

# In situ and ex situ conservation gap analyses of West African priority crop wild relatives

Nduche, M. U.; Magos brehm, J.; Parra-Quijano, M.; Maxted, N.

DOI:

[10.1007/s10722-022-01507-2](https://doi.org/10.1007/s10722-022-01507-2)

License:

Creative Commons: Attribution (CC BY)

*Document Version*

Publisher's PDF, also known as Version of record

*Citation for published version (Harvard):*

Nduche, MU, Magos brehm, J, Parra-Quijano, M & Maxted, N 2022, 'In situ and ex situ conservation gap analyses of West African priority crop wild relatives', *Genetic Resources and Crop Evolution*.  
<https://doi.org/10.1007/s10722-022-01507-2>

[Link to publication on Research at Birmingham portal](#)

## General rights

Unless a licence is specified above, all rights (including copyright and moral rights) in this document are retained by the authors and/or the copyright holders. The express permission of the copyright holder must be obtained for any use of this material other than for purposes permitted by law.

- Users may freely distribute the URL that is used to identify this publication.
- Users may download and/or print one copy of the publication from the University of Birmingham research portal for the purpose of private study or non-commercial research.
- User may use extracts from the document in line with the concept of 'fair dealing' under the Copyright, Designs and Patents Act 1988 (?)
- Users may not further distribute the material nor use it for the purposes of commercial gain.

Where a licence is displayed above, please note the terms and conditions of the licence govern your use of this document.

When citing, please reference the published version.

## Take down policy

While the University of Birmingham exercises care and attention in making items available there are rare occasions when an item has been uploaded in error or has been deemed to be commercially or otherwise sensitive.

If you believe that this is the case for this document, please contact [UBIRA@lists.bham.ac.uk](mailto:UBIRA@lists.bham.ac.uk) providing details and we will remove access to the work immediately and investigate.



# In situ and ex situ conservation gap analyses of West African priority crop wild relatives

M. U. Nduche · J. Magos Brehm ·  
M. Parra-Quijano · N. Maxted

Received: 11 August 2022 / Accepted: 20 November 2022  
© The Author(s) 2022

**Abstract** Crop wild relatives are genetically related wild taxa of crops with unique resources for crop improvement through the transfer of novel and profitable genes. The in situ and ex situ conservation gap analyses for priority crop wild relatives from West Africa were evaluated using species distribution modelling, ecogeographic diversity, and complementary analyses. A total of 20, 125 unique occurrence records were used for the conservation gap analysis, however, 26 taxa had no occurrence data. 64 taxa (62.7%) occurred in protected areas, 56 taxa (55%) were conserved ex situ, while 76.7% (43) of the accessions are underrepresented with less than 50 accessions conserved ex situ. Areas of highest potential diversity were found in the Woroba and Montangnes districts in Cote d'Ivoire, Nzerekore, Faranah, Kindia, and Boke regions of Guinea, South-South, and North-East zones of Nigeria, and Kono and Koinadugu districts in Sierra Leone. Hotspots were found in Atlantic, Littoral, Mono, Kouffo, Atakora, Donga, and

Colline provinces of Benin, Accra, and Volta regions of Ghana, North–Central Nigeria, and Lacs district of Cote d'Ivoire and Nzerekore region of Guinea. 29 reserve sites for active in situ conservation were identified, 11 occur in protected areas, while 18 are located outside protected areas. The establishment of the reserve sites will complement existing PAs and ensure long-term active in situ and ex situ conservation and sustainable utilization of priority crop wild relative to underpin food security and mitigate climate change in the region.

**Keywords** CAPFITOGEN · Crop wild relatives · Diversity analysis · Ex situ · Genetic conservation · In situ · Species distribution modelling

## Introduction

The flora of West Africa is diverse, heterogeneous, and abundant with numerous plant species. The region harbours over 9000 vascular plants with an estimated 1800 species native to West Africa (Carr et al. 2015). The climate of West Africa is characterized by abundant year-round rainfall in the Gulf of Guinea to a mean annual rainfall of 165 mm in the Agadez of Niger (USGS 2017). Five bioclimate regions have been recognized in West Africa; Saharan, Sahelian, Sudanian, Guinean, and Guinea–Congolian regions (USGS 2017). As such West African plant species are adapted and resilient to the region's

---

**Supplementary Information** The online version contains supplementary material available at <https://doi.org/10.1007/s10722-022-01507-2>.

---

M. U. Nduche (✉) · J. Magos Brehm · N. Maxted  
School of Biosciences, University of Birmingham,  
Edgbaston, Birmingham B15 2TT, UK  
e-mail: nduche.michael@mouau.edu.ng

M. Parra-Quijano  
Facultad de Ciencias Agrarias, Universidad Nacional de  
Colombia, Ciudad Universitaria, Bogota, Colombia

erratic, and diverse ecogeographic conditions and may possess useful genes/traits for crop improvement. West Africa is recognized as a region that played a significant role in crop diversity, origin and domestication, and still retains significant crop landraces and CWR diversity (Castañeda-Álvarez et al. 2016; Vincent et al. 2019; Maxted and Vincent 2021). For instance, archaeological records shows that cowpea (*Vigna unguiculata* (L.) Walp.), originated from Ghana (D'Andrea et al. 2007), kola nut (*Kola nitida* (Vent.) Schott. and Endl.) originated from West to Central Africa, from Sierra Leone to Congo (Lovejoy 1980), African oil palm (*Elaeis guineensis* Jacq.) originated from West and Central Africa, from Nigeria and Cameroon to Congo (Carney 2001; Hall 2008), while *Coffea canephora* Pierre ex A. Froehner (bitter and caffeinated coffee) originated from Central Africa to West Africa (between Congo, Central African Republic, Cameroon, Cote d'Ivoire and Guinea) (Leroy et al. 2014). Similarly, fonio [*Digitaria exilis* (Kippist) Stapf] was domesticated in Senegal (Harlan 1992) and Pearl millet was domesticated between Mali and Mauritania (Burgarella et al. 2018). The zone between Ghana and Nigeria, down to Cameroon have been identified as the source of yam domestication (Scarcelli et al. 2019), fleshy watermelon [*Citrullus lanatus* (Thunb.) Matsum. and Nakai] was domesticated in West Africa from *C. mucospermus* (Fursa) Fursa (Guo et al. 2013, 2019; Chomici et al. 2019). Other crops domesticated in West Africa include Garden egg (*Solanum macrocarpon* L.), Locust bean [*Parkia biglobosa* (Jacq.) G. Don], Pigeon pea [*Cajanus cajan* (L.) Millsp], Cotton (*Gossypium herbaceum* L.), Okra [*Abelmoschus esculenta* (L.) Moench], Piper seed (*Piper guineensis* Schumacher and Thonn.), Tamarind (*Sesamum indicum* L.), and Gourd (*Telfairia occidentalis* Hook. f.) (MacNeish 1992; Vaughan and Geissler 1999; Carney 2001). Seed cotton, domesticated in West Africa is ranked among the first ten crops in feeding in the world, while watermelon is among the five most economically valuable fruits in the world (FAOSTAT 2020). The extent of crop diversity in West Africa through these crops, has helped to expand the agricultural repertoire beyond the reliance on few global food crops (Champion and Fuller 2018; Kay et al. 2019). The importance of West Africa in terms of crop and intra-crop diversity, and origin and domestication of cultivated crops has recently been recognized by the

adding of an additional Vavilov Centre in the west African region (Maxted and Vincent 2021).

Global food production in the next few decades will be determined by several factors including climate change. Climate change will negatively impact agricultural productivity in a global yield decline of an estimated 1.5% per decade (David and Sharon 2012). This trend can at least be partially mitigated by the genetic and agronomic improvement of cultivated crops using trait diversity from crop wild relatives (CWR) (Maxted et al. 2008a, b, c; David and Sharon 2012). CWR are wild plant species relatively closely related to crops, including crop's wild ancestors, that retain indirect use value as gene donors for crop improvement and a high level of genetic diversity having not passed through the genetic bottleneck of domestication. Maxted et al. (2006) defined CWR broadly as all taxa within the same genus as a crop and more precise as wild plant taxon that have indirect use derived from its relatively close genetic relationship to a crop; this relationship is defined in terms of the CWR belonging to gene pools 1 or 2, or taxon groups 1 to 4 of the related crop. CWR contain resilient genes for crop improvement with several domesticated crops in West Africa improved using adaptive genes from CWR (Nduche et al. 2021). Such crops include cassava (David and Sharon 2012; Kawuki et al. 2016), maize (David and Sharon 2012), yam (Lopez-Montes et al. 2012; Saini et al. 2016), cowpea (Andargie et al. 2014; Badiane et al. 2014), millet (Sood et al. 2015), sorghum (Park et al. 2015), rice (Jena 2010; Atwell et al. 2014), barley (Wendler et al. 2015), and for an overview (Nduche et al. 2021).

Despite the important role of CWR in food security in the West African region and the world, their conservation has received little attention. The neglect of CWR is because of lack of appreciation of its potential value in breeding and has resulted in underutilization of its profitable genetic diversity in crop improvement. The adaptive diversity of CWR is a safety net for urgent global food security needs. Globally, in situ conservation of CWR in protected area (PAs) is inadequate, with insufficient number of genetic reserves established (Iriondo et al. 2012). In West Africa, 1938 nationally protected sites exist covering about 9.6% of the region. Another 53 internationally designated protected areas are also found in the region (Mallon et al. 2015). The number of CWR accessions conserved ex situ in genebanks is

relatively low compared to accessions of cultivated crops. Globally, there are an estimated 7 million plant accessions conserved in 1750 genebanks (FAO 2010a; Fu 2017), however, about 29% of CWR lack genebank accessions, while over 24% have less than ten accessions represented in genebanks (Castañeda-Álvarez et al. 2016). Despite this shortfall in ex situ conservation of CWR, a comprehensive collection of CWR is still lacking. The combined use of in situ and ex situ conservation of plant genetic diversity will lessen the erosion of valuable genetic diversity (Maxted et al. 1997a; Zegeye 2017).

Despite the wide agreement that in situ and ex situ techniques should be applied in a complementary manner (CBD 1992), almost 100% of CWR diversity when conserved are conserved using ex situ seed storage alone (Maxted et al. 2016). In situ conservation is only recently being implemented and involves the designation of and management of populations to preserve a particular plant species in its natural abode where its intrinsic features are found (Maxted et al. 1997c). To help ensure more ex situ and in situ conservation coverage more recently, gap analysis has been applied for the planning of CWR conservation (Maxted et al. 2013). It involves identifying CWR diversity that is not well represented in conservation action and prioritizing these ‘gaps’ for more active conservation (Maxted et al. 2008a; Magos Brehm et al. 2017a; Ng’uni et al. 2019; Mponya et al. 2020; Magos Brehm et al. 2022).

The aim of this study was to undertake in situ and ex situ conservation gap analyses of West African priority CWR, through (a) Evaluating the spatial distribution of West African priority CWR (b) Modelling the predicted distribution of the priority CWR (c) Identifying the reserve sites in PAs for active in situ conservation of priority CWR and locations with inadequate occurrence records (d) Identifying taxa that are not present in PAs and those absent or under-represented in genebanks, for further ex situ collection and effective preservation in genebanks within the region.

## Materials and methods

### Collation and verification of occurrence data

The distributional data for the 102 West African priority CWR defined by Nduche et al. (2021) was collated using a standard occurrence data template

(Magos Brehm et al. 2017b). The occurrence data of the West African priority CWR were collated from Global Biodiversity Information Facility (GBIF 2020), Genesys Global Portal on Plant Genetic Resources (Genesys 2020), Royal Botanical Gardens, Kew (<https://www.kew.org/kew-gardens>), and Rain-Bio (Dauby et al. 2016). A total of 54,924 distributional records were collated for the 102 West African priority CWR. Records that lacked coordinates but with collection sites information were georeferenced, using Google maps (<https://www.maps.google.com>). A quality check was done on the distributional data to ensure all records were expressed in decimal degrees. Locational records without decimal degree coordinates were converted to a decimal degree using Canadensys (<https://www.data.canadensys.net/tools/coordinates>). Duplicate records were removed before the analysis, and records that lied abnormally in neighbouring countries were reviewed. Duplicate records are distributional records that are associated with the same record but from different sources or was documented twice from the same source (Magos Brehm et al. 2017a). The West African countries included in this study are Benin, Burkina Faso, Cote D’Ivoire, Gambia, Ghana, Guinea, Guinea-Bissau, Liberia, Mali, Mauritania, Niger, Nigeria, Senegal, Sierra Leone and Togo. The 20,125 records without duplicate records were entered in the occurrence data template required by the CAPFITOGEN tool which makes use of the FAO- Biodiversity’s multi-crop descriptor (FAO-BIOVERSITY 2015). The ‘Testable tool’ of CAPFITOGEN3 was used to verify the occurrence data table to ensure it meets the requirements for other CAPFITOGEN3 tools analyses. GEOQUAL tool of CAPFITOGEN3 was used to assess the quality of coordinates and collection sites of the records (Parra-Quijano et al. 2021).

