substantial number of the released improved cowpea varieties have been adopted by Nigerian farmers (IITA 2013; Ogundapo 2016).

Although the primary role of IITA's genebank is the maintenance of crop diversity outside its natural environment, there are two important studies that attempted to investigate its impact on farms. Ogundapo et al. (2020) use a combination of DNA fingerprinting and economic surplus model to demonstrate the outcomes of Cowpea Genetic Resource (CGR) conservation and improvement efforts on smallholder farmers in Kano State, Nigeria. The results reveal increased productivity of low-income cowpea farmers that adopted improved cowpea varieties, increased net present value for cowpea germplasm conservation, and 487,219 persons lifted out of poverty between 1980 and 2015. Manda et al. (2019) rigorously estimates 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. The results indicate that adoption of improved cowpea varieties increase per capita household income and asset ownership. In addition, the results based on the observed and counterfactual income and asset distributions show that adoption reduces both income poverty 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 varieties in Nigeria. We build on from these two studies and utilize the same data from Manda et al. (2019) to explore the linkage to the genebank and to variety diversity on farms and other measures of farmers' welfare.

Our objective is twofold. First, we establish the link between the IITA's genebank and the development of improved cowpea varieties. We relate this link to measures of on-farm cowpea varietal diversity in Nigeria. Second, we examine the impact of IITA's genebank, through the adoption of improved varieties, on cowpea yield and farmers' welfare in Nigeria.

3 Econometric methods

We apply several econometric models to conduct our analysis. First, we apply a system of two equations to measure the impact of IITA's genebank to on-farm cowpea varietal diversity. Second, we apply a multinomial endogenous treatment effect model to measure the impact of IITA's genebank on Nigerian farmers' welfare.

The system of two equations helps capture (1) farmers' decisions to grow a cowpea variety that has a genebank ancestor and the (2) impact of growing this variety on the spatial diversity of cowpea varieties. We hypothesize 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. 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 other cowpea varieties—reducing the spatial diversity of cowpea varieties. The model is formulated for the *i*th farmer as:

$$\begin{cases} G_i^* = \boldsymbol{\alpha X_i} + e_i \quad (1) \\ I_i^* = \beta G_i + \boldsymbol{\gamma Z_i} + u_i \ (2) \end{cases}$$

where G_i^* is a latent variable that captures the farmer's benefit from the decision to grow a cowpea variety that has a genebank ancestor. The farmer's observed choice is a binary variable:

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

where G_i is a binary variable that indicates whether the farmer is growing a cowpea variety that has a genebank ancestor. X_i represents a vector of factors that affect G_i^*, with an associated vector of parameters α, and an error term e_i.

I_i^* is also a latent variable that captures farmer's diversification strategy. The farmer's observed diversification strategy is a cowpea varietal diversity index I_i, which has the minimum value $\underline{I}$ and the maximum value $\bar{I}$:

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

In equation (2), I_i^* is affected by G_i, with the associated parameter β. Z_i represents a vector of factors that affect I_i^*, with a vector of associated parameters γ, and an error term u_i.

We use the conditional recursive mixed-process (CMP) framework (Roodman 2011) to estimate the parameters of the two-equation system. The use of the CMP approach is motivated by the following reasons. First, our system is a multiequation mixed model (the two equations have different types of dependent variables), Equations 1 and 2 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 (Equation 1), the probit/logit model, captures farmer's decision to grow a cowpea variety that has a genebank ancestor, whereas Stage 2 (Equation 2), the tobit model, captures the effect of farmer's decision on spatial diversity of cowpea varieties. The system of equations is estimated using a maximum likelihood (ML) approach (Roodman 2011).

In settings with potential selection on unobservable characteristics and a treatment variable that has more than two categories, both multinomial endogenous treatment effect model and multinomial endogenous switching regression model may be used to measure a treatment effect. We select the multinomial endogenous treatment model, as we are interested in the average treatment effect and testing the significance of selection effects. 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, 2006b). We hypothesize that farmers are growing one of the three types of cowpea varieties: an (improved) cowpea variety that has a genebank ancestor, an (improved) cowpea variety that does not have a genebank ancestor, and a cowpea landrace. Each type of cowpea variety has a distinct 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

$$EV_{ij}^{*} = z_i'\alpha_j + \delta_j l_{ij} + \eta_{ij} \qquad (3)$$

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

Let $j = 0$ denotes the control group, farmers who are growing a cowpea landrace, and $EV_{i0}^{*} = 0$. While EV_{ij}^{*} is not observed, we observe farmer *i's* cowpea variety choice (treatment choice). Let d_j be binary variables representing the observed cowpea variety choice (observed treatment choice) and $\boldsymbol{d_i} = (d_{i0}, d_{i1}, d_{i2})$. Also let $\boldsymbol{l_i} = (l_{i0}, l_{i1}, l_{i2})$. 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)[1]:

$$Pr(\boldsymbol{d_i}|\boldsymbol{z_i},\boldsymbol{l_i}) = \frac{exp(z_i'\alpha_j+\delta_j l_{ij})}{1+\sum_{k=1}^{2} exp(z_i'\alpha_k+\delta_k l_{ik})} \quad (4)$$

The second stage of the model assesses the impact of growing a specific type of cowpea variety on three outcome variables: cowpea yield, cowpea consumption, and cowpea sale. The expected outcome equation for farmer *i* is formulated as follows:

$$E(y_i|\boldsymbol{d_i},\boldsymbol{x_i},\boldsymbol{l_i}) = \boldsymbol{x}_i'\beta + \sum_{j=1}^{2}\gamma_j d_{ij} + \sum_{j=1}^{2}\lambda_j l_{ij} \quad (5)$$

where $\boldsymbol{x_i}$ is a set of exogenous covariates with associated parameter vectors β, and γ_j denoting the treatment effects relative to the control. λ_j show the impacts of unobserved characteristics (common to farmer i's cowpea variety choice and outcome) on the outcome. We also assume that the outcome variables are continuous[2] and follow a normal (Gaussian) probability distribution.[3]

The model is 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).

4 Data and variables description

4.1 Data

The data for the study come from two sources. The first source is the IITA's Tropical Legumes III Project: a household survey conducted in Northern Nigeria in 2016 and 2017 and used by Manda et al. (2019). The survey was conducted in 10 states (Borno, Bauchi, Gombe, Jigawa, Kaduna, Kano, Katsina, Kebbi, Sokoto, and Zamfara), which represent about 75% of the total cowpea production in Nigeria. Enumerators collected information from 1,524 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 (NPC) and the extension agents from the Agricultural Development Program (ADP), respectively.

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[1] Please note that the mixed multinomial logit structure (MMNL) is an assumption. Other multinomial probability distributions could also be considered.

[2] 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.

[3] Using ln(.) helps have normal distributions of outcome variables.

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 second source of data is the genebank of IITA. 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).

4.2 **Variables description**

To investigate the impact of IITA's genebank on varietal diversity of cowpeas on farms in Nigeria, we use similar dependent and independent variables as discussed in Bellon et al. (2020), Benin et al. (2004), and Smale (2006), which analyze the determinants of crop diversity on farms (in African countries). We also use similar dependent and independent variables with Bozzola and Smale (2020), which investigates the welfare effects of crop biodiversity. Definitions of the variables used for our econometric analysis are presented in table 1.

Following Magurran (2004) and Smale (2006), we measure 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 is 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 are collected).

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 plot. 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 is computed as follows:

$$d^r = S/\sqrt{A}$$

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

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:

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

In our case, p_i is the area share planted to cowpea 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 compute the Berger-Parker index as follows:

$$d^d = 1/max(p_i)$$

where $max(p_i)$ is the maximum 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 economics analysis of industrial organizations. As applied here, it expresses specialization and tells us whether a single variety occupies most of the planted area. We calculate the Herfindahl index as follows:

$$d^c = \sum_{i=1}^{n} p_i^2$$

where p_i is area share occupied by cowpea variety *i.*

We account 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 helps establish the link between the genebank and improved cowpea varieties grown by farmers.

We also select cowpea *Yield*. *Yield* is obtained by dividing the total cowpea harvested on the farm size (the sum of plots), expressed in kg/ha.

Two variables are 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. And *Sale* is a sale (or revenue) indicator, which refers to the quantity of cowpea grain sold by the household, expressed in kg.

The other variables that are used for our econometric analysis are 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).

5 Results

We first present descriptive statistics on households and household heads (section 5.1). We then move to our research objectives (sections 5.2, 5.3, 5.4 and 5.5).

5.1 Descriptive statistics

The study surveyed 1,524 cowpea producing households. Our analysis is based on these households and the characteristics of their household heads. Table 2 presents a summary of descriptive statistics of independent variables. We find significant differences between the North East and North West regions, where the survey was conducted. With respect to socioeconomic characteristics, we find that household heads from the North West regions are older and need more credit compared with households from the North East region. In addition, in the North West region, fewer women (4%) are heads of cowpea-producing households than in the North East region (10%). However, the two regions are similar in terms of level of education of the household head. On average, household heads of both regions have five years of education.

Regarding the pedigree information of cowpea varieties grown by farmers, we find that more households from the North West region are growing improved cowpea varieties that have a genebank ancestor. In the North West region 44% of households are growing improved cowpea varieties that have 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 have more genebank ancestors (12) than those grown in the North East region (8). Finally, regarding farm and market characteristics, farms are bigger and have flat soils in the North East region, but households living in this region are farther away from village and district markets.

5.2 Spatial diversity of cowpea varieties on farms

The first research objective consists of measuring spatial diversity of cowpea varieties on farms, and testing its association with genebank ancestry in the pedigrees of improved cowpea varieties. On average, most of Nigerian households are growing one cowpea variety per plot. Only nine households (0.58%) are growing two different cowpea varieties per plot. In addition, 41.29% of households are growing at least one improved cowpea variety as main crop, whereas 40.91% are growing at least one improved cowpea variety that has a genebank ancestor as main crop. Finally, 68.50% of households are growing at least one cowpea landrace as 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 (2.161) is higher in the North West region (two-sample two-sided t-test: p = 0.000), than in the North East region (1.780), suggesting greater richness of cowpea varieties in the North West region, when standardized by area. For instance, Table 4, which shows the repartition of households over main cowpea varieties grown, indicates that some improved cowpea varieties (UAM09-1046-6-1 and other improved cowpea varieties) are not grown as main cowpea variety by households from the North East region, whereas 15 households are growing them as main cowpea varieties in the North West region.

The average value of the Shannon index (0.340) is lower in the North West region than in the North East region (0.344) (two-sample two-sided t-test: p = 0.03), indicating that cowpea varieties grown are less equally abundant in the North West region than the North East region.

Finally, in term of dominance, we find that the difference between the average values of the Berger-Parker index in the North East region and in the North West region is weakly significant (two-sample two-sided t-test: p = 0.075), suggesting that no single variety strongly dominates both regions. While Kananado White/Dan Bokolo is the most widely grown cowpea variety in both regions, farmers cultivate other varieties too.