### Ecogeographical land characterization map

Ecogeographic land characterization (ELC) (Parra-Quijano et al. 2021) was used to evaluate the delineation and depiction of ecogeographic variables and determine appropriate sites for in situ and ex situ conservation of priority CWR (Parra-Quijano et al. 2011; Magos Brehm et al. 2022). Eighteen environmental variables (6 bioclimatic, 6 edaphic, and 6 geophysical) were selected in the selecVar tool of CAPFITOGEN3, to generate the generalist ELC map. A total

of 24 ELC zones were produced, which represents the predicted ecogeographic scenarios of the region (Fig. 5) (Parra-Quijano et al. 2012a; Mponya et al. 2020). To accommodate those taxa with distributional records of < 10, a generalist ELC map was generated using the ELC maps tool of CAPFITOGEN3. This is because these taxa cannot generate species – specific ELC map. Using the kmeanbic method, at a resolution of the ecogeographic layer of 10 × 10 km (approximately 5 arc – minutes), the ELC map was created. The kmeanbic method was used because it identifies an optimal number of groups with discriminant analysis of principal components.

### Species distribution modelling

Based on environmental layers of various components of ecogeographic variables, predicted taxa distribution was identified by the distribution models produced by the individual taxa with more than 10 occurrence records in Maximum Entropy Algorithm (MaxEnt) (Phillips et al. 2006) (Table S6), and by circular buffer (CA<sub>50</sub>) for taxa with less than 10 occurrence records used in the species distribution modelling (SDM), MaxEnt is a common SDM algorithm used to predict taxa distribution (Fourcade et al. 2014). The species distribution data of the taxa for model calibration was classified into a training set (75% of total occurrence data) and test set (25% of total occurrence records) for design evaluation. Raster files of bioclimatic variables were obtained from WorldClim (<https://www.worldclim.org/biocl>im), edaphic variables, from ISRIC – World Soil Information (<https://files.isric.org/soilgrids/>), while geophysical data were downloaded as Digital Elevation Map (DEM) files from the National Aeronautics and Space Administration (NASA) (<https://www.nasa.gov>.) All ecogeographic raster files were clipped to the same extent, resampled to the same cell size (0.41666666667 m), and reprojected to the same grid (WGS—84), in ASCII raster grid format, using Arc-Map 10.4.1 (ESRI 2015). With Random Forest, integrated in the SelectVar of the CAPFITOGEN tools, variables for each ecogeographic component (bioclimatic, edaphic and geophysical) at resolution of 10 × 10 km (approximately 5 arc minutes at Equator) were selected for each priority taxon (Parra-Quijano et al. 2016). Bivariate correlation analysis was also evaluated in SelecVar, to reduce dimensionality, and only

variables with weak correlation ( $p$ -value ≤ 0.33) or not correlated ( $p$ -value = 0) were used to create the distribution model for each taxon (Tables S7 and S8). Maximum training sensitivity plus specificity threshold was applied, as recommended by Liu et al. (2005). The robustness of the models were evaluated using three criteria: (a) Average area under the test receiver operating characteristics curve [(ATAUC) > 0.7] (b) Standard deviation of ATAUC (STAUC) < 0.15 (c) The proportion of potential distribution area with a STAUC > 0.15, being < 10% were stable and used for evaluating taxa predicted distribution (Ramírez-Villegas et al. 2010; Mponya et al. 2020). All three criteria had to be met for a model to be valid. However, for those taxa that failed the above MaxEnt model validation criteria, and for taxa with occurrence records < 10, predicted distribution were identified by a circular buffer technique, using a radius of 50 km (CA<sub>50</sub>) around each observational point as recommended by Hijmans and Spooner (2001). In this case, intersecting sites are not counted more than once.

### In Situ conservation gap analysis

Gap analysis is a method of evaluation of the extent of conservation which helps to hierarchize CWR for preservation by locating gaps in the conservation (Rodrigues et al. 2004; Langhammer et al. 2007; Magos Brehm et al. 2017a). In situ conservation gap analysis involves a comparative study of intrinsic diversity and the element of diversity that is under active conservation action (Maxted et al. 2008b; Magos Brehm et al. 2017a) The method was described by Maxted et al. (2008a, b, c), Scheldeman and van Zonneveld (2010) and Parra-Quijano et al. (2012b), where in situ and ex situ conservation gap analyses were determined at taxon and ecogeographic levels. At the taxon level, the West African PA map was overlapped with the passport data in QGIS. Subsequently, using ‘the join attribute by location’ in the ‘data management tool’ of QGIS, the West African PA maps was intersected to identify records within and outside PA. The in situ conservation gaps were obtained by comparing the number of populations of taxa present in PAs against those not represented in PAs (Mponya et al. 2020). To estimate the extent of representativeness of in situ conservation of priority CWR at the ecogeographic level, the ELC zones from the ELC map tool analysis and the occurrence data

were inputted in the ‘Representa tool’ of CAPFITOGEN3 (Parra-Quijano et al. 2021). The West African PA maps were overlapped with the ELC maps produced in the ‘Representa tool’ to determine the representativeness of the ELC zones in PAs.

Complementarity analysis was done to identify potential sites for in situ conservation of priority CWR. Maxted et al. (1997b) described these sites as genetic reserve for long – term active conservation of plant genetic resources. They are defined designated locations either within PAs or outside PAs as informal sites for CWR conservation (Magos Brehm et al. 2017a). Such locations are aimed at conserving a large number of CWR taxa in the smallest available area (Kati et al. 2004). Using the ‘Reserve selection’ tool in DIVA – GIS 7.5, at resolution of 10×10 km (approximately 5 arc minutes), potential genetic reserve sites were identified according to their priority for the conservation of priority CWR. The PA map for West Africa, obtained from UNEP-WCMC (2019) was overlapped with the complementarity genetic reserve site and taxon richness maps to determine the level of current passive in situ conservation of the priority CWR and identify areas that require further active in situ conservation actions. Passive in situ conservation means that CWR in PAs are not actively monitored and managed to preserve their genetic diversity and protect them from pest, diseases, fragmentation, habitat degradation and natural disaster (Vincent et al. 2019). The maps produced were visualized in DIVA-GIS 7.5 (Hijmans et al. 2012) and QGIS 3.16.8 (QGIS-Development Team 2021).

#### Ex situ conservation gap analysis

Ex situ conservation gap analyses were determined at taxon and ecogeographic levels. At the taxon level, a map of observed ex situ collection was subtracted from the predicted distribution map to obtain the gap in current ex situ conservation and locate the priority site for further ex situ collection. To determine the current germplasm representativeness of the ecogeographic diversity, the resulting ELC map and passport data were inputted in the ‘Representa’ tool of CAPFITOGEN to assess the degree of representativeness of the ELC categories in the ex situ collection (Parra-Quijano et al. 2016). The maps were processed in DIVA-GIS 7.5 (Hijmans et al. 2012), ArcMap 10.7 (ESRI 2011) and QGIS 3.16.8 (QGIS-Development

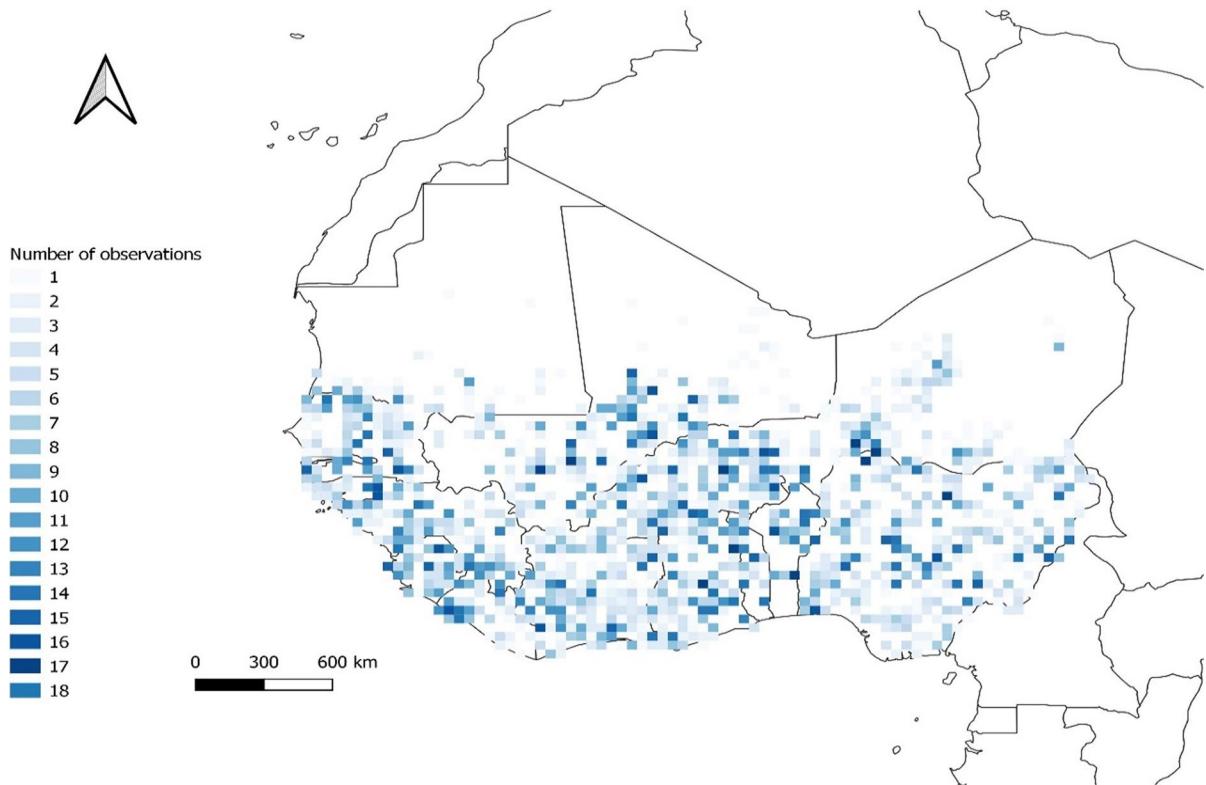
Team 2021) at a resolution of 10×10 km (approximately 5 arc minutes). At the ecogeographic level, the categories of representativeness of the diversity were analysed using the ‘Representa tool’ of CAPFITOGEN3 (Parra-Quijano et al. 2021). Based on the frequencies of the ELC map, the ELC map was categorized into quartiles, using the ELC zones in the ELC map. The four frequency classes were low, mid-low, mid-high, and high. However, zones where occurrence records were not found were categorized as ‘null’. Ex situ conservation gap were determined by estimating the diversity present in ex situ conservation against that conserved in situ (Mponya et al. 2020; Parra-Quijano et al. 2021).

## Results

### In situ gap analysis

A total of 20,125 unique occurrence points were used for the in situ conservation gap analysis, however 26 CWR had no occurrence data. The highest occurrence points were recorded in Benin and Nigeria with 31.9% (6428) and 11.7% (2,358) present points, respectively (Fig. 1 and S1). Hotspots were found in Atlantique, Littoral, Mono, Kouffo, Atakora, Donga and Colline provinces of Benin. These areas correspond to the location of protected areas with the highest number of taxa such as Pendjari (28), Quari Maro (18), La Lama Nord (16), Monts Kouffe and Boucle de la Pendjari (18) (Table S1) There were also hotspots in Accra and Volta regions of Ghana, corresponding to the location of the Volta River reserve site. Location of high diversity were also spotted around Nasarawa, Plateau States of North- Central Nigeria, where Nasarawa Forest Reserve is located and South- Western zone of Nigeria. High species richness is also observed at the Lacs district of Cote d’Ivoire where the Mando forest reserve is situated, Montagnes district of Cote d’Ivoire where Mont Nimba is located and Nzerekore region of Guinea where Mont Nimba, Pic de Fon and Pic de Tibe Classified Forests are located (Fig. 2).

Analysis of the occurrence records showed that 18.5% (3,730) of the total unique present points were recorded in PAs. PAs with the highest number of taxa are Pendjari in Benin (28), Comoe National Park in Cote d’Ivoire (24), Niokolo – Koba National Park in Senegal (21), Quari Maro in Benin (18) and

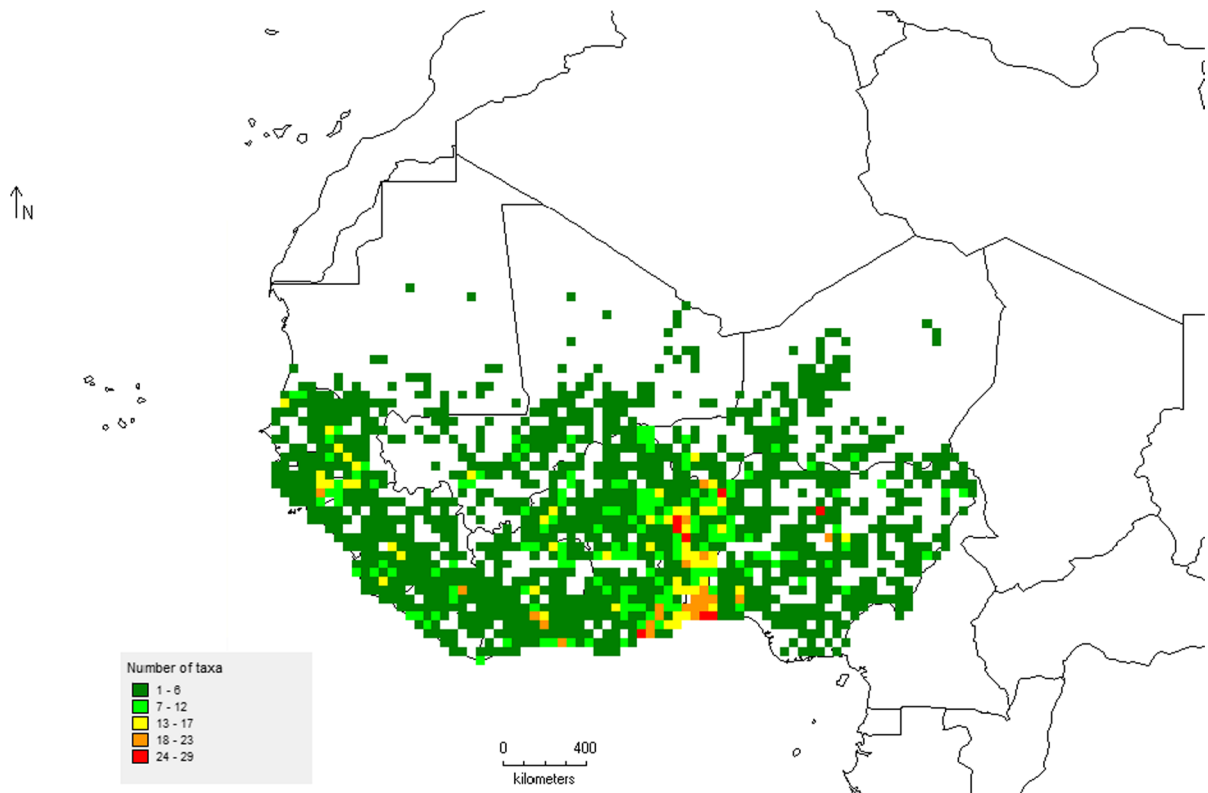


**Fig. 1** Observed records of 102 priority CWR in West Africa

Queme Superieur in Benin (18), while PAs with the highest population of taxa are Sahel (708), Comoe National Park (407), Kouffe (250) and Pemdjari (239) (Table S1). 62.7% (64) of the priority taxa were represented in a PA, 34.3% (35) of the taxa were present in  $\geq 5$  PA, while the remaining 27.4% (28) had less than five populations in different PA (Table S2). However, 38 taxa (37.3%) did not occur in any PA. *Digitaria ciliaris* (Retz) Koeler, *Vigna racemosa* (G. Don) Hutch and *Eragrostis pilosa* (L.) P. Beauv., had the highest number of taxa populations in PA network with 443, 425 and 234 taxa population, respectively. Similarly, *Vigna racemosa* (G. Don) Hutch, *Eleusine indica* (L.) Gaertn. and *Oryza glaberrima* Steud. occurred in more PAs, appearing in 40, 38 and 37 PAs, respectively, while all the rice crop genepool occurred in the PA network. Cowpea (17), yam (13), and potato (9) crop genepools were the highest number of priority taxa that occurred in PA (Table S2). Nigeria, Benin and Cote d' Ivoire had the highest number of PAs where taxa are present, with 46, 25 and 18 PAs, respectively. Conversely, no PA with

taxa was identified in Mauritania (Fig. S2). Similarly, the highest number of taxa population in PAs were found in Benin, Burkina-Faso and Cote d'Ivoire had, with 1351, 768 and 463 populations, respectively. Also, Benin, Nigeria and Guinea had the highest number of CWR in PAs, numbering 207, 87 and 76 taxa respectively (Fig. S3)). 38 taxa (37.3%) did not occur in any PA, similarly none of the Sorghum, fonio and yam wild relatives occurred in PA. Other taxa not represented in PA are *Echinochloa crus-galli* (L.) P. Beauv., *Gossypium herbaceum* var. *acerifolium* (Guill. and Perr.) A. Chev., *Ipomoea ochracea* (Lindl.) Sweet, *Manihot dichotoma* Ule, *Triticum turgidum* L. and *Vigna unguiculata* subsp. *stenophylla* (Harv.) Marechal et al. (Table S2).

Complementarity analysis identified 29 potential genetic reserve sites with grid square size of 0.4 degrees for the conservation of West African priority CWR (Fig. 3). Apart from Burkina-Faso, Liberia, Mauritania and Gambia, genetic reserve sites were identified in all the other West African countries. The highest number of reserve sites were found in Nigeria



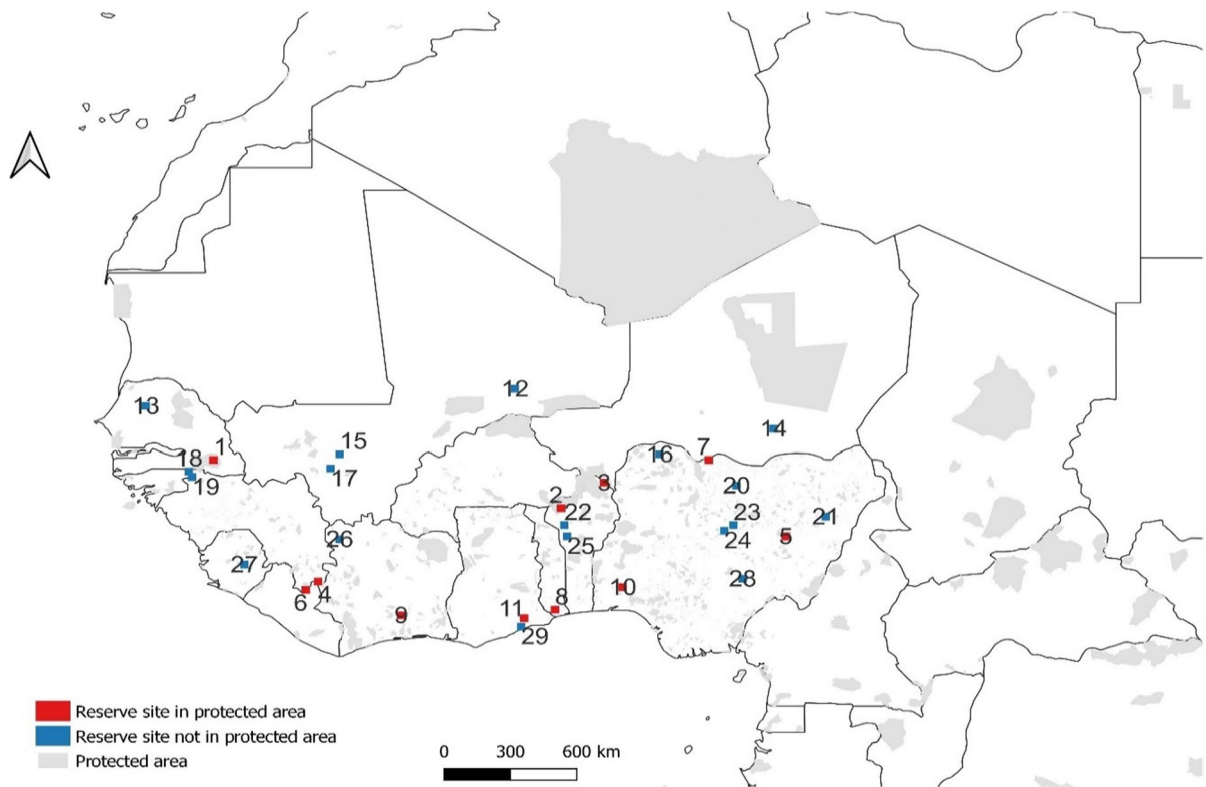
**Fig. 2** Observed taxa richness map of 102 priority West African CWR

with 9, while Benin and Guinea have 4 each (Fig. 3). Eleven reserve sites are located in PA (Table 1), with 9 of the sites conserving 37% (38) of the CWR, however priority CWR were absent in Eleiyele and Volta River (Table S1 and S3). A total of 458 records were present in 9 of the reserve sites with taxa. 36.3% (37 taxa) of the priority CWR were found in the reserve sites (Table S3). *Vigna racemosa* (G. Don) Hutch. and Dalz., *Oryza glaberrima* Steud., *Vigna gracilis* (Guill. and Perr.) Hoof. f. and *O. barthi* A. Chev. had the highest number of taxa population; 56, 51, 46 and 35 respectively in the genetic reserve sites (Table S2 and Table S5). Cowpea (10), yam (7), sweet potato (7), and rice (4), are the crop genepools with the highest number of CWR present in the reserve sites (Table S). Conversely, cowpea (13), yam (8), sweet potato (6) and cassava (5) are the crop genepools with the highest number of taxa not represented in reserve sites. *V. racemosa* (G. Don) Hutch and Dalz., *O. barthi* A. Chev., *Ipomoea aquatica* Forssk., *O. longistiminata* A. Chev. and Roehr and *Eleusine indica*

(L.) Gaertn were found in more genetic reserve sites than other taxa and were found in 4 reserve sites each (Table S3 and S5).