5.3 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 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. We find that most of improved cowpea varieties grown by Nigerian farmers have been released recently (between 2005 and 2015) and have a genebank ancestor. On average, an improved cowpea variety grown by Nigerian farmers has 39 and 9 IITA's genebank ancestors, relative to number of appearances and unique counts, respectively. For instance, the most recently released improved cowpea variety, UAM09-1055-6, has 56 and 8 IITA's genebank ancestors, relative to number appearances and unique counts, respectively, whereas, the least recent improved cowpea variety, IT90K-277-2 (Sasakawa), has 14 and 7 IITA's genebank ancestors, relative to number of appearances and unique counts, respectively. UAM09-1055-6 is the result of a single cross between Borno Brown and IT97K-499-35, whereas IT90K-277-2 (Sasakawa) is the result of the breeding between the IITA's genebank accession IT87F-1777-2 and IT84S-2246-4, crossed with TVx3236. Annexes show diagrams depicting improved cowpea varieties pedigree trees, including UAM09-1055-6 and IT90K-277-2 .

The improved cowpea variety, IT89KD-288/Sampea-11, released in 2009 is the most adopted by Nigerian farmers, in terms of main cowpea variety grown on plots (it is grown as main cowpea variety on 7.24% of plots), whereas IT07K-318-33/Sampea 17, released in 2015, is the least adopted by Nigerian farmers, in terms of main cowpea variety grown on plots (it is grown on 0.08% of plots). IT89KD-288/Sampea-11 is the result of the combination between an IITA's genebank accession, IT87F-1777-2, and IT84s-2246-4, while IT07K-318-33/Sampea 17 has been developed through the cross of IT98K-131-2 with IT95K-238-3. Annexes show diagrams depicting 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 generate bred lines used in the final breeding of improved cowpea varieties grown by Nigerian farmers.

5.4 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 run the recursive mixed-process model (Equations 1 and 2), using an ML estimation approach.[4] Table 6 presents the estimates of the model. Based on the first specification, we find that growing an improved cowpea variety that has a genebank ancestor is not significantly associated with richness—either positively or negatively.

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

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[4] The model is estimated using the Stata command *cmp*

on farms is higher in the North West region and in households with small farms, a higher number of flat plots, or whose members reside not far from their plots.

Results also show 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 are more likely to grow improved cowpea varieties that have a genebank ancestor. This is in line with Manda et al. (2019), who find that the number of years a farmer has been exposed to improved cowpea varieties is an important determinant of the adoption of improved cowpea varieties.

Results from the second specification indicate that the adoption of an improved cowpea variety that has a genebank ancestor has a positive and significant effect on the inverse dominance index. Farm characteristics, including farm size and distance to farm, and household size are also determinants of the inverse dominance index. Farmers who have either large farms, a high number of household members, or are far from their farms devote less area to their preferred variety.

A new important determinant of growing a cowpea variety that has a genebank ancestor is soil fertility. Farmers are more likely to grow an improved cowpea variety that has a genebank ancestor when they have a higher number of plots with perceived poor soil quality. This suggests a possible association with traits conferred through diverse ancestry.

Finally, the third specification indicates that growing an improved cowpea variety that has a genebank ancestor has a negative and significant effect on the concentration index. This is consistent with the results for the Berger-Parker index.

To sum up, genebank ancestry does not contribute to more specialization or dominance of any particular cowpea variety on farms or lead to the displacement of other cowpea varieties. The results also indicate that certain farm characteristics are more important determinants of greater richness among cowpea varieties.

5.5 IITA's genebank, cowpea yield and farmers' welfare

To investigate the effect of IITA's genebank on cowpea yield and farmers' welfare, we run a multinomial endogenous treatment effect model, using a maximum simulated likelihood (MSL) approach.[5] Table 7 presents the results of multinomial endogenous treatment effects model estimates of impacts on cowpea yield. We find a positive and significant treatment effect of growing an

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[5] The model is estimated using the Stata command *mtreatreg*. We use 500 simulation draws.

improved cowpea variety having a genebank ancestor. Growing an improved cowpea variety having a genebank ancestor increases by 197.427% the yield of cowpea, compared to growing a cowpea landrace. However, the significant value (-1.279) of the coefficient on the latent factor indicates a possible negative selection effect. In other words, farmers who are more likely to grow a cowpea variety having a genebank ancestor relative to a cowpea landrace, on the basis of their unobserved characteristics, may experience a decline in cowpea yield.

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) have a significant effect on cowpea yield.

Table 8 presents the results of multinomial endogenous treatment effects model estimates of impacts on cowpea consumption. We find a positive and significant treatment effect of growing an improved cowpea variety with a genebank ancestor on cowpea consumption. Growing an improved cowpea variety having a genebank ancestor increases by 52.653% the home food cowpea consumption, compared to growing a cowpea landrace. However, the significant value (-0.479) of the coefficient on the latent factor indicates a possible negative selection effect. In other words, farmers who are more likely to grow a cowpea variety having a genebank ancestor relative to a cowpea landrace, on the basis of their unobserved characteristics, may reduce their home food cowpea consumption.

Other factors like farm characteristics (size, slope, distance to field, and soil fertility) and market characteristics (distance to district market) have a significant effect on home food cowpea consumption.

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

In summary, growing a cowpea variety that has a genebank ancestor has a positive and significant impact on cowpea yield and cowpea consumption at home, but not on cowpea sale.

6 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 confirm that genebanks in Africa contribute to the development of improved crop varieties and the conservation and distribution of tree germplasms (Kitonga et al. 2020; Sellitti et al. 2020).

Evidence also shows that genebank ancestry does not contribute to specialization or dominance of any particular variety but is not significantly associated with greater richness among cowpea varieties grown by farmers in Nigeria. Therefore, although IITA's genebank accessions are used for the development of improved cowpea varieties that have been adopted by farmers in Nigeria, other factors like household size, farm characteristics and geographical zone are more important to explain the specialization/dominance/richness of cowpea varieties grown. This is in line 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 (Bellon et al. 2020; Benin et al. 2004; Smale et al. 2003).

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), which finds that a number of years a farmer has been exposed to improved cowpea varieties is an important determinant of the adoption of improved cowpea varieties. We find 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 find 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 find that the geographical zone has an effect on the adoption of improved cowpea varieties in Nigeria. Finally, as expected, growing a cowpea variety that has a genebank ancestor has an effect on cowpea yield and farmers' welfare. Evidence shows a positive and significant effect on cowpea yield and cowpea consumption. It is acknowledged that improved crop varieties or agricultural technologies have a positive and significant impact on agricultural productivity in Africa (Abdulai and Huffman 2014; Duflo et al. 2008; Kassie et al. 2008; Pender and Gebremedhin 2007).

7 Conclusion

Cowpea is an important food legume that provides food and fodder as well as improving soil fertility and contributing 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 2016 and 2017, and data from IITA's cowpea breeding program, we measure varietal diversity, link improved cowpea varieties grown to IITA's genebank and investigate the effect of IITA's genebank on varietal diversity of cowpeas on farms. We also examine 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 that some IITA's genebank accessions are used by different breeders to generate bred lines used in the final breeding of 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 is not significantly associated with greater richness among cowpea varieties. However, 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 suggest that, on farms, IITA's genebank contributes to cowpea yield and farmers' welfare, showing additional benefits from IITA's genebank in Nigeria. In addition, this study shows that growing cowpea varieties with genebank ancestry does not displace other varieties, including cowpea landraces.

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.

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9 Figures and tables

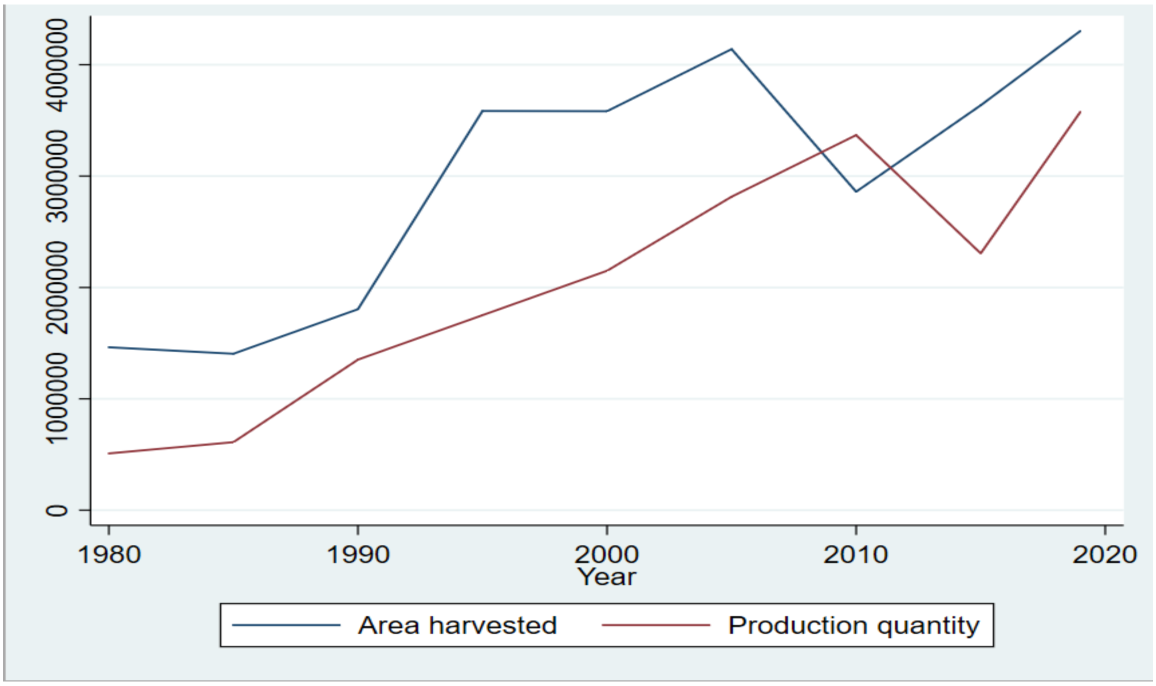


Figure 1. Land area harvested (ha) and production quantity (tons) of cowpea in Nigeria (1980-2020). Source: FAOSTAT data on crops production.

Table 1. Definition of variables used in 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
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

Source: Authors

Table 2. Descriptive statistics for independent (control) variables

Variable	All	North West (N=994)	North East (N=530)
Household characteristics			
Age***	43.759	44.823	41.758
Sex***	0.941	0.961	0.904
Education	5.248	5.304	5.142
Household size***	8.292	8.558	7.793
Experience***	0.957	0.942	0.985
Need credit***	0.514	0.480	0.577
Pedigree information			
Anc***	0.409	0.436	0.358
NumAnc***	10.708	11.907	8.395
Farm characteristics			
Size***	1.938	1.736	2.317
Slope***	1.241	1.303	1.124
Soil fertility	0.072	0.069	0.077
Distance to field*	26.215	25.551	27.464
Market characteristics			
Distance to seed dealer	68.952	67.058	72.498
Distance to village market***	42.510	39.424	48.290
Distance to district market***	85.898	79.670	97.563

Source: Authors. Notes: ***,**,*: differences in means or proportions are statistically significant at 1, 5, or 10% significance level, respectively.

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	2.032	1.120	0.404	15.811
Shannon index	0.341	0.041	0	0.693
Berger-Parker index	3.142	1.825	1	33.333
Herfindahl index	0.165	0.123	0.001	1
	North West region			
Menhinick index	2.161	1.187	0.404	15.811
Shannon index	0.340	0.043	0	0.693
Berger-Parker index	3.190	1.919	1	33.333
Herfindahl index	0.165	0.128	0.001	1
	North East region			
Menhinick index	1.780	0.925	0.442	12.910
Shannon index	0.344	0.034	0	0.367
Berger-Parker index	3.044	1.615	1	25
Herfindahl index	0.165	0.112	0.002	1

Source: Authors

Table 4. Repartition of households over main cowpea varieties grown.

Cowpea varieties	**North West**		**North East**	
	Total are 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

Source: Authors.

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? (0/1)**	**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)	1	14	7	2005
IT89KD-288/Sampea-11	1	13	7	2009
IT99K-216-24-2 (Kwankwaso)	1	22	7	Not yet released
IT89KD-391/Sampea12	1	16	8	2009
IT97K-499-35/Sampea-10	1	55	8	2008
IT93K-452-1/Sampea8	1	29	13	2005
IT99K-573-1-1/Sampea-14	1	43	12	2011
IT99K-573-2-1/Sampea-15	1	43	12	2011
IT98K-131-2	1	33	7	Not yet released
UAM09-1046-6-1	1	56	8	Not yet released
UAM09-1055-6	1	56	8	2016
IT98K-205-8	1	55	9	Not yet released
IAR48 /Sampea 7	Not Available	Not Available	Not Available	Not available
IT98K-491-4	1	Not Available	Not Available	Not Available
IT07K-318-33/Sampea 17	1	50	13	2015
IT07K-292-10/Sampea 16	1	67	14	2015

Source: Authors. Notes: Retrieving from the database of the cowpea program of IITA.

Table 6. Recursive mixed-process model estimates.

Explanatory variable	***First specification***	
	Richness index (d^r)	**Anc**
Endogenous variable		
Anc	0.104	----- -----
Household characteristics		
Age	-----	-0.001
Sex	-----	-0.118
Education	-----	0.011
Education^2		-0.001
Household size	-0.005	-----
Need credit	-----	-0.157**
Experience	-----	1.032***
Farm characteristics		
Size	-0.175***	-----
Slope	0.189***	-----
Distance to farm	-0.002**	-----
Soil fertility	-----	0.378
Market characteristics		
Distance to seed dealer	-----	0.000
Distance to village market	-----	0.000
Distance to district market	-----	0.001
Geographical zone		
North East	-0.263***	-0.253***
Constant	2.248***	-0.954***
Prob > chi^2	0.000	
N	1,557	

Explanatory variable	*Second specification*		*Third specification*	
	Inverse Dominance index (d^d)	Anc	Concentration index (d^c)	Anc
Endogenous variable				
Anc	2.473***	-----	-0.065**	-----
Household characteristics				
Age	-----	0.003	-----	0.000
Sex	-----	-0.097	-----	-0.139
Education	-----	-0.011	-----	-0.002

Education^2		-0.005		-0.001
Household size	0.016*	-0.000	-0.002**	
Need credit	-----	-0.189***	-----	-0.190***
Experience	-----	0.481***	-----	0.999***
Farm characteristics				
Size	0.040**	-----	-0.003**	
Slope	0.024	-----	-0.005	
Distance to farm	0.003*	-----	-0.000	
Soil fertility	-----	0.276***	-----	0.399***
Market characteristics				
Distance to seed dealer	-----	0.000	-----	0.000
Distance to village market	-----	0.001***	-----	0.000
Distance to district market	-----	0.000	-----	0.001
Geographical zone				
North East	0.040	-0.202***	-0.005	-0.244***
Constant	1.740***	-0.555***	0.231***	-0.924***
Prob > chi^2	0.000		0.000	
N	1,559		1,559	

Source: Authors. Notes: ***,**,*: Significance at 1, 5, or 10% significance level, respectively.

Table 7. Multinomial endogenous treatment effects model estimates of impacts on cowpea yield.

	Outcome model	
Explanatory variable	Ln cowpea yield	
Treatment variable		
Adoption of cowpea variety without genebank ancestor	-1.277	
Adoption of cowpea variety having genebank ancestor	1.090***	
Household characteristics		
Age	-0.018	
Age^2	0.000	
Sex	0.739***	
Education	0.008	
Education^2	0.000	
Need credit	0.390***	
Farm characteristics		
Size	-0.172***	
Slope	0.035	
Distance to farm	-0.006***	
Soil fertility	-0.345**	
Market characteristics		
Distance to village market	-0.003***	
Distance to district market	-0.001*	
Constant	3.081***	
Selection terms (λ)		
Adoption of cowpea variety without genebank ancestor	0.664	
Adoption of cowpea variety having genebank ancestor	-1.279**	
	Treatment models	
Explanatory variable	Adoption of cowpea variety without genebank ancestor	Adoption of cowpea variety having genebank ancestor
Household characteristics		
Age	0.161	-0.002
Age^2	-0.001	0.000
Sex	1.029	-0.422
Education	-0.113	0.013
Education^2	0.009**	-0.002
Need credit	-0.522	-0.230*
Experience	-1.528	2.150***
Farm characteristics		

Size	0.084	-0.012
Slope	0.093	0.371***
Distance to farm	-0.017	-0.004
Soil fertility	0.794	0.673***
Market characteristics		
Distance to seed dealer	-0.003	0.000
Distance to village market	-0.000	0.001
Distance to district market	0.003	0.001
Geographical zone		
North East	-1.776	-0.225
Constant	-8.772*	-2.203**
Prob > chi^2	0.000	
N	1,442	

Source: Authors. Notes: The control group is households that grow a cowpea landrace. 500 simulation draws were used. ***,**,*: Significance at 1, 5, or 10% significance level, respectively.

Table 8. Multinomial endogenous treatment effects model estimates of impacts on cowpea consumption.

	Outcome model	
Explanatory variable	Ln cowpea consumption	
Treatment variable		
Adoption of cowpea variety without genebank ancestor	-0.283	
Adoption of cowpea variety having genebank ancestor	0.423***	
Household characteristics		
Age	0.012	
Age^2	-0.000	
Sex	0.083	
Education	-0.013	
$Education^2$	0.000	
Need credit	0.060	
Farm characteristics		
Size	0.065***	
Slope	-0.046*	
Distance to farm	0.001*	
Soil fertility	-0.136**	
Market characteristics		
Distance to village market	-0.000	
Distance to district market	0.0004*	
Constant	0.803***	
Selection terms (λ)		
Adoption of cowpea variety without genebank ancestor	0.117	
Adoption of cowpea variety having genebank ancestor	-0.479***	
	Treatment models	
Explanatory variable	Adoption of cowpea variety without genebank ancestor	Adoption of cowpea variety having genebank ancestor
Household characteristics		
Age	0.153	0.008
Age^2	-0.001	-0.000
Sex	-18.656**	-0.366
Education	-0.201*	0.025
$Education^2$	0.010**	-0.003
Need credit	-0.337	-0.203
Experience	-1.699*	2.186***

Farm characteristics		
Size	0.081	-0.022
Slope	0.139	0.384***
Distance to farm	-0.010	-0.005*
Soil fertility	0.824	0.696***
Market characteristics		
Distance to seed dealer	-0.004	0.000
Distance to village market	-0.000	0.000
Distance to district market	0.003**	0.000
Geographical zone		
North East	-1.156	-0.346**
Constant	11.025-	-2.572***
Prob > chi^2	0.000	
N	1,376	

Source: Authors. Notes: The control group is households that grow a cowpea landrace. 500 simulation draws were used. ***,**,*: Significance at 1, 5, or 10% significance level, respectively.

Table 9. Multinomial endogenous treatment effects model estimates of impacts on cowpea sale.

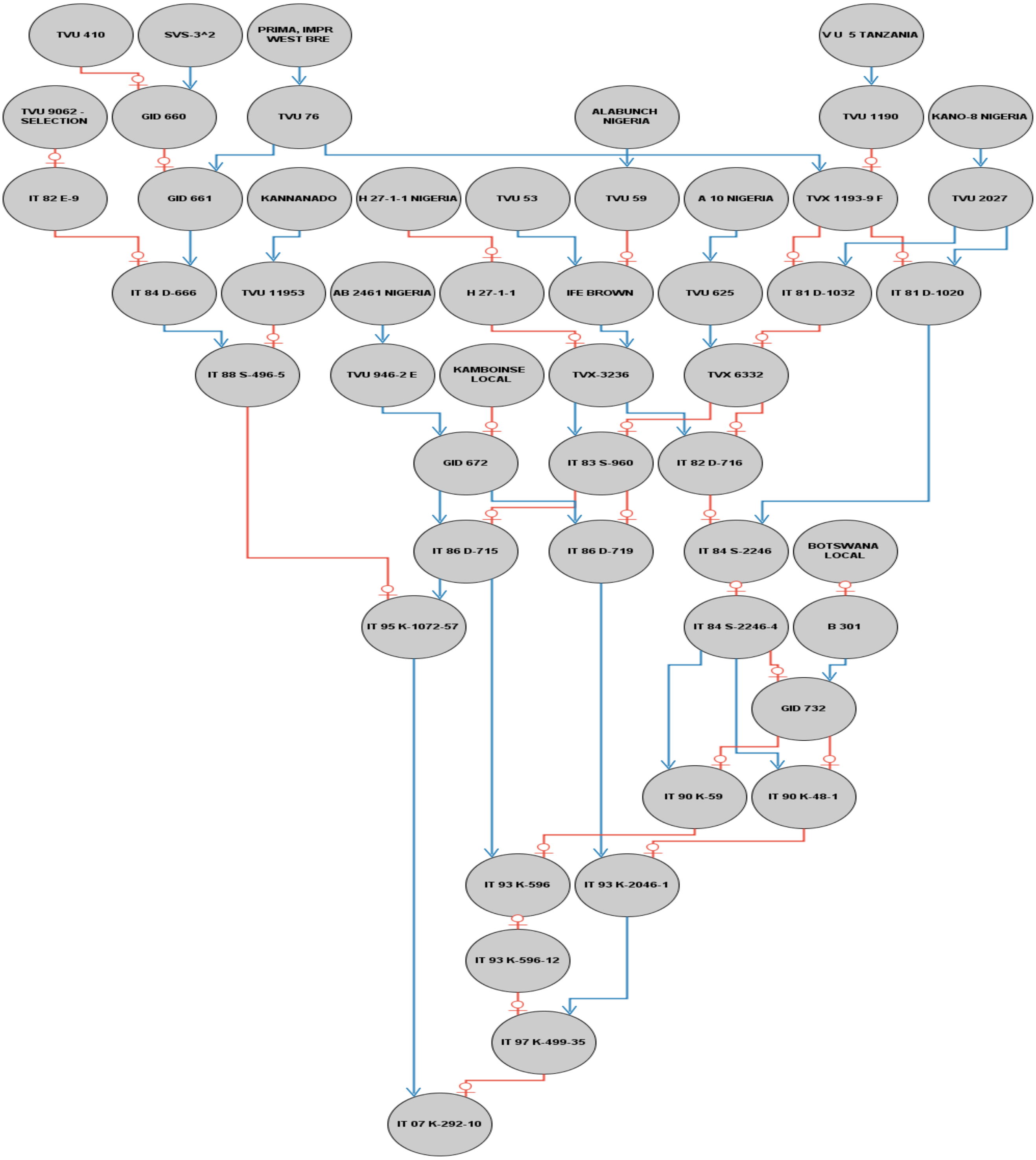
	Outcome model	
Explanatory variable	Ln cowpea sale	
Treatment variable		
Adoption of cowpea variety without genebank ancestor	-0.578	
Adoption of cowpea variety having genebank ancestor	-0.027	
Household characteristics		
Age	0.001	
Age^2	-0.000	
Sex	-0.116	
Education	0.017	
Education^2	-0.002	
Need credit	-0.631***	
Farm characteristics		
Size	-0.000	
Slope	0.105	
Distance to farm	0.003	
Soil fertility	0.133	
Market characteristics		
Distance to village market	-0.004***	
Distance to district market	0.000	
Constant	5.399***	
Selection terms (***λ***)		
Adoption of cowpea variety without genebank ancestor	0.000	
Adoption of cowpea variety having genebank ancestor	-0.000	
	Treatment models	
Explanatory variable	Adoption of cowpea variety without genebank ancestor	Adoption of cowpea variety having genebank ancestor
Household characteristics		
Age	16.210***	-0.029
Age^2	-0.142***	0.000
Sex	0.675	-0.759
Education	-60.040***	-0.123*
Education^2	3.396***	0.005
Need credit	59.044***	-0.131
Experience		1.702**