In situ conservation gap analysis of the 102 priority CWR showed that the areas of predicted distribution is present in all the West African countries (Fig. 4). The areas of highest potential diversity was found at Woroba and Montagnes districts of Cote d'Ivoire where some protected areas such as Mont Tia, Mont Sangbe, Pic de Fon, Pic de Tibe, Mt Yonon and Mont Nimba reserve site are located (Fig. 4). Also of high predicted CWR taxon richness are Nzerekore, Faranah, Kindia and Boke regions of Guinea where the Mont Nimba and Diecke reserve sites are situated. Other areas of high predicted taxon richness are in the South – South zone of Nigeria around Cross River National Park, North Eastern Nigeria, Kono and Koinadugu districts in Sierra Leone (Fig. 4), where these areas are predicted to harbour 51 to 63 CWR. However, areas from Abidjan in Cote d'Ivoire, Ghana, Togo, Benin to South- West Nigeria had low areas





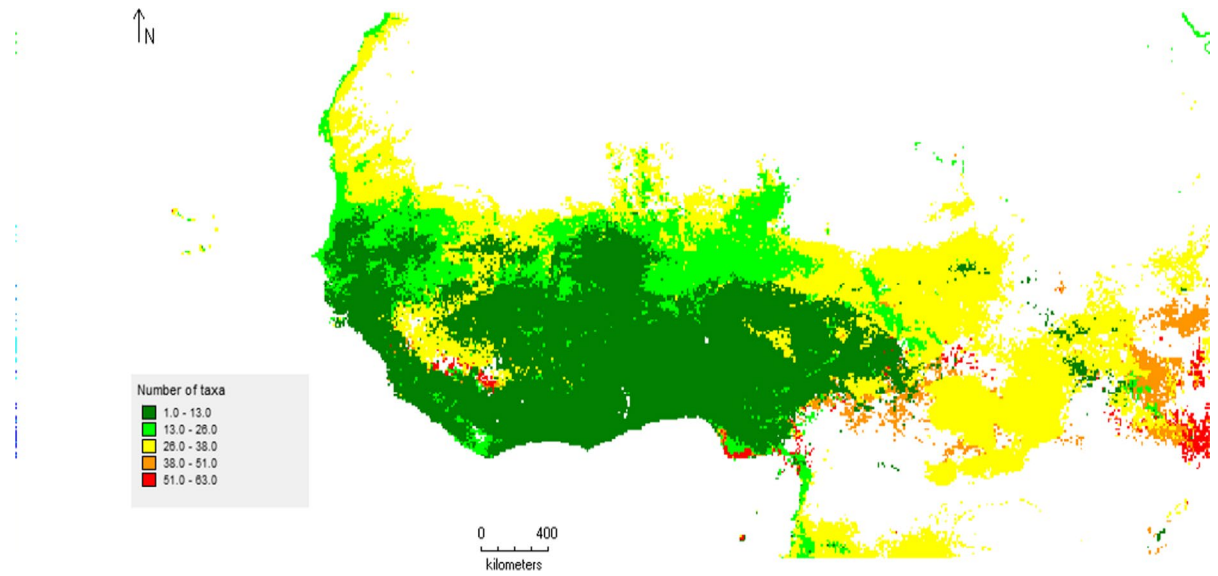
**Fig. 3** Complementary analysis showing areas of proposed genetic reserve sites of West African priority CWR. Numbers are in order of conservation priority for the reserve sites. Grid cell size is 0.4 degrees, Geographic coordinate system is WCS 1984

of predicted distribution (Fig. 4). The ecogeographic diversity of 17 ELC zones are present in 152 PAs,

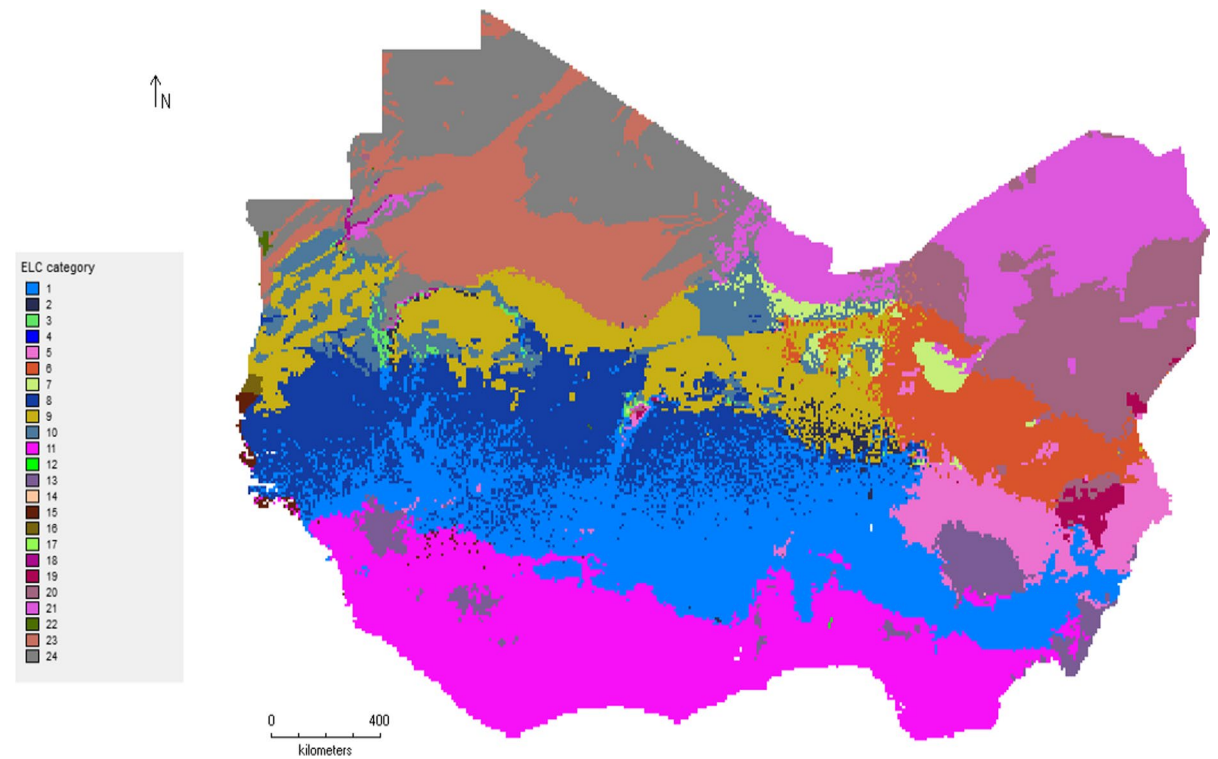
while ELC zones 11 and 2 had the highest diversity in PAs (Table S4 and Figs. 5, 6).

**Table 1** Reserve sites for in situ conservation of West African CWR and protected areas where they are located

Reserve site	Protected area	Total occurrence record	Number of CWR	ELC zones	Total area (Km <sup>2</sup> )	Total area (ha)	Country
1	Niokolo – Koba National Park	252	21	1,7	9130	913,000	Senegal
2	Boucle de la Pendjari	65	16	1	2755	275,500	Benin
3	Dosso	48	13	1,7	5,440.87	5,440,870	Niger
4	Mount Nimba	63	11	10,12	175.40	17,540	Guinea
5	Yankari	24	9	1,4	2254	225,400	Nigeria
6	Diecke	2	2	–	640	64,000	Guinea
7	Nasarawa	1	1	6	15,076,526	150,765,260	Nigeria
8	Eto	2	1	10	116.02	14,763	Togo
9	Goudi	1	1	10	96	9600	Cote d'Ivoire
10	Eleiyele	–	–	–	5.261	526.092	Nigeria
11	Volta River	–	–	–	–	–	Ghana

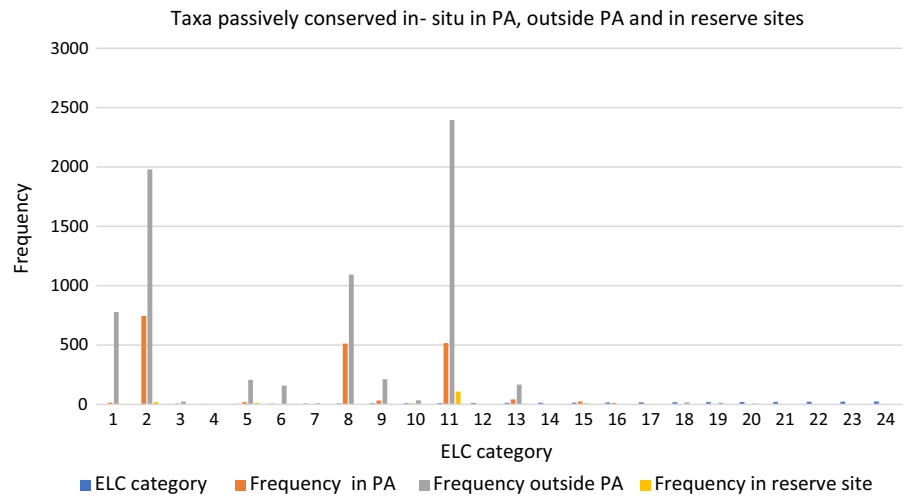


**Fig. 4** Taxa richness based on predicted distribution of 102 priority CWR in West Africa



**Fig. 5** Ecogeographic Land Characterization (ELC) generalist map of West Africa based on ecogeographic variables using the method described by Parra-Quijano et al. (2021)

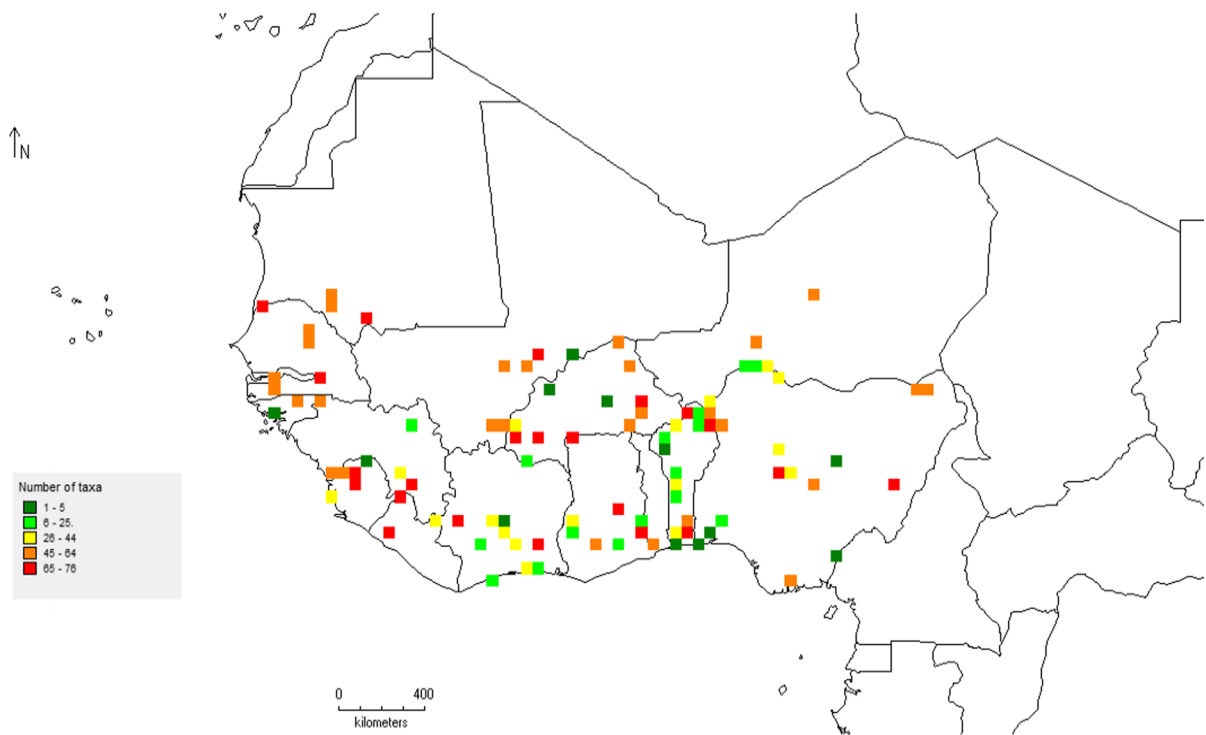
**Fig. 6** In situ conservation gap of priority CWR based on taxa passively conserved in, outside PA and reserve sites across the 24 ELC categories



### Ex situ gap analysis

The SDM of 55 taxa met the validation whereas for the remaining 8 CWR, a  $CA_{50}$  buffer area created around each occurrence point (Table S6). The number of ecogeographic variables for the SDM varied from

15 in *Vigna filicaulis* Hepper and *V. desmodiodes* Wilczek to 43 in *Ipomoea aquatica* Forssk (Table S7 and Table S8). A total of 5720 (28.4%) accessions from 56 (55%) priority CWR are represented ex situ. 13 taxa had occurrence data but did not pass the validation criteria for predicted distribution map



**Fig. 7** Priority area for further ex situ collection of 102 West African priority CWR based on species distribution models

(Table S6). 55% (56) priority CWR had at least one accession represented in genebank, of these, 23% (13) of the taxa had at least 50 accessions conserved ex situ, while 76.7% (43) of the accessions are under-represented with less than 50 accessions conserved in genebanks. Nigeria had the highest number of accessions in genebanks, with 23.8% (1366) accessions, while Mauritania had the least 0.2% (13) (Fig. S1). Benin had the highest number of occurrence data (6428), while Mauritania had the least (150) (Fig. 1 and Fig. S1). *Oryza glaberrima* Steud., *O. barthii* A. Chev. and *O. longistaminata* A. Chev. and Roehr. had the highest number of accessions conserved in genebanks, with 2670, 610 and 562 accessions respectively (Table S2). All the *Hordeum* and *Phaseolus* CWR species had no occurrence data. Of the taxa that have occurrence data, 20 were not represented in genebanks, while *Cola nitida* (Vent.) Schott. and Endl. (3), *D. rotundata* Poir (3), *I. batatas* (L.) Lam. (3), *Sorghum bicolor* (L.) Moench (3) and *Vigna unguiculata* (Linn.) Walp. (3) represent the crop gene-pools with the highest number that were not present in both genebanks and PA (Table S9). Similarly, of the 13 taxa that did not occur in PA, 7 were not also represented in genebanks. However, all the taxa with  $\geq 50$  accessions in genebanks also occurred in  $\geq 5$  PAs (Table S2 and Table S3).