Farm characteristics		
Size	15.610***	-0.002
Slope	-94.746***	0.452***
Distance to farm	0.755***	-0.013**
Soil fertility	4.613***	0.568
Market characteristics		
Distance to seed dealer	-0.743***	0.001
Distance to village market	0.184***	-0.002
Distance to district market	0.202***	0.002
Geographical zone		
North East	-68.994***	-0.373
Constant	--520.468***	-0.482
Prob > chi^2	0.000	
N	500	

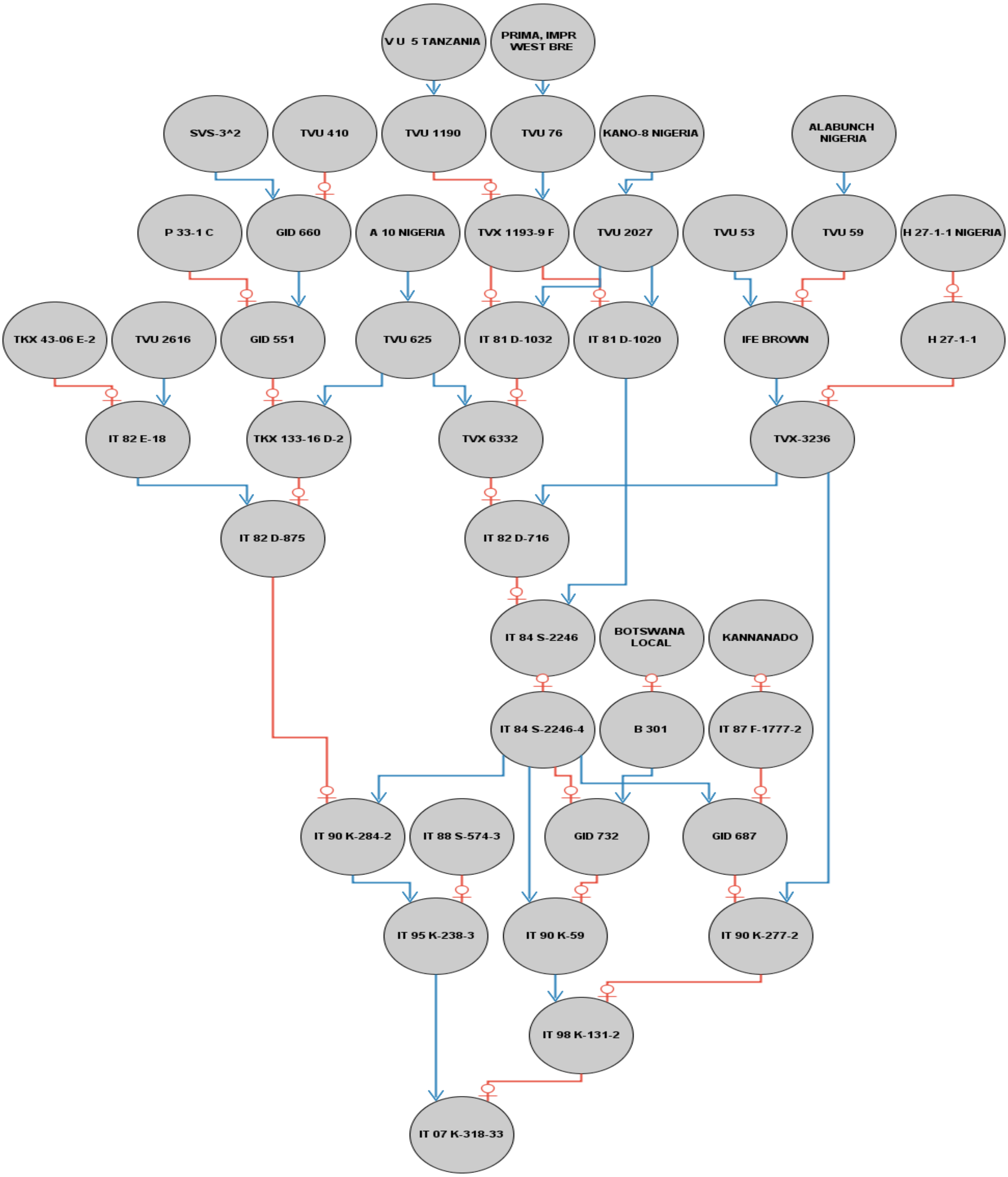
Source: Authors. Notes: The control group is households that grow a cowpea landrace. 500 simulation draws were used. ***,**,*: Significance at 1, 5, or 10% significance level, respectively.

10 Annexes

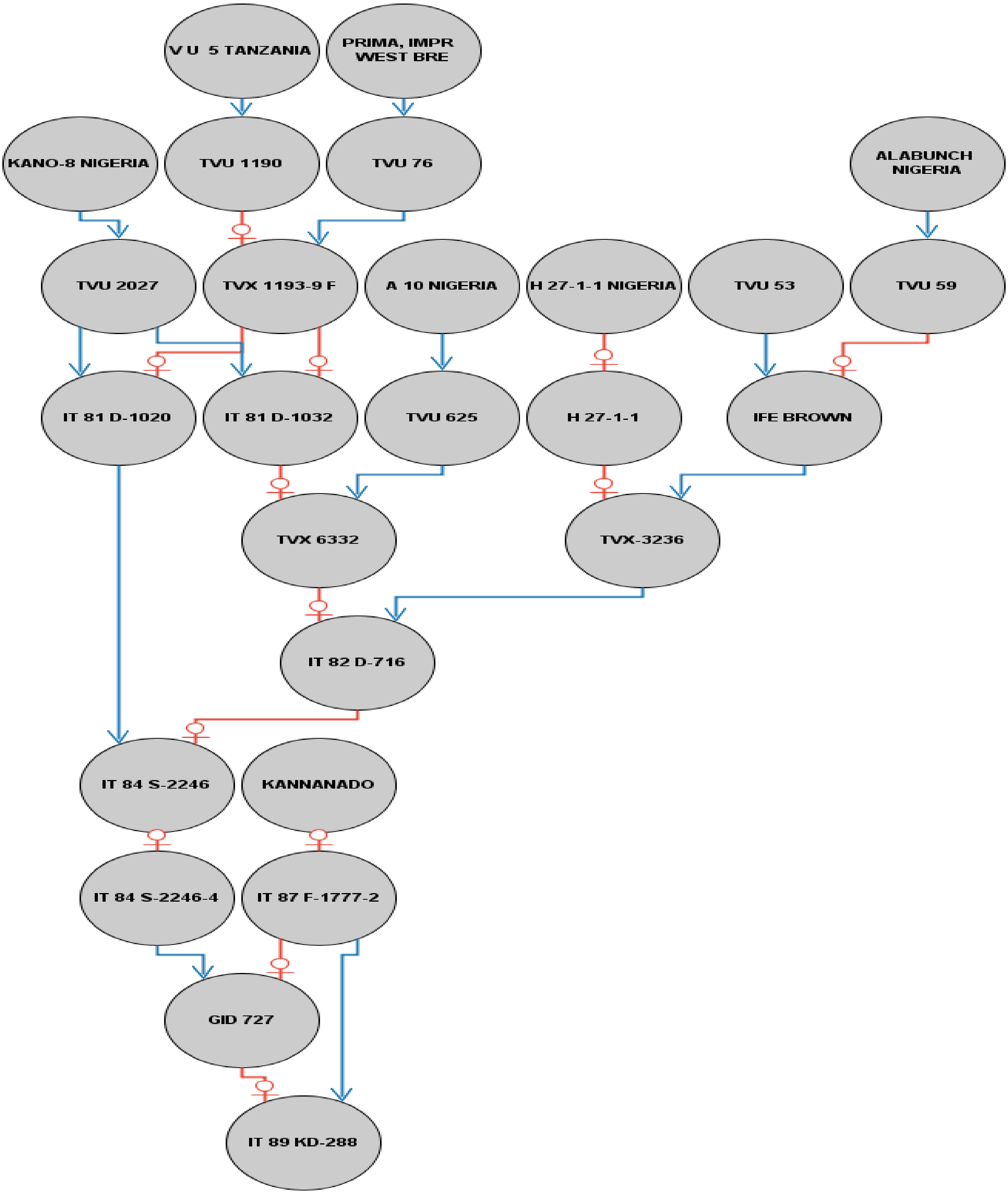
Annex 1. Diagrams depicting adopted improved cowpea varieties pedigree trees



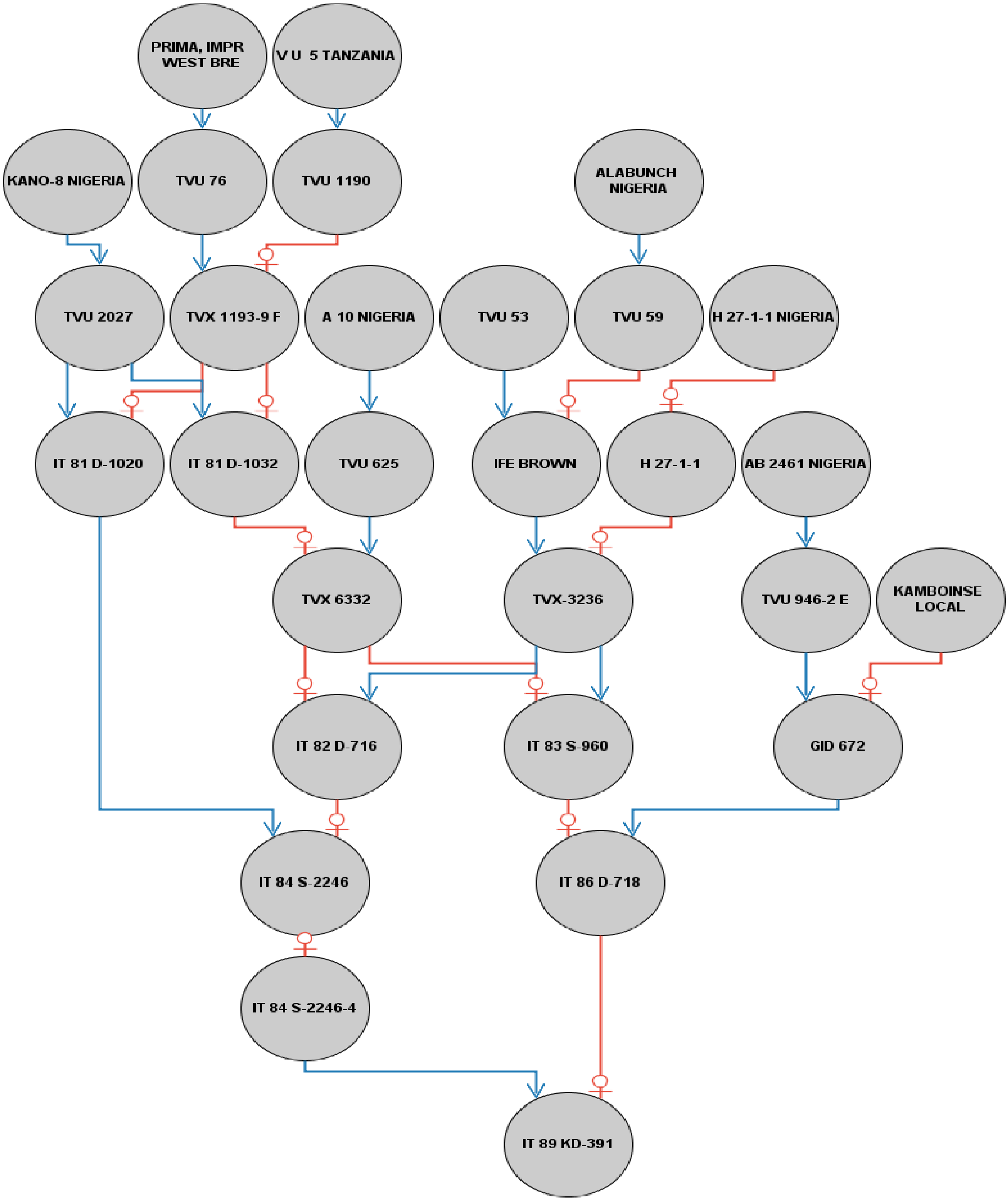
IT07K-292-10/Sampea 16



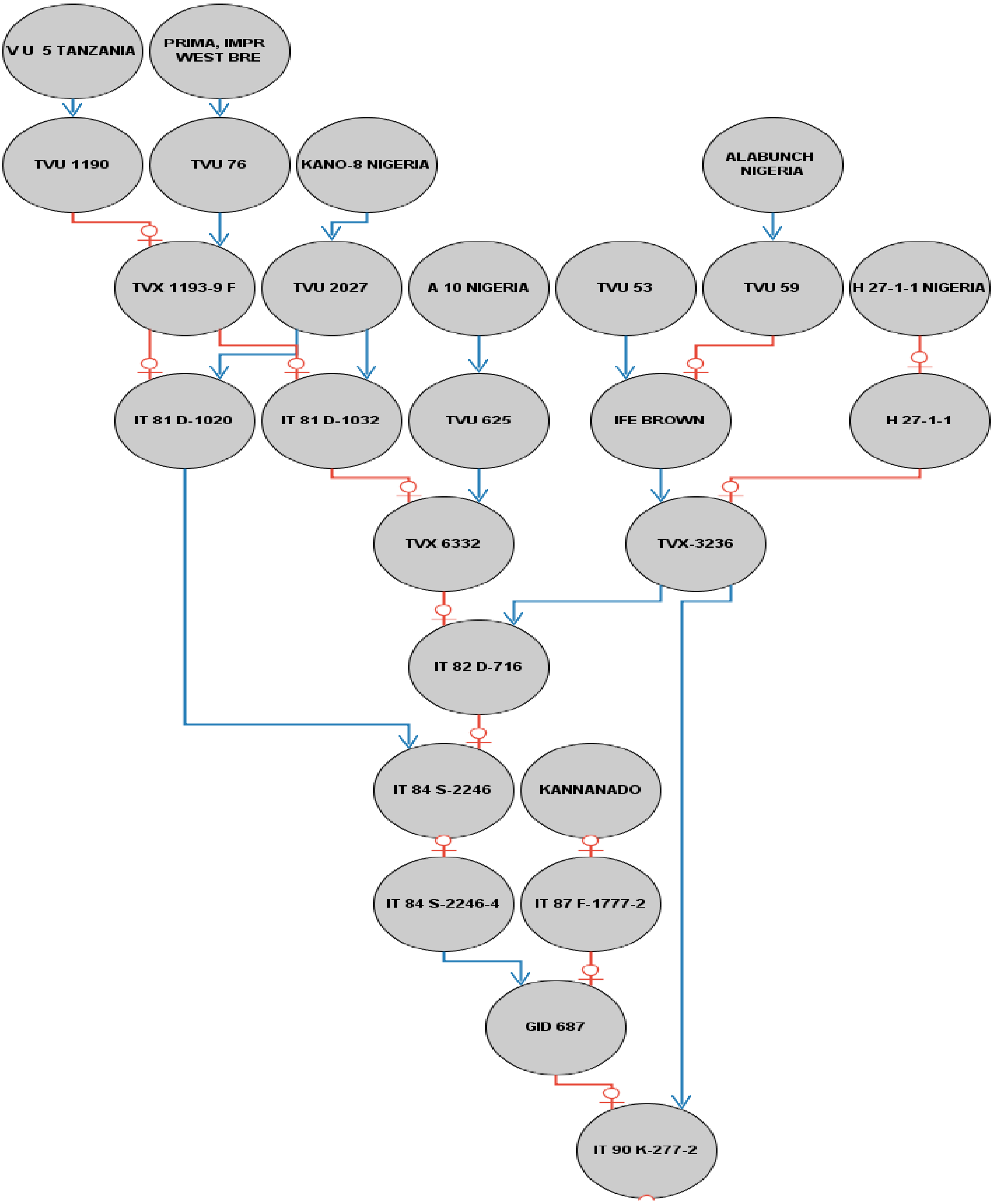
IT07K-318-33/Sampea 17



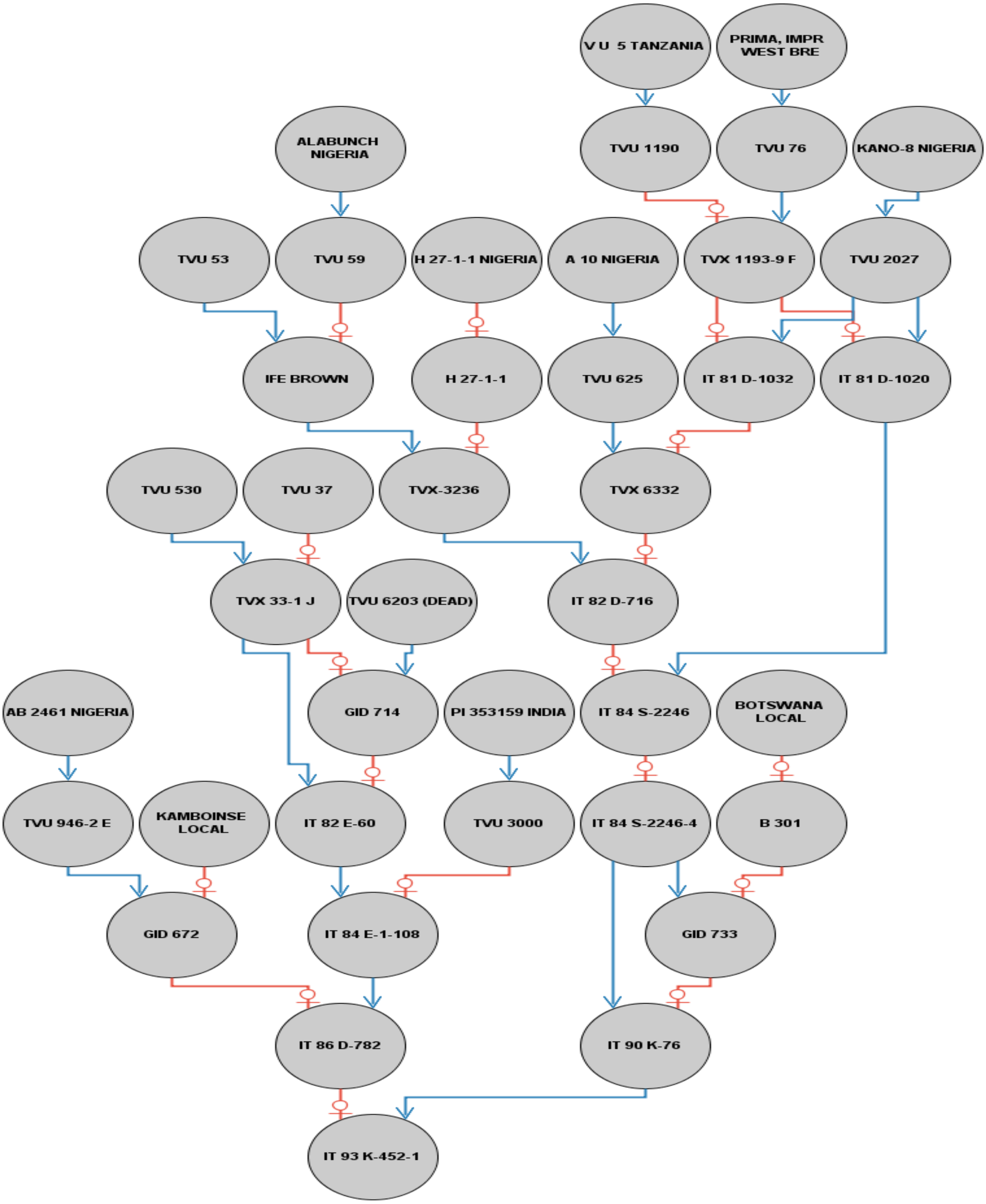
IT 89 KD-288/Sampea-11



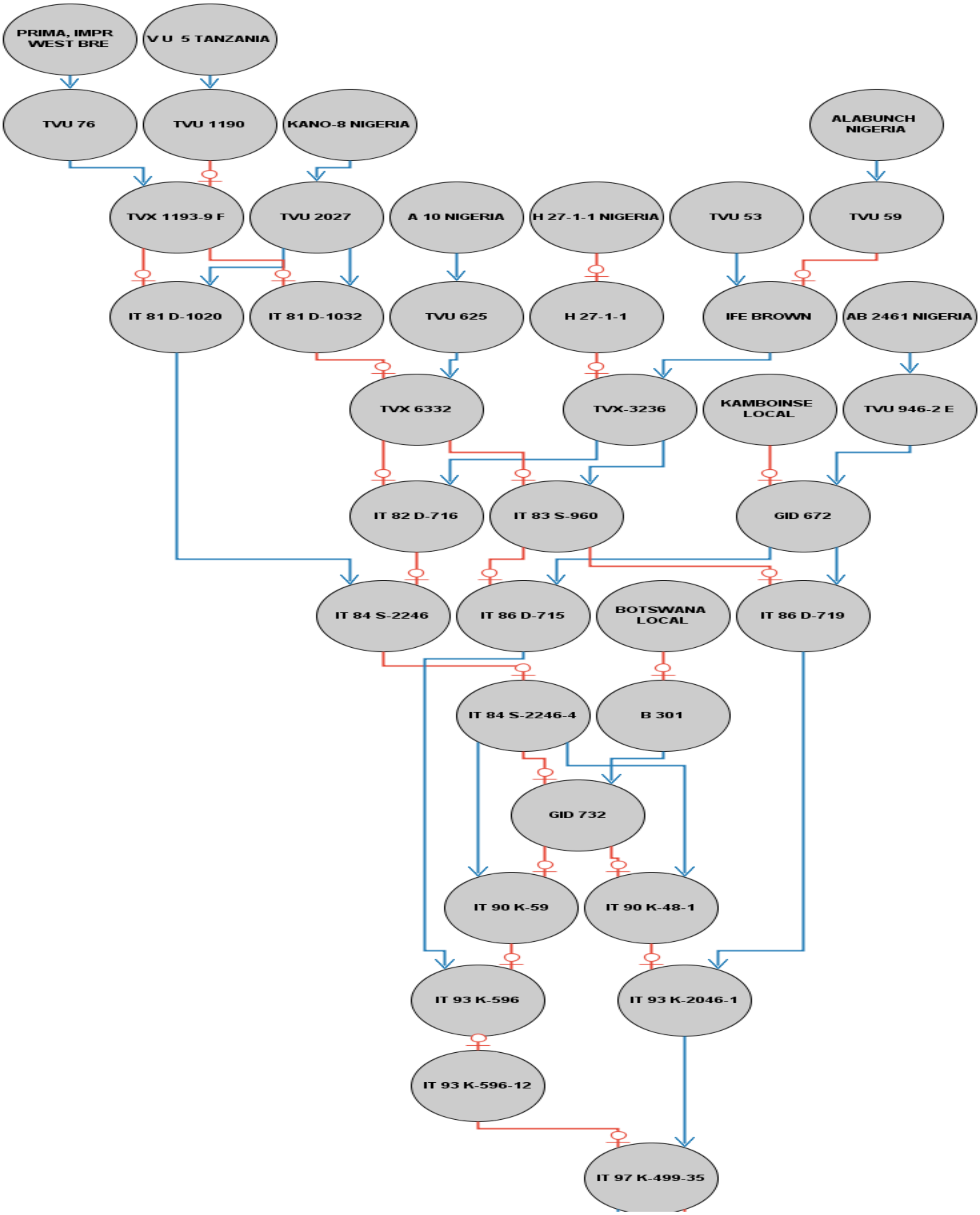
IT89KD-391/Sampea12



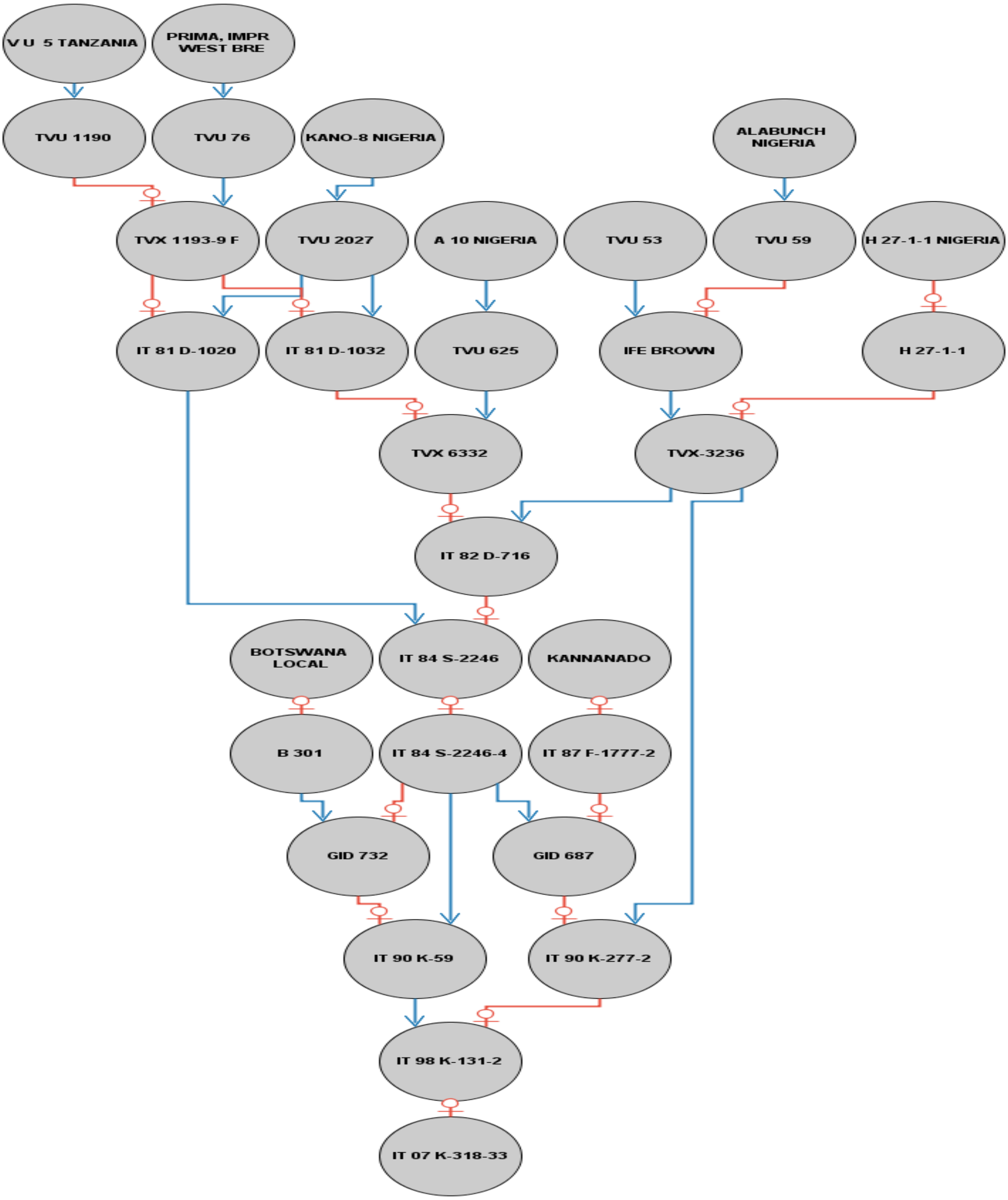
IT 90 K-277-2 (Sasakawa)



IT93K-452-1/Sampea8



IT97K-499-35/Sampea-10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TVU 76