The areas of further collection are found in all the West African countries (Fig. 7), while 87.27% (89) priority CWR needs further collecting (Table S2). Areas of further collection are Assaba and Guidimaka provinces of Mauritania; Saint – Louis and Tambounda regions in Senegal. Nzerekore region of Guinea; Koinadugu, Bombali and Tonkolili districts of Sierra Leone. Loffa, Bomi, Montserrado and Grand Cape Mount counties of Liberia. Montagnes, Lacs and Lagunes districts of Cote d' Ivoire; Mopti region of Mali; Upper West, Bono East, Eastern, Volta and Ashanti regions of Ghana. Other areas are Haut – Bassins, Cascades, Est and Centre – Est regions of Burkina Faso; Plateau, Queme, Atlantique and Alibori provinces of Benin; North – East and North – Central zones of Nigeria (Fig. 7) Ecogeographic diversity of 16 ELC zones are conserved in genebanks (Table S9), while the CWR diversity of 8 zones are not represented. ELC zones 2,8 and 11 had the highest population which corresponds to the ELC map category. 50% of the ELC zones had  $\geq 25\%$  of

their accessions represented in genebanks (Table S4), while ELC zones 2 and 11 had the highest collection.

## Discussion

West Africa is rich with taxa diversity, endemism and biodiversity heritage, while CWR diversity and flora distribution of the region have been reported in various studies (Huchinson and Dalziel 1958; Oates et al. 2004; Bergl et al. 2007; Idohou et al. 2013; Hounsou-Dindin et al. 2022). However, as a purpose of this, further study is needed to determine the gaps in in situ and ex situ conservation action in the region, as this will complement and consolidate the national efforts of the individual countries. According to recent CWR ecogeographic diversity analysis, West Africa has been identified as a region of global importance with high CWR diversity for food security (Castañeda-Álvarez et al. 2016; Vincent et al. 2019). The highest CWR diversity identified in the provinces of Benin, is because of the recent Flora of Benin (Akoègninou et al. 2006), and the high number of occurrence records found in Benin, relative to other countries in the region (Fig. 1 and S1). High CWR diversity was also identified at Accra and Volta regions of Ghana, North – Central and South- Western zone of Nigeria. Other areas include Lacs district of Cote d' Ivoire and Nzerekore region of Guinea (Fig. 2). These areas correspond to some areas of predicted distribution such as Nzerekore region of Guinea where Mont Nimba, Diecke, Pic de Fon, Pic de Tibe Classified Forests are located (Fig. 4). Similarly, these areas of species richness are in congruence with the Guinean forest, categorized as one of the 36 biodiversity hotspots in the world (Maxted and Vincent 2021; Vincent et al. 2022) and the highest conservation value in Africa (Luiselli et al. 2019). The Guinean Forest covers an area of 621,705 km<sup>2</sup>, extending from Guinea, Sierra Leone, Liberia, Cote d' Ivoire, Ghana, Togo, Benin to Nigeria. However, Guinean Forest is one of the most exploited biodiversity hotspots in the world, though 15% of the original forest is still unexploited (Conservation International 2007).

The network of PAs in West Africa conserves a substantial number of the priority CWR with 61% (63) of the taxa found in PAs (Table S2). However, further field survey should be carried out to ascertain

the presence of the priority CWR in those PAs where they were identified. For the 28 taxa (27.4%) that were found in less than five PAs, field survey should be done in areas of predicted distribution to determine their locations and to identify more taxa populations in network of PAs, to ensure they meet or surpass the required minimum number for active in situ conservation. Brown and Briggs (1991) and Dulloo et al. (2008) suggested the presence of five population of a taxa in different PAs as the minimum for in situ conservation in PA. Also, effective management and monitoring should be put in place to ensure active in situ conservation of the priority CWR in their respective PAs (Maxted et al. 2008b). Relevant institutions, stakeholders, non – governmental organizations (NGOs), and protected area managers should synergistically, ensure the maintenance of the PAs for optimal and active conservation action. Pendjari National Park in Benin with an area of 2765 km<sup>2</sup> and Comoe National Park in Cote d' Ivoire occupying an area of 11,500km<sup>2</sup> are the PAs with the highest number of CWR (Table S1). The presence of more CWR in Pendjari National Park may have resulted from the fact that the site was better surveyed than other PAs, as shown in the number of occurrence data recorded in Benin as compared to other countries (Fig. 1 and S1). UNESCO (2019) reported that 620 plant species are found in Comoe National Park, which agrees with the high number of CWR present in Comoe National Park. The site contains great diversity of plants, endemic species and diverse ecological habitats ranging from savannah, forest to grasslands. (UNESCO 2019). Large PAs such as Sahel (30,693 km<sup>2</sup>), Comoe National Park (11,500 km<sup>2</sup>), W National Park Benin (10,000 km<sup>2</sup>), Niokolo – Koba National Park (9130 km<sup>2</sup>), were design to conserve diverse ecogeographical populations, which CWR is a subset. However, they contain only small of CWR population per unit area. The designation and development of the 18 reserve site found outside PAs, as other effective based conservation measures (OECM) will augment the preservation of CWR population outside PA network (Iriondo et al. 2021).

Identifying priority sites for the in situ conservation of CWR, based on species richness may be misleading since the approach relays only on taxa richness sites neglecting those taxa that require urgent protection (Brooks et al. 2006). However, to overcome this challenge, complementarity analysis

through reserve site selection is used (Fielder et al. 2015; Contreras-Toledo et al. 2019; Mponya et al. 2020). Complementarity analysis have been used to identity priority site in regions such as Southern African Development Commission (SADC) (Magos Brehm et al. 2022) and Middle East (Zair et al. 2021). Twenty-nine reserve sites were identified in this study, with 11 in PA and 18 spotted outside PAs. The 11 reserve sites located in PAs will require minimal cost to establish and manage, being in existing PAs. It will augment and complement the protective function offered by the existing PAs and provide benefits to the local communities (Maxted et al. 2008b; Maxted and Kell 2009). The remaining 18 reserve sites not located in PAs also present an opportunity for those countries with low number of PAs where taxa were found such as Guinea – Bissau (3), Mali (4), Niger (5), Sierra Leone (7) and Senegal (9) (Fig. 3). The outcome of the complementary analysis showed that the location of some reserve sites corresponds with some CWR hotspots in West Africa. These areas are Atakora, Alibori, Donga and Bongou provinces in Benin; Accra region of Ghana; North – Central and South – West zones of Nigeria and Lacs district of Cote d' Ivoire (Figs. 2 and 3).

The areas of predicted distribution were highest in Woroba and Montagnes districts of Cote d'Ivoire where the reserve site; Mont Nimba is located and some protected areas such as Mont Tia, Mont Sangbe, Pic de Fon, Pic de Tibe, Mt Yonon are found. The area of high predicted distribution also extended to the Nzerekore, Faranah, Kindia, and Boko regions of Guinea, where the reserve site; Mont Nimba and Diecke Classified Forest are located (Fig. 4). Mont Nimba is strategic because it is located between Guinea and Cote d' Ivoire. It occupies a total land area of 175.4 km<sup>2</sup>, with 125.4 km<sup>2</sup> in Guinea and 50 km<sup>2</sup> in Cote d' Ivoire. UNESCO (2019) reported diverse flora and endemic plant species in the site, including epiphytes and over 2000 vascular plant species. Similarly, Diecke Classified Forest is one of the largest undisturbed areas of the Guinee For-estiere with diverse plant species including several threatened tree species. The presence of *Cola attien-sis* Aubrev. Pellegr. in the site (Table S3) was also reported by (Couch and Haba 2021). The area of predicted distribution appears to be larger than the area of observed distribution, which shows that the region is under surveyed. Efforts should be made for ex situ

collection of taxa in predicted areas outside PAs, as they may be under threat by urbanization, change in land use and habitat destruction (Mponya et al. 2020).

For active in situ CWR conservation, effective ex situ conservation is needed to complement it. Ex situ conservation methods include seed bank, genebank, DNA bank, cryopreservation, botanical garden and *in-vitro* conservation (Maxted et al. 1997c; Maxted 2013). 55% (56) of the priority taxa were represented in genebanks, however more accessions need to be collected for ex situ conservation. Further collection actions should be undertaken for the 20 taxa with occurrence records but not present in genebanks, the 26 taxa without occurrence data and the 44 taxa underrepresented in genebanks to reflect the recommendation by (Brown and Marshall 1995) and (Guerrant et al. 2004) of 50 taxa population for effective representation in genebank. Additionally, taxa already present in PAs should be conserved ex situ in genebanks as a back – up to the in situ conservation to protect them in the event of natural disaster, war or fire outbreak (Ford-Lloyd and Maxted 1993). Genebank accessions should be duplicated regionally and internationally to ensure effective and long term ex situ conservation (FAO 2014; Magos Brehm et al. 2022).

The crop gene pools with the highest number of taxa not represented in genebanks are yam (3), potato (3), sorghum (3), cowpea (3) and cola (3). Among the taxa that are not present in genebanks are *Dioscorea abyssinica* Hochst. ex. Kunth, used to improve yam for resistance against yam mosaic virus and anthranose (Lopez-Montes et al. 2012), *Manihot carthagenesis* (Jacq.) Mull. Arg, *M. dichotoma* Ule, *M. esculenta* subsp. *peruviana* Crantz and *M. esculenta* subsp. *flabellifolia* Crantz, used to improve for resistance against cassava brown streak disease (Kawuki et al. 2016). *Echinichloa frumentacea* Link and Eleusine Africana Kenn – O’Byne are used to breed Barnyard millet (Sood et al. 2015) and finger millet (Dida and Devos 2006), respectively for high yield. Other taxa that are not present in genebanks include *Phaseolus vulgaris* var. *aborigineus* (Burkart) Baude, used for the improvement of common bean against bruchid (Osborn et al. 2003), white mould (Mkwaila et al. 2011), web and bacterial blight (Beaver et al. 2012) and for high yield (Wright and Kelly 2011). *Sorghum purpureosericeum* (Hochst ex. A. Rich) Schweinf and Asch. has confirmed used in the improvement

of sorghum for resistance against sorghum shoot fly (Nwanze et al. 1990), while *Sorghum bicolor* subsp. *verticiliformum* (L.) Moench is used in breeding sorghum for resistance against stem and leaf rust (Fetch et al. 2009; Park et al. 2015), increase in seed size and weight (Pillen et al. 2004). *Hordeum bulbosum* L. is used in breeding barley for resistance against barley mild mosaic virus (Ruge et al. 2003; Wendler et al. 2015), barley yellow virus (Wendler et al. 2015), powdery mildew (Pickering and Johnston 2005; Johnston et al. 2009), stem and leaf rust (Fetch et al. 2009; Johnston et al. 2013; Park et al. 2015) and leaf scald (Pickering et al. 2006). Ex situ conservation will be a safety net for some CWR that have their adaptive scenario outside PA. For instance, some herbs and shrubs thrive on lawns, waste lands, swamps and agricultural lands (Maxted and Kell 2009).

A major objective of in situ conservation is to confirm and preserve diverse CWR genes in a defined location for optimal used in crop improvement to ensure food and nutrient security. Ecogeographical diversity can work as proxy for genetic diversity (Korona 1996; Parra-Quijano et al. 2012a). The frequency of ecogeographical diversity outside PAs is higher, compared to that in PA. Therefore, ex situ collection of priority CWR outside PAs will capture taxa in ELC zones not represented or underrepresented in network of PA. The ELC map shows all resilient environmental conditions present within the geographical location of the target taxa population. ELC zone 2 had more accessions in genebanks and the highest frequency of occurrence in PA compared to other ELC categories (Table S4 and Fig. 6). However, taxa found in rare ELC zones present unique genes (Contreras-Toledo et al. 2019; Parra-Quijano et al. 2021) and should be prioritized in ex situ collection and conservation for use in crop improvement of their related crops. Complementarity analysis showed that 11 ELC categories were present in the reserve sites within PA, compared to 15 ELC categories represented in all PAs. This shows a high degree of complementarity in capturing the ecogeographical categories diversity of the priority CWR. On the average, the diversity of ELC categories per taxa was higher (26.3%) compared to that for all PA network (23.4%) (Table S4). For ELC zones 12,14,16,17,19,22,23,24 where taxa were not represented in genebanks and ELC zones 4,7,20,21 with low genebank representation, based of frequency of occurrence (Table S9), further collection action should be carried out to ensure

their representation. Similarly, ex situ collection should be done to represent all the ELC zones and ensure the preservation of novel and vital genes (Rubio-Teso et al. 2013; Parra-Quijano et al. 2021). The presence of these taxa in different ELC zones helps to identify those that thrive in adverse and marginal environments, as they may possess profitable genes for adapting their related crops to erratic climatic conditions (Garcia et al. 2017).