KANO-8 NIGERIA
ALABUNCH NIGERIA
TVX 1193-9 F
TVU 2027
A 10 NIGERIA
TVU 53
TVU 59
H 27-1-1 NIGERIA
IT 81 D-1020
IT 81 D-1032
TVU 625
IFE BROWN
H 27-1-1
TVX 6332
TVX-3236
IT 82 D-716
BOTSWANA LOCAL
IT 84 S-2246
KANNANADO
B 301
IT 84 S-2246-4
IT 87 F-1777-2
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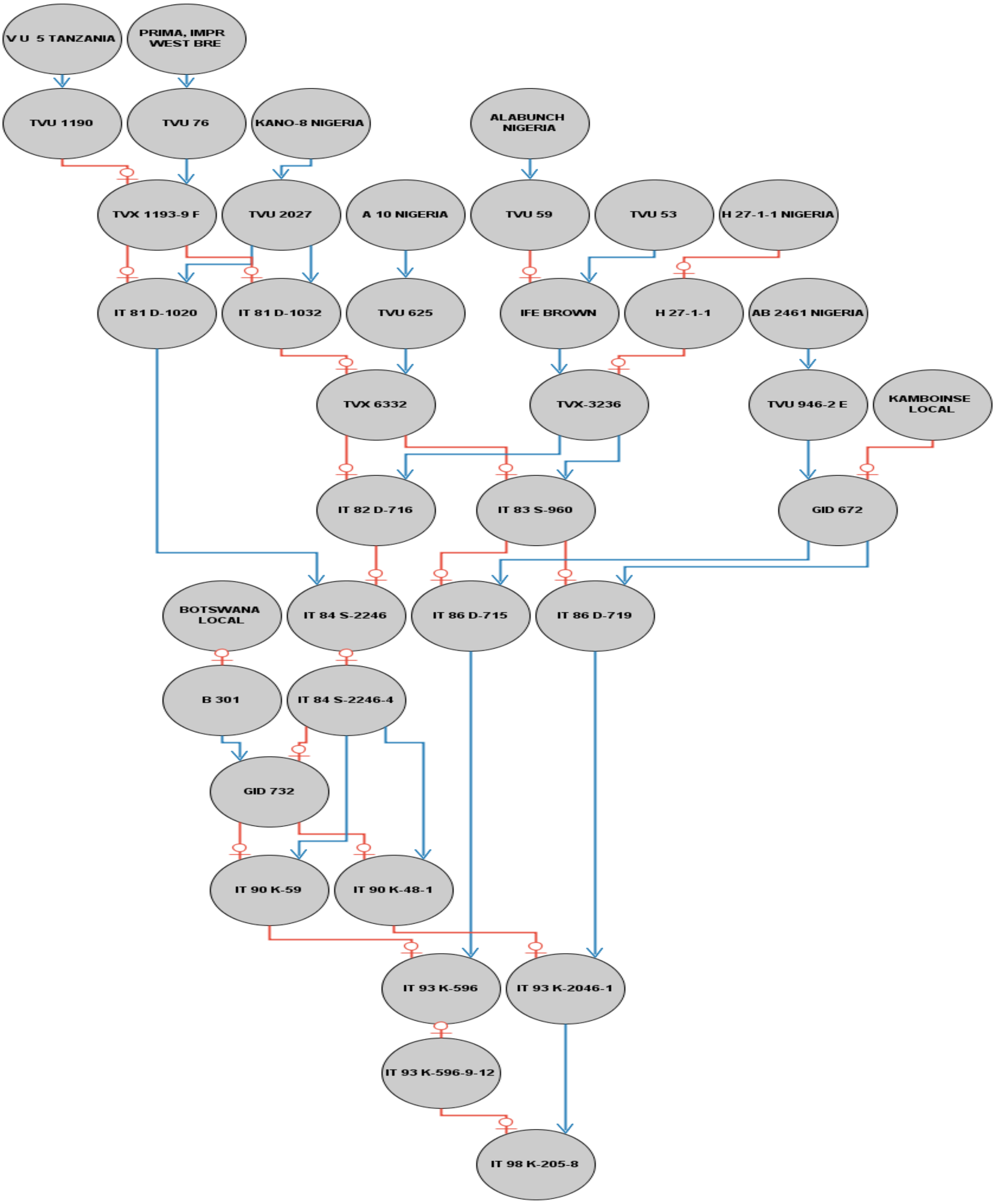
IT 07 K-318-33

IT98K-131-2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TVU 2027
A 10 NIGERIA
TVU 59
TVU 53
H 27-1-1 NIGERIA
IT 81 D-1020
IT 81 D-1032
TVU 625
IFE BROWN
H 27-1-1
AB 2461 NIGERIA
TVX 6332
TVX-3236
TVU 946-2 E
KAMBOINSE LOCAL
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IT 83 S-960
GID 672
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IT 86 D-715
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B 301
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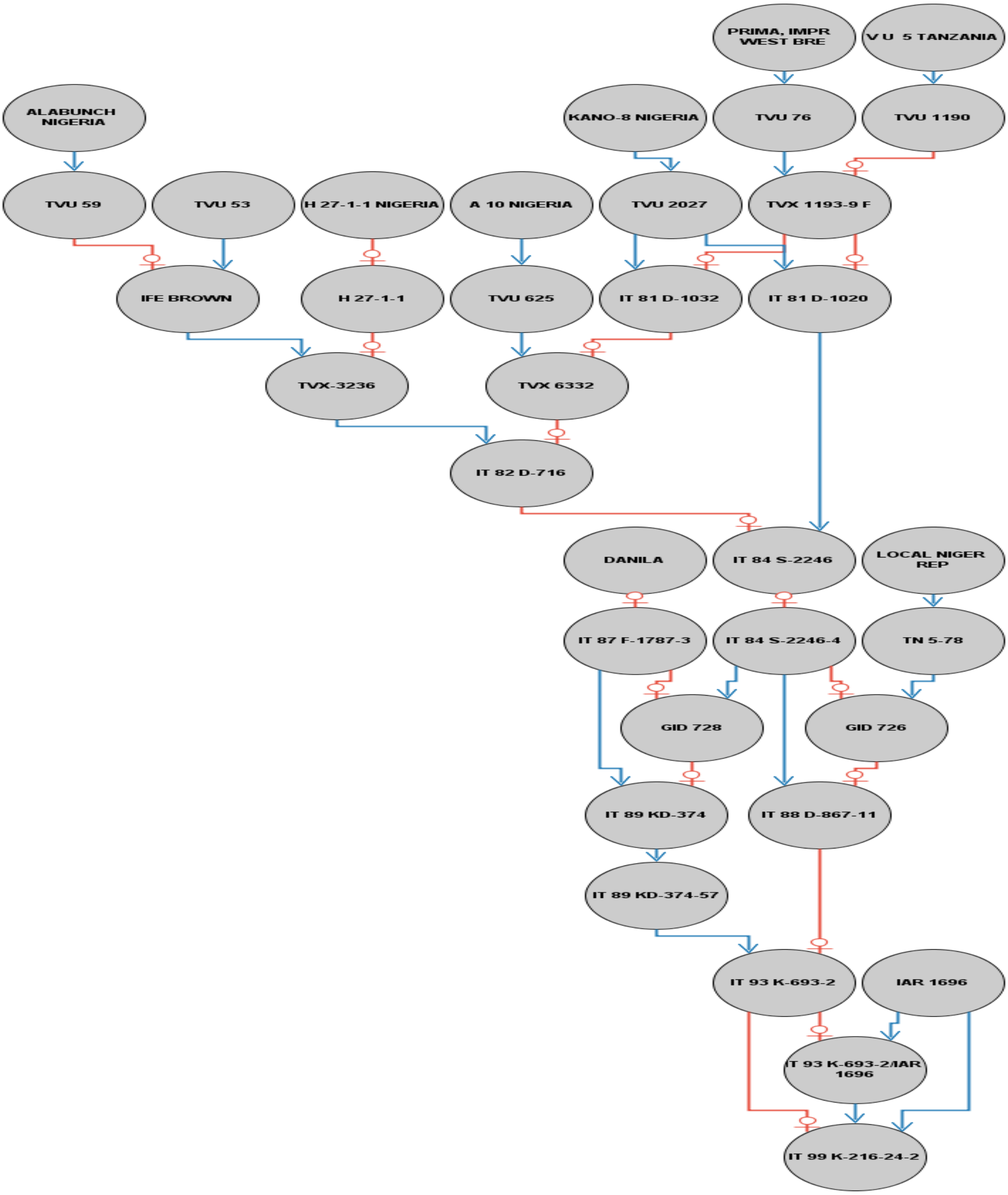
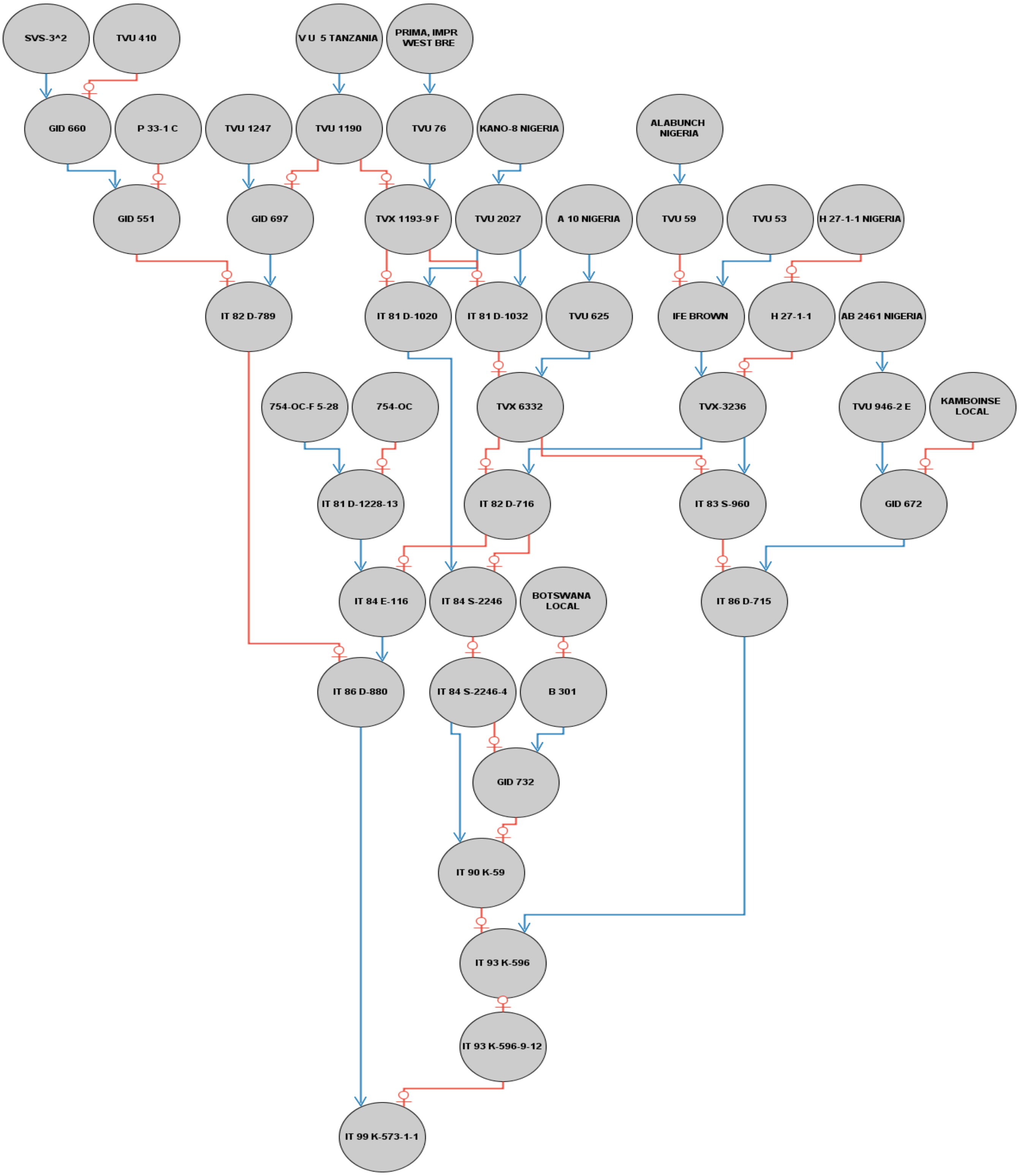
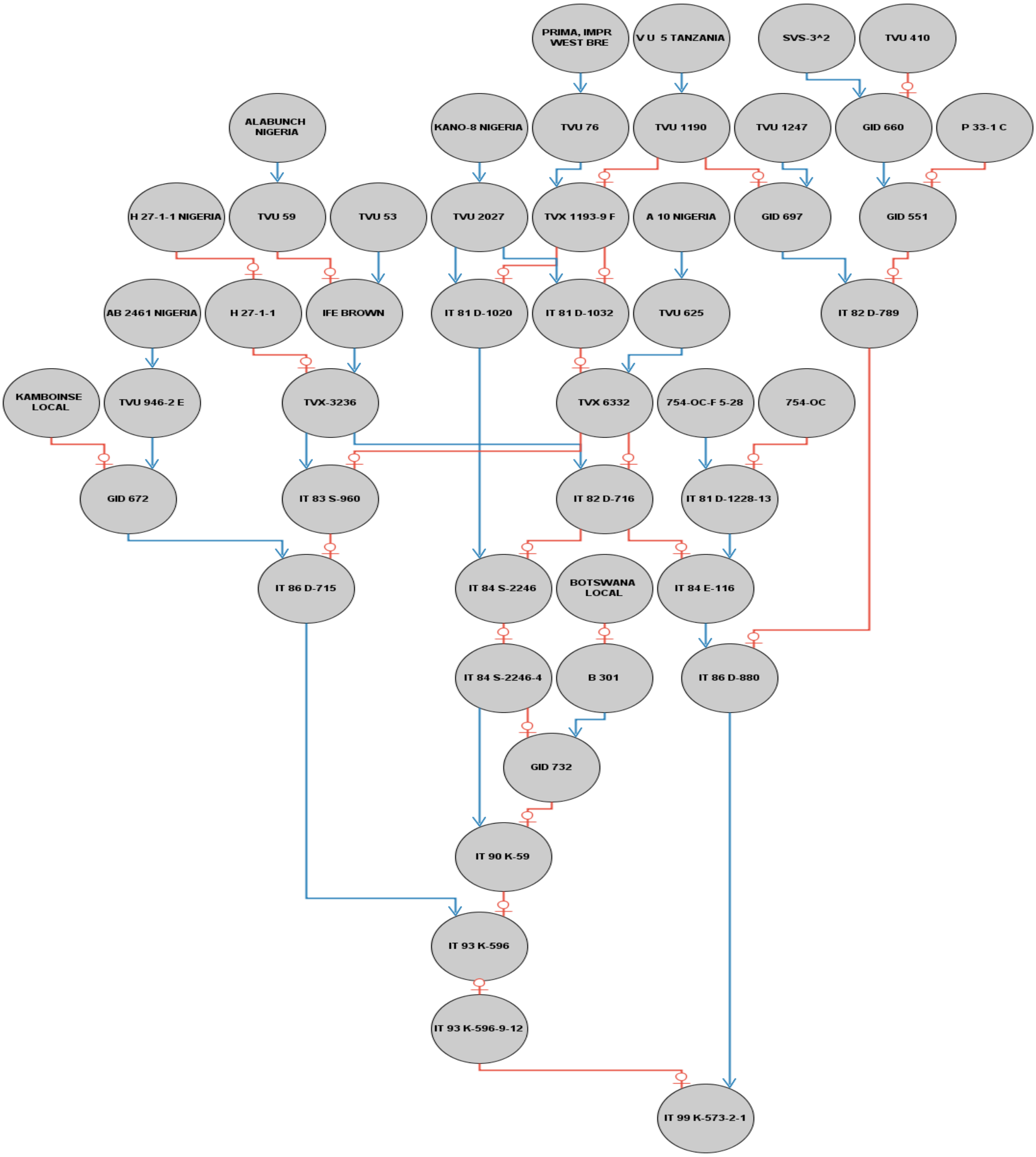
IT98K-205-8