### Recommendations

Based on the outcome of this study, the following recommendations for the in situ and ex situ conservation of West African priority CWR are proposed:

- (1) Improved the efficacy of reserve sites in PAs for active in situ conservation through effective management and monitoring of the target CWR to ensure long term preservation. Small PAs should be expanded to ensure full and optimal conservation area and to include CWR diversity that occurs next to them. The eleven reserve sites in PAs should be prioritized for the in situ conservation of West African priority CWR. Ascertain the suitability of the location of the 18 reserve sites that are not in PA, including the topography, accessibility and demography of the taxa in the area. Then initiate the establishment of reserve sites for the in situ conservation of priority CWR not conserved in PAs, to augment the functions of existing PAs. New PAs are crucial for countries with limited PAs such as Guinea – Bissau, Mali, Niger, Sierra Leone and Senegal (Fig S2 and Table S1). The identification of the 29 reserve sites is significant and a footprint for the in situ conservation of the priority CWR.
- (2) Conduct field survey for the 38 taxa that did not occur in PA to ensure they are present in at least five PAs to meet the minimum number of representations in PAs for active in situ conservation (Dulloo et al. 2008). Priority PAs for further field survey are those where CWR are predicted to be present such as Mont Tia, Mont Sangbe, Pic de Fon, Pic de Tibe, Mt Yonon, Cross River National Park and reserve sites such as Mont Nimba and Diecke. Attention should be given to CWR diversity and general biodiversity present in reserve sites located in PAs to ensure the conservation of all available plant genetic diversity.
- (3) Maintain international genebanks in West Africa such as the International Institute of Tropical Agriculture (IITA) (IITA 2022), Nigeria which conserve accessions of African food crops, AfricaRice M'be Cote d' Ivoire with over 22, 000 accessions (CGIAR 2022) and ICRISAT, Niger (ICRISAT 2022). Establish national genebank in the areas with high ex situ collection and predicted distribution for the ex situ conservation of priority CWR, while national genebanks like National Centre for Genetic Resources and Biotechnology (NACGRAB) Ibadan, Nigeria with 13, 839 accessions (Crop Trust 2022), National Agricultural Research Center, Cote d' Ivoire holding 8,000 accessions of coffee (World Coffee Research 2021) and Ghana National Genebank should be upgraded to hold more accessions. Also, genebank accessions should be duplicated in different facilities, while accessions present only in genebanks outside West Africa should be retrieved from internationally genebanks (Table S10) and conserved in area where the taxa have their intrinsic features and taxon richness.
- (4) Search for occurrence data for the 26 taxa without occurrence records and for those with less than 10 records in their countries of endemism. Conduct field survey for countries with inadequate number of occurrence data such as Mauritania, Gambia, Guinea – Bissau, Liberia, Togo and Sierra Leone (Fig. S1), to identify the location of more priority CWR and taxa population both within and outside PAs for ex situ collection and active in situ conservation. SDM and buffer CA<sub>50</sub> can serve as a guide in locating the taxa in the areas of predicted distribution.
- (5) Prioritize the ex situ collection of the 43 taxa with less than 50 accessions in genebanks, using the SDM and CA<sub>50</sub> as a guide to ensure their effective representation ex situ. Also, of priority are the 13 taxa with occurrence data but did not pass the validation criteria. Diversity in ex situ conservation should be increased to include seed banks, cryopreservation, *in – vitro* storage for recalcitrant taxa, and botanical garden. Government agencies, institutions, local communities, national and international genebanks should be involved in the collection mission.

- (6) Conduct field survey to identify priority CWR in the ELC zones with low frequency to ensure that a full range of ELC zones are captured so as to preserve unique and novel genes for use in crop improvement (Parra-Quijano et al. 2021).
- (7) Make crosses between plants from collected seeds and their related crops, as well as between CWR found in PA and their related crops based on gene pool levels (Table S11). Advanced methods such as embryo rescue, *in-vitro* gene transfer can be used for CWR that shows difficulty with conventional methods. This may help in resolving the challenge of hunger and food insecurity in the densely populated West African region.
- (8) Periodic revision, review and upgrade of the outcome of this study and the recommendations in the event of change in conservation priorities as a result of availability of more occurrence records and a more precise algorithm for ecogeographic modelling and occurrence data analysis.

## Conclusion

In this study, the *in situ* and *ex situ* conservation gaps for the 102 West African CWR were evaluated. The 26 taxa without occurrence data, 20 taxa with occurrence records but not present in genebanks, and the 44 taxa underrepresented in genebanks have been prioritized for further *ex situ* collection to ensure their effective representation in genebanks. The areas of high predicted distribution within PAs such as Mont Tia, Mont Sangbe, Pic de Fon, Pic de Tibe, Mt Yonon, Cross River National Park and reserve site such as Mont Nimba and Diecke were also prioritized for *ex situ* collection. The 38 taxa that are not present in PA and the 28 taxa with less than five population in different PAs were also target taxa for identification and *in situ* conservation action. Establishment of the 29 identified reserve sites will further strengthen the CWR *in situ* conservation effort at national and regional level. Similarly, filling the identified *in situ* and *ex situ* conservation gaps will ensure that the priority CWR and agrobiodiversity are availability for use as food, feed and fibre. Additionally, the implementation of the proposed recommendations will enhance the active conservation and sustainable utilization of the priority CWR for crop improvement to mitigate climate change and underpin food security for the rising population in West Africa.

**Acknowledgements** The authors would like to thank the Tertiary Education Trust Fund (TETFUND), Nigeria for the scholarship awarded to Michael Nduche which ensured the funding of this study.

**Author Contributions** N Maxted and J Mago Brehm designed the study. All the authors contributed in the data analysis and revising of the manuscript, while MU Nduche wrote the manuscript.

**Funding** Tertiary Education Trust Fund (TETFUND), Nigeria provided funding for this study as a scholarship awarded to the corresponding author.

**Data Availability** Data area available from the author upon reasonable request.

## Declarations

**Conflict of Interest** The authors declare that they have no conflict of interest.

**Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>.

## References

- Akoègninou A, Van Der Burg WJ, Van Der Maesen LJG (2006) *Flore Analytique Du Bénin*. Backhuys Publishers, Leiden, p 1034
- Andargie M, Pasquet RS, Gowda BS, Muluvi GM, Timko MP (2014) Molecular mapping of Qtls for domestication-related traits in Cowpea (*V. Unguiculata* (L.) Walp.). *Euphytica* 200(3):401–412
- Atwell BJ, Wang H, Scafaro AP (2014) Could abiotic stress tolerance in wild relatives of rice be used to improve *Oryza Sativa*? *Plant Sci* 215:248–258
- Badiane FA, Diouf M, Diouf D (2014) Cowpea. Broadening the genetic base of grain legumes. Springer, India, pp 95–111
- Beaver JS, Zapata M, Alameda M, Porch TG, Rosas JC (2012) Registration Of Pr0401-259 And Pr0650-31 Dry Bean Germplasm Lines. *Journal of Plant Registrations* 6(1):81–84
- Bergl RA, Oates JF, Fotso R (2007) Distribution And Protected Area Coverage Of Endemic Taxa In West Africa's Biafran Forests And Highlands. *Biol Cons* 134:195–208



- Brooks TM, Mittermeier RA, Da-Fonseca GAB, Geriach J, Hoffmann M, Lamoreux JF, Mittermeier CG, Pilgrim JD, Rodrigues ASL (2006) Global biodiversity conservation priorities. *Science* 313:58–61. <https://doi.org/10.1126/Science.1127609>
- Brown AHD, Briggs JD (1991) Sampling strategies for genetic variation in *ex situ* collections of endangered plant species. In: Falk DA, Holsinger KE (eds) *Genetics and conservation of rare plants*. Oxford University Press, New York, pp 99–119
- Brown AHD, Marshall DR (1995) A basic sampling strategy: theory and practice. In: Guarino L, Ramantha RV, Reid R (eds) *Collecting plant genetic diversity: technical guidelines*. Cabi Publishing, Wallingford, pp 75–92
- Burgarella C, Cubry P, Kane NA, Varshney RK, Mariac C, Liu X, Shi C, Thudi M, Couderc M, Xu X, Chitikineni A, Scarcelli N, Barnaud A, Rhoné B, Dupuy C, François O, Berthouly-Salazar C, Vigouroux Y (2018) A Western Sahara centre of domestication inferred from pearl Millet genomes. *Nat Ecol Evol* 2:1377–1380
- Carney J (2001) African rice in the Columbian exchange. *J Afr Hist* 42:377–396. <https://doi.org/10.1017/S0021853701007940>
- Carr J, Adeleke A, Angu K, Belle E, Burgess N, Carrizo S, Choimes A, Coulthard N, Darwall W, Foden W (2015) Ecosystem profile guinean forests of West Africa biodiversity hotspot. Critical Ecosystem Partnership Fund, USA
- Castañeda-Álvarez NP, Khoury CK, Achicanoy HA, Bernau V, Dempewolf H, Eastwood RJ (2016) Global conservation priorities for crop wild relatives. *Nat Plants* 2(4):16022
- Cbd (1992) Convention on biological diversity. <http://www.Cbd.Int/Doc/Legal/Cbd-En.Pdf>. Accessed May 2022
- Cgiar (2022) Genebank - Africa Rice Center (Africarice), Genetic Resources Unit <https://www.Genebanks.org/Genebanks/Africarice/> Accessed 28 June 2022
- Champion L, Fuller D (2018) Archaeobotanical remains. In: Haour A (ed) *Two thousand years in Dendi, Northern Benin. Archaeology, history and memory*. Brill, Leiden, pp 216–233
- Chomicki G, Schaefer H, Renner S (2019) Origin and domestication of Cucurbitaceae crops: insights from phylogenies, genomics, and archaeology. *New Phytol* 226:1240–1255. <https://doi.org/10.1111/Nph.16015>
- Conservation International (2007) Guinean forests of West Africa. In *Biodiversity Hotspots*. Accessed June 21, 2022
- Contreras-Toledo AR, Cortés-Cruz M, Costich DE, Rico-Arce ML, Magos Brehm J, Maxted N (2019) Diversity and conservation priorities of crop wild relatives in Mexico. *Plant Genet Res*. <https://doi.org/10.1017/S1479262118000540>
- Couch C, Haba PM (2021) Tipa assessment: diecke classified forest, Yomou Prefecture [http://www.Herbiiergee.org/Uploads/2/6/3/0/26303479/2.\\_Tipas\\_Report\\_Diecke\\_En\\_New\\_Final.Pdf](http://www.Herbiiergee.org/Uploads/2/6/3/0/26303479/2._Tipas_Report_Diecke_En_New_Final.Pdf).
- Crop Trust (2022) Pgrfa Hub - Crops, Countries And Genebanks, Nigeria <https://www.Croptrust.org/Pgrfa-Hub/Crops-Countries-And-Genebanks/Countries/Nigeria/> Accessed 28 June 2022
- D'andrea A, Kahlheber S, Logan A, Watson D (2007) Early domesticated Cowpea (*Vigna unguiculata*) from Central Ghana. *Antiquity* 81:686–698. <https://doi.org/10.1017/S0003598x00095661>
- Dauby G, Zaiss R, Blach O, Catarino L, Damen T, Deblauwe V, Dessin S, Dransfield J, Droissart V, Duarte MC, Engledow H, Fadeur G, Figueira R, Gereau RE, Hardy OJ, Harris DJ, De Heij J, Janssens SB, Klomberg Y, Ley AC, Mackinder BA, Meerts P, Van De Poel JL, Sonké B, Sosef MSM, Stévant T, Stoffelen P, Svenning JC, Sepulchre P, Van Der Burgt XM, Wieringa JJ, Couvreur TLP (2016) Rainbio: a mega-database of Tropical African vascular plants distributions. *Phytokeys* 74:1–18
- David BL, Sharon MG (2012) The influence of climate change on global crop productivity. *Am Soc Plant Biol, Plant Physiol*. <https://doi.org/10.1104/PP.112.208298>
- Dida MM, Devos KM (2006) *Finger Millet*. In *Cereals and Millets* Springer, Berlin Heidelberg
- Dulloo ME, Labokas J, Iriondo JM, Maxted N, Lane A, Laguna E, Jarvis A, Kell S (2008) Chapter 2. Genetic reserve location and design. In: Iriondo JM, Maxted N, Dulloo ME (eds) *Conserving plant genetic diversity in protected areas*. Cabi, Wallingford, pp 23–64
- Em W, Kelly J (2011) Mapping Qtl for seed yield and canning quality following processing of black bean (*Phaseolus vulgaris* L.). *Euphytica* 179(3):471–484
- Esri (2011) Arcgis desktop release version 10.7. Environmental Systems Research Institute, Redlands, Ca
- Esri (2015) Arcmap for desktop release version 10.4.1. Environmental Systems Research Institute, Redlands, California.
- Fao (2010a) Second report on the state of the world's plant genetic resources for food and agriculture. Food and agriculture organization of the United Nations, Rome, Italy. Available Online: <https://www.Fao.org/Agriculture/Seed/Sow2/En/> Accessed 25 July 2021
- Fao (2014) Genebank standards for plant genetic resources for food and agriculture. Fao. <https://www.Fao.org/3/A-I3704e.Pdf>
- Fao-Bioversity (2015) Fao/Bioversity multi-crop passport descriptors V.2. Url: <https://Bioversityinternational.org/E-Library/Publications/Detail/Faobioversity-Multi-Crop-Passport-Descriptors-V21-Mcpd-V21/> Accessed 27 July 2022
- Faostat (2020) Food and agricultural organization of the United Nations. Rome, Italy <http://www.Fao.org/Statistics/En> (Accessed August 2020)
- Fetch T, Johnston PA, Pickering R (2009) Chromosomal location and inheritance of stem rust resistance transferred from *Hordeum bulbosum* into cultivated Barley (*H. vulgare*). *Phytopathology* 99(4):339–343
- Fielder H, Brotherton P, Hosking J, Hopkins JJ, Ford-Lloyd B, Maxted N (2015) Enhancing the conservation of crop wild relatives in England. *Plos One* 10(6):e0130804
- Ford-Lloyd BV, Maxted N (1993) Preserving diversity. *Nature* 361:579. <https://doi.org/10.1038/361579a0>
- Fourcade Y, Engler JO, Rödder D, Secondi J (2014) Mapping species distributions with maxent using a geographically biased sample of presence data: a performance assessment of methods for correcting sampling bias. *PLoS ONE* 9:E97122
- Garcia RM, Parra-Quijano M, Iriondo JM (2017) Identification of ecogeographical gaps in the Spanish *Aegilops* collections with potential tolerance to drought and salinity. *Peer J* 5:E3494

- Genesys (2020) Global portal on plant genetic resources, Genesys. <https://www.Genesys-Pgr.org/Welcome>. Accessed 20 November 2020
- Gbif (2020) Global biodiversity information facility, Gbif Occurrence Data Download <https://www.Gbif.org/Occurrence/Search> Accessed 24 October 2020
- Guerrant EO, Fiedler PL, Havens K, Maunder M (2004) Revised genetic sampling guidelines for conservation collections of rare and endangered plants. In: Guerrant EO, Havens K, Maunder M (eds) *Ex situ* plant conservation: supporting species survival in the wild. Island Press, Washington, pp 419–441
- Guo S, Zhang J, Sun H, Salse J, Lucas W, Zhang H, Zheng Y, Mao L, Ren Y, Wang Z, Min J, Guo X, Murat F, Ham B, Zhang Z, Gao S, Huang M, Xu Y, Zhong S, Bombarely A, Mueller L, Zhao H, He H, Zhang Y, Zhang H, Tan T, Pang E, Lin K, Hu Q, Kuang H, Ni P, Wang B, Liu J, Kou Q, Hou W, Zou X, Jiang J, Gong G, Klee K, Schoof H, Huang Y, Hu X, Dong S, Liang D, Wang J, Wu K, Xia Y, Zhao X, Zheng Z, Xing M, Liang X, Huang B, Lv T, Wang J, Yin Y, Yi H, Li R, Wu M, Levi A, Zhang X, Giovannoni J, Wang J, Li Y, Fei Z, Xu Y (2013) The draft genome of watermelon (*Citrullus Lanatus*) and resequencing of 20 diverse accessions. *Nat Genet* 45:51–58. <https://doi.org/10.1038/Ng.2470>
- Guo S, Zhao S, Sun H, Wang X, Wu S, Lin T, Ren Y, Gao L, Deng Y, Zhang J, Lu X, Zhang H, Shang J, Gong G, Wen C, He N, Tian S, Li M, Liu J, Wang Y, Zhu Y, Jarret R, Levi A, Zhang X, Huang S, Fei Z, Liu W, Xu Y (2019) Resequencing of 414 cultivated and wild watermelon accessions identifies selection for fruit quality traits. *Nat Genet* 51:1616–1623. <https://doi.org/10.1038/S41588-019-0518-4>
- Hall R (2008) Food crops, medicinal plants, and the atlantic slave trade, In: African American foodways: explorations of history and culture A. L. Bower (Eds.). University Of Illinois Press, Urbana, Il., pp. 17–44
- Harlan JR (1992) Crops and man. American society of agronomy, Ed. 2.
- Hijmans R, Guarino L, Mathur P (2012) Diva-Gis.7.5.0. <https://www.Diva-Gis.org/Documentation>. Accessed 26 July 2021
- Hijmans RJ, Spooner DM (2001) Geographic distribution of wild potato species. *Am J Bot* 88:2101–2112
- Hounsou-Dindin G, Idohou R, Akakpo AD, Adome N, Adomou AC, Assogbadjo AE, Kakaï RG (2022) Assessment of wild oil plants diversity and prioritization for valorization in Benin (West Africa): a multivariate approach. *Trees, Forests People*. <https://doi.org/10.1016/J.Tfp.2022.100210>
- Huchinson J, Dalziel JM (1958) Flora of West Tropical Africa, Vol. 1, Part II. Crown agents for overseas governments and administrations. London, pp. 335 – 587
- Icrisat (2022) International crops research institute for the semi-arid tropics. Tag, Niger <https://www.Icrisat.org/Tag/Niger/>
- Idohou R, Assogbadjo A, Fandohan A, Gouwakinnou G, Glele-Kakaï RL, Sinsin B, Maxted N (2013) National inventory and prioritization of crop wild relatives: case study for Benin. *Genet Res Crop Evol* 60:1337–1352. <https://doi.org/10.1007/S10722-012-9923-6>
- Lita (2022) Our genetic resources. international institute of tropical agriculture <https://www.lita.org/Research/Genetic-Resources/> Accessed 28 June 2022
- Iriondo JM, Maxted N, Kell SP, Ford-Lloyd BV, Lara-Romano C, Labokas J, Magos Brehm J (2012) Quality standards for genetic reserve conservation of crop wild relatives. In: Maxted N, Dulloo ME, Ford-Lloyd BV, Frese L, Iriondo JM, Pinheiro De Carvalho MAA (eds) *Agrobiodiversity Conservation: securing the diversity of crop wild relatives and landraces*. Cabi Publishing, Wallingford, pp 72–77
- Iriondo JM, Magos Brehm J, Dulloo ME, Maxted N (Eds.) (2021) Crop wild relative population management guidelines. Farmer's Pride: networking, partnerships, and tools to enhance in situ conservation of European plant genetic resources <https://www.Farmerspride.Eu/> Accessed July 10 2022
- Jena KK (2010) The species of the genus *Oryza* and transfer of useful genes from wild species into cultivated rice *O. Sativa*. *Breeding Science* 60(5):518–523
- Johnston PA, Timmerman-Vaughan GM, Farnden KJ, Pickering R (2009) Marker development and characterisation of *Hordeum Bulbosum* introgression lines: a resource for barley improvement. *Theor Appl Genet* 118(8):1429–1437
- Johnston PA, Niks RE, Meiyalaghan V, Blanchet E, Pickering R (2013) Rph22: Mapping of a novel leaf rust resistance gene introgressed from the Non-Host *Hordeum Bulbosum* L. into cultivated Barley (*Hordeum Vulgare* L.). *Theor Appl Genet* 126(6):1613–1625
- Kati V, Devillers P, Dufrière M, Legakis A, Vokou D, Lebrun P (2004) Hotspots, complementarity or representativeness? designing optimal small-scale reserves for biodiversity conservation. *Biol Cons* 120(4):471–480
- Kawuki RS, Kaweesi T, Esuma W, Pariyo A, Kayondo IS, Ozimati A, Kyaligonza V, Abaca A, Orone J, Tumuhimbise R, Nuwamanya E, Abidrabo P, Amuge T, Ogwok E, Okao G, Wagaba H, Adiga G, Alicai T, Omongo C, Bua A, Ferguson M, Kanju E, Banguma Y (2016) Eleven years of breeding efforts to combat cassava brown streak disease. *Breed Sci* 66(4):560–571
- Kay A, Fuller D, Neumann K, Eichhorn B, Höhn A, Morin-Rivat J, Champion L, Linseele V, Huysecorn E, Ozainne S, Lespez L (2019) Diversification, Intensification and specialization: changing land use in Western Africa from 1800 Bc to Ad 1500. *J World Prehist* 32(2):179–228
- Korona R (1996) Adaptation to structurally different environments. *Proc R Soc Lond Ser B Biol Sci* 263:1665–1669. <https://doi.org/10.1098/Rspb.1996.0243>
- Langhammer PF, Bakarr MI, Bennun LA, Brooks TM, Clay RP, Darwall W, De Silva N, Edgar GJ, Eken G, Fishpool LDC, Fonseca GAB, Foster MN, Knox DH, Matiku P, Radford EA, Rodrigues ASL, Salaman P, Sechrest W, Tordoff AW (2007) Identification and gap analysis of key biodiversity areas: targets for comprehensive protected area systems. *Best Practice Protected Area Guidelines Series 15*. Iucn, Gland, Switzerland
- Leroy T, De Bellis F, Legnate H, Musoli P, Kalonji A, Solórzano R, Cubry P (2014) Developing core collections to optimize the management and the exploitation of diversity of the coffee *Coffea Canephora*.