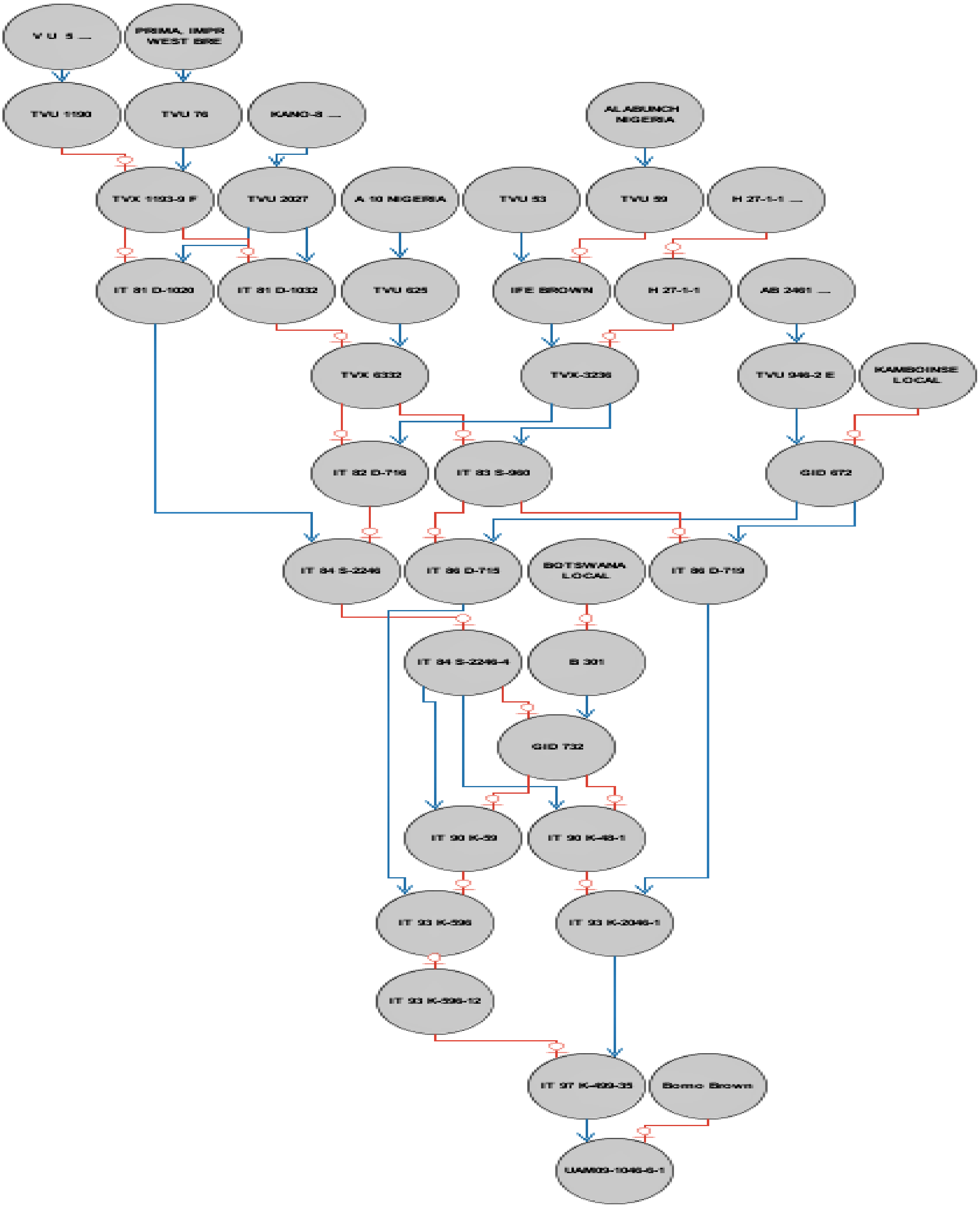
IT99K-216-24-2 (Kwankwaso)



IT99K-573-1-1/Sampea-14



IT99K-573-2-1/Sampea-15



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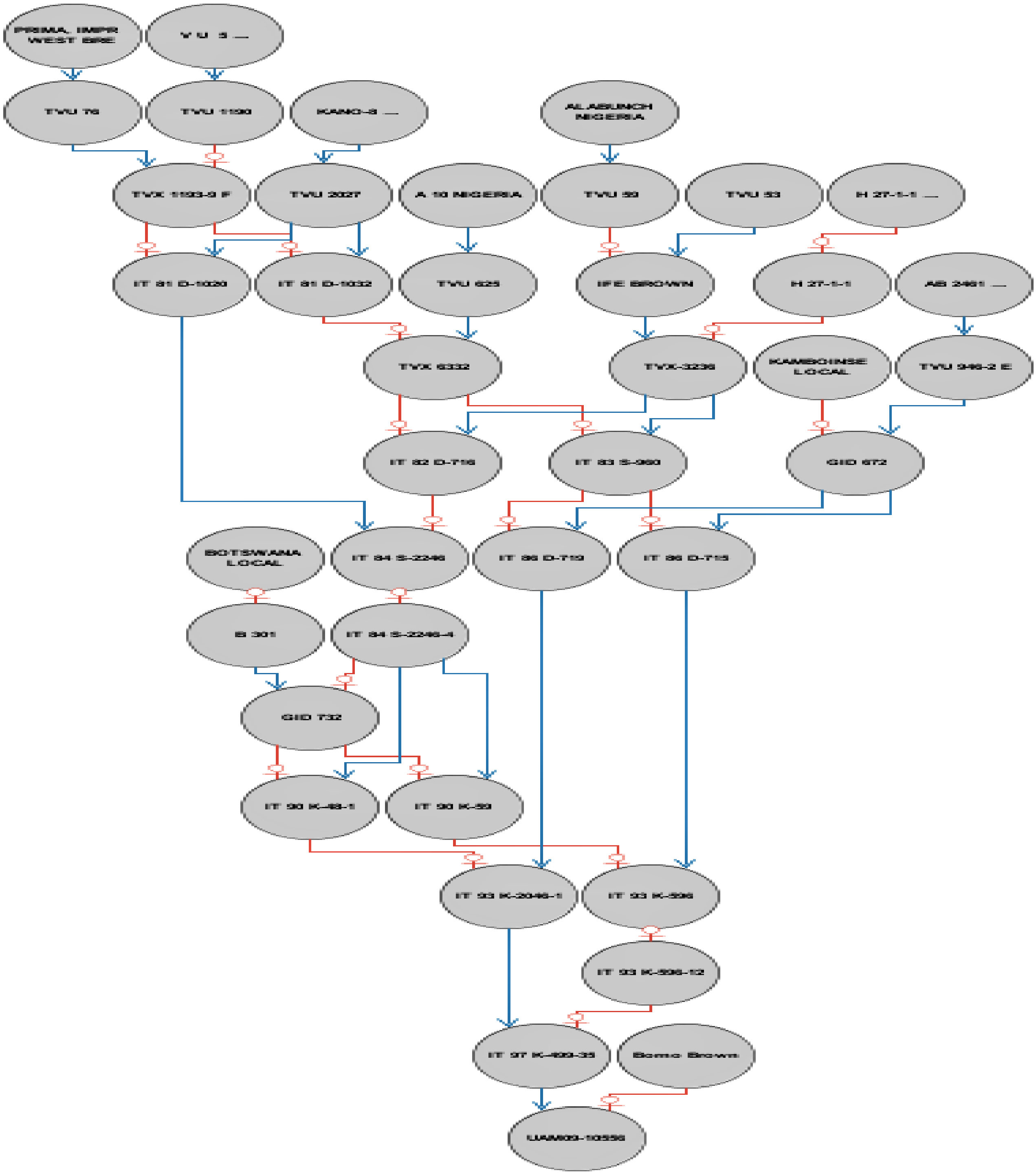

UAM09-10556

Source: Retrieved from the database of the cowpea program of IITA, using Helium