- Genetica 142:185–199. <https://doi.org/10.1007/S10709-014-9766-5>
- Liu C, Berry PM, Dawson TP, Pearson RG (2005) Selecting thresholds of occurrence in the prediction of species distributions. *Ecography* 28:385–393
- Lopez- Montes A, Bhattacharjee R, Tessema G (2012) Yam Breeding At Iita: Achievements, Challenges And Prospects. <https://R4dreview.iita.org/Index.Php/Tag/Yam-Breeding/>
- Lovejoy P (1980) Kola in the history of West Africa (La Kola Dans L'histoire De L'afrique Occidentale). *Cahiers D'études Afr* 20:97–134. <https://doi.org/10.3406/Cea.1980.2353>
- Luiselli L, Dendi D, Eniang EA, Fakae BB, Akani GC, Fa JE (2019) State of knowledge of research in the Guinean forests of West Africa region. *Acta Oecologica* 94:3–11. <https://doi.org/10.1016/J.Actao.2017.08.006>
- Macneish R (1992) The origins of agriculture and settled life. University Of Oklahoma Press, Norman, pp 298–318
- Magos Brehm J, Gaisberger H, Kell S, Parra-Quijano M, Thormann I, Dulloo ME, Maxted N (2022) Planning complementary conservation of crop wild relative diversity in Southern Africa. *Diversity Distributions*. <https://doi.org/10.1111/Ddi.13512>
- Magos Brehm J, Kell S, Thormann I, Gaisberger H, Dulloo ME, Maxted N (2017a) Interactive toolkit for crop wild relative conservation planning university of Birmingham, Birmingham, Uk And Bioversity International, Rome, Italy <https://www.Cropwildrelatives.org/Conservation-Toolkit>
- Magos Brehm J, Kell SP, Thormann I, Gaisberger H, Dulloo E, Maxted N (2017b) Occurrence data collation template V.1. <https://doi.org/10.7910/Dvn/5b9iv5>, Harvard Database, V1
- Mallon CA, Poly F, Roux XL, Marring I, Van Elsas JD, Salles JF (2015) Resource pulses can alleviate the biodiversity-invasion relationship in soil microbial communities. *Ecol Ecol Soci Am*. <https://doi.org/10.1890/14-1001.1>
- Maxted N (2013) In situ, ex situ conservation. *Encyclopedia of biodiversity*. Elsevier, pp 313–323. <https://doi.org/10.1016/B978-0-12-384719-5.00049-6>
- Maxted N, Vincent H (2021) Review of congruence between global crop wild relative hotspots and centres of crop Origin/Diversity. *Genet Resour Crop Evol* 68:1283–1297. <https://doi.org/10.1007/S10722-021-01114-7>
- Maxted N, Bv F-L, Jg H (1997a) Plant genetic conservation: the in situ approach. Chapman and Hall, London
- Maxted N, Ford-Lloyd BV, Hawkes JG (1997) Complementary conservation strategies. In: Maxted N, Ford-Lloyd BV, Hawkes JG (eds) *Plant genetic conservation: The In Situ approach*. Chapman and Hall, London, pp 20–55
- Maxted N, Hawkes JG, Guarino L, Sawkins M (1997) Towards the selection of data for plant genetic conservation. *Genet Resour Crop Evol* 44(337):348
- Maxted N, Ford-Lloyd BV, Jury S, Kell SP, Scholten MA (2006) Towards a definition of crop wild relative. *Biodiversity Conservation* 15:2673–2685
- Maxted N, Dulloo E, Ford-Lloyd BV, Iriondo JM, Jarvis A (2008) Gap analysis: a tool for complementary genetic conservation assessment. *Diversity Distributions* 14:1018–1030
- Maxted N, Ford-Lloyd B, Kell SP, Iriondo Jm, Dulloo ME, Turok J (2008b) Crop wild relative conservation and use. In: International conference on crop wild relative, conservation and use, C. A. B. International
- Maxted N, Iriondo JM, De Hond L, Dulloo ME, Lefèvre F, Asdal A, Kell SP, Guarino L (2008) Genetic reserve management. In: Iriondo JM, Dulloo ME, Maxted N (eds) *Conserving plant genetic diversity in protected areas*. Cab International, Wallingford, pp 65–87
- Maxted N, Kell SP (2009) Establishment of a global network for the in situ conservation of crop wild relatives: status and needs. Commission on genetic resources for food and agriculture, Food and agriculture organization of the United Nations, Rome, Italy
- Maxted N, Magos BJ, Kell S (2013) Resource book for preparation of national conservation plans for crop wild relatives and landraces. . In: Magos Brehm J, Kell S, Thormann I, Gaisberger H, Dulloo ME and Maxted N (2017). *Interactive toolkit for crop wild relative conservation planning version 1.0*. University Of Birmingham, Birmingham, Uk And Bioversity International, Rome, Italy
- Maxted N, Dulloo ME, Ford-Lloyd B (2016) Enhancing crop genepool use : capturing wild relative and landrace diversity for crop improvement, C. A. B. International
- Mkwaila W, Terpstra KA, Ender M, Kelly JD (2011) Identification of Qtl for agronomic traits and resistance to white mold in wild and landrace germplasm of common bean. *Plant Breeding* 130:665–672
- Mponya NK, Chanyenga T, Brehm JM, Maxted N (2020) In situ and ex situ conservation gap analyses of crop wild relatives from Malawi. *Genet Res Crop Evolut* 68:759–771
- Nduche M, Brehm JM, Abberton M, Omosun G, Maxted N (2021) West African crop wild relative checklist, prioritization and inventory. *Genetic Resources* 2(4):55–65
- Ng'uni D, Munkombwe G, Mwila G, Gaisberger H (2019) Spatial analyses of occurrence data of crop wild relatives (CWR) Taxa as tools for selection of sites for conservation of priority CWR in Zambia. *Plant Genet Resour Charact Util* 17:103–114
- Nwanze KF, Rao KE, Soman P (1990) Understanding and manipulating resistance mechanisms in sorghum for control of the shoot-fly. In: *Proceedings of international symposium on molecular and genetic approaches to plant stress*. New Delhi 14:17th Feb 1990
- Oates JF, Bergl RA, Linder JM (2004) Africa's Gulf of Guinea forests: biodiversity patterns and conservation priorities. *Advances in Applied Biodiversity Science. Conservation International*, pp 9–91. <https://doi.org/10.1896/1-881173-82-8.9>
- Osborn TC, Hartweck LM, Harmsen RH, Vogelzang RD, Kmiecik KA, Bliss FA (2003) Registration of phaseolus Vulgaris genetic stocks with altered seed protein compositions. *Crop Science* 43(4):1570–1572
- Park RF, Golegaonkar PG, Derevnina L, Sandhu KS, Karooglu H, Elmansour HM, Singh D (2011) Ecogeographical land characterization maps as a tool for assessing plant adaptation and their implications in agrobiodiversity studies. *Genet Resour Crop Evol*. <https://doi.org/10.1007/S10722-011-9676-7>
- Park RF, Golegaonkar PG, Derevnina L, Sandhu KS, Karooglu H, Elmansour HM, Singh D (2015) Leaf rust of

- cultivated barley: pathology and control. *Annu Rev Phytopathol* 53:565–589
- Parra-Quijano M, Iriondo JM, Torres E (2012) Ecogeographical land characterization maps as a tool for assessing plant adaptation and their implications in agrobiodiversity studies. *Genet Res Crop Evol* 59:205–217
- Parra-Quijano M, Iriondo JM, Torres E (2012) Improving representativeness of genebank collections through species distribution models, gap analysis, and ecogeographical maps. *Biodiversity Conservation* 21:79–96
- Parra-Quijano M, Torres E, Iriondo JM, López F, Molina PA (2016) Capfitogen tools. User Manual Version 2.0. International treaty on plant genetic resources for food and agriculture. *Fao. Rome Pp 251* <https://www.Capfitogen.Net/En/> (Accessed 29 July 2022)
- Parra-Quijano M, Iriondo JM, Torres ME, López F, Maxted N, Kell SP (2021) Capfitogen3: A toolbox for the conservation and promotion of the use of agricultural biodiversity. Bogotá, Colombia, Pp 45 - 194 <https://www.Capfitogen.Net/En/>. Accessed 23 December 2021
- Phillips SJ, Anderson RP, Schapire RE (2006) Maximum entropy modelling of species geographic distributions. *Ecol Model* 190(3–4):23
- Pickering R, Pa J (2005) Recent progress in barley improvement using wild species of *Hordeum*. *Cytogenet Genome Res* 109:344–349
- Pickering R, Ruge-Wehling B, Johnston PA, Schweizer G, Ackermann P, Wehling P (2006) The transfer of a gene conferring resistance to scald (*Rhynchosporium Secalis*) from *hordeum bulbosum* into *H. vulgare* chromosome 4hs. *Plant Breeding* 125(6):576–579
- Pillen K, Zacharias A, Lon J (2004) Comparative Ab-Qtl analysis in barley using a single exotic donor of *hordeum vulgare* Ssp *Spontaneum*. *Theor Appl Genet* 108(8):1591–1601
- Qgis-Development Team (2021) Qgis 3.16. 8 Geographic information system open source geospatial foundation Project. <https://qgis.Osgeo.org>
- Ramírez-Villegas J, Khoury K, Jarvis A, Dg D, Guarino L (2010) A gap analysis methodology for collecting crop genebanks: a case study with phaseolus beans. *PLoS ONE* 5:E13497
- Rodrigues ASL, Andelman SJ, Bakarr MI, Boitani L, Brooks TM, Cowling RM, Fishpool LDC, Fonseca GAB, Gaston KJ, Hoffmann M, Long JS, Marquet PA, Pilgrim JD, Pressey RL, Schipper J, Sechrest W, Stuart SN, Underhill LG, Waller RW, Watts MEJ, Yan X (2004) Effectiveness of the global protected area network in representing species diversity. *Nature* 428:640–643
- Rubio-Teso MI, Iriondo JM, Parra-Quijano M, Torres E (2013) National strategy for the conservation of crop wild relatives Of Spain. *Pgr Secure*. [https://www.Pgrsecure.Bham.Ac.Uk/Sites/Default/Files/Documents/Public/National\\_Cwr\\_Conservation\\_Strategy\\_Spain.Pdf](https://www.Pgrsecure.Bham.Ac.Uk/Sites/Default/Files/Documents/Public/National_Cwr_Conservation_Strategy_Spain.Pdf) Accessed 18 Jun 2022
- Ruge B, Linz A, Pickering R, Proeseler G, Greif P, Wehling P (2003) Mapping Of Rym14 Hb, a gene introgressed from *hordeum bulbosum* and conferring resistance to Bammv and Baymv In Barley. *Theor Appl Genet* 107(6):965–971
- Saini H, Kashihara Y, Aj L-M, Robert A (2016) Interspecific crossing between yam species (*Dioscorea Rotundata* and *Dioscorea Bulbifera*) through in vitro ovule culture. *Am J Plant Sci* 07(08):1268–1274
- Scarcelli N, Cubry P, Akakpo R, Thuillet A, Obidiegwu J, Baco MN, Otoo E, Sonké B, Dans A, Djedatin G, Mariac C, Couderc M, Causse S, Alix K, Chair H, François O, Vigouroux Y (2019) Yam genomics supports West Africa as a major cradle of crop domestication. *Science Advances*. <https://doi.org/10.1126/sciadv.aaw1947>
- Scheldeman X, Van Zonneveld M (2010) Training Manual On Spatial Analysis Of Plant Diversity And Distribution. Rome, Italy: Bioversity International. [https://www.Bioversityinternational.org/Fileadmin/User\\_Upload/Online\\_Library/Publications/Pdfs/1431.Pdf](https://www.Bioversityinternational.org/Fileadmin/User_Upload/Online_Library/Publications/Pdfs/1431.Pdf) Accessed 18 June 2022.
- Sood S, Khulbe RK, Gupta AK, Grawal PA, Upadhyaya HD, Bhatt JC (2015) Barnyard Millet – a potential food and feed crop of future. *Plant Breeding* 134:135–147
- Unep-Wcmc (2019) The world database on protected areas (Wdpa). Cambridge, UK. <https://www.Protectedplanet.Net/>. Accessed 9 Jan 2022
- Unesco (2019) Mount nimba strict nature reserve. World Heritage Convention <https://whc.Unesco.org/En/List/155/> Accessed 24 June 2022
- Usgs (2017) West Africa: land use and land cover dynamics, agricultural expansion across West Africa. *Us Geographical Survey* <https://eros.Usgs.Gov/WestAfrica/Agriculture-Expansion>
- Vaughan J, Geissler C (1999) The new Oxford book of food plants. Oxford University Press, Oxford, pp 10–174
- Vincent H, Amri A, Np C-A, Dempewolf H, Dulloo E, Guarino L, Hole D, Mba C, Toledo A, Maxted N (2019) Modeling of crop wild relative species identifies areas globally for in situ conservation. *Commun Biol* 2:136
- Vincent H, Hole D, Maxted N (2022) Congruence between global crop wild relative hotspots and biodiversity hotspots. *Biol Cons* 265:109432. <https://doi.org/10.1016/J.Biocon.2021.109432>
- Wendler N, Mascher M, Himmelbach A, Johnston P, Pickering R, Stein N (2015) *Bulbosum* to go: a toolbox to utilize *Hordeum Vulgare/Bulbosum* introgressions for breeding and beyond. *Mol Plant* 8(10):1507–1519
- World Coffee Research (2021) Cote D'ivoire Genebank digitizes coffee collection <https://worldcoffeeresearch.org/News/2021/> Accessed 28 June 2022
- Yb Fu (2017) The vulnerability of plant genetic resources conserved ex situ. *Crop Science*. <https://doi.org/10.2135/Cropsci2017.01.0014>
- Zair W, Maxted N, Magos Brehm J, Amri A (2021) Ex situ and in situ conservation gap analysis of crop wild relative diversity in the fertile crescent of the middle east. *Genet Resour Crop Evolut* 68:693–709
- Zegeye H (2017) In situ and ex situ conservation: complementary approaches for maintaining biodiversity. *Int J Res Environ Stud* 4:1–12

**Publisher's Note** Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.