

Global Genepool Conservation and Use Strategy for Dioscorea (Yam)

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Abstract

The global genepool conservation and use strategy for yam were developed in this study. Diversity analysis, and *in situ* and *ex situ* conservation gap analyses were carried out for the 27 globally priority yam crop wild relatives (CWR) at taxon and ecogeographic levels to determine their representativeness in conservation actions. Hotspots were found in Nzerekore region of Guinea, Nimba and Grand Gedeh regions of Liberia, Montagnes, Sassandra- Marahouse, and Bas – Sassandra regions of Cote d'Ivoire, Volta, Greater Accra and Eastern regions of Ghana, Centrale and Plateau regions of Togo, Donga, Oueme, Atlantique, Littoral and Plateau provinces of Benin, South West zone of Nigeria, Es region of Cameroon, Sangha- Mbaere region of Central Africa Republic. Likouala and Sangha regions of Congo, and Shan province of Myanmar and Thailand. A total of 13 reserve sites were found in 13 countries, with four locations in the network of PA. Out of the 81% of the priority CWR, 7.10% of the taxa were represented in *ex situ* collections, with 14.8% of the taxa with at least 50 accessions in genebanks, while 66.6% of the priority CWR are underrepresented in genebanks, with less than 50 accessions conserved *ex situ*, and 18.5% of the species are not represented in *ex situ* collections. The findings and recommendations of this study will guide the production and implementation of effective long term conservation action and sustainable utilization of globally priority yam CWR. The active conservation of the global yam priority species will underpin food security and mitigate climate change.

Introduction

Yams are important nutrient- dense food security crops (Danquah et al., 2022). They are starchy staple food for many people across the globe, especially in tropical and subtropical countries. A total of 75.14 million tonnes of yams were harvested in 8.68 million hectares of land in 2021, with Nigeria, Benin, Ghana and Cote d'Ivoire contributing to about 93% of the total production. West Africa accounted for 8.1 million hectares (94.4%) of the total area harvested in the same year (FAOSTAT, 2021). Yams are the second most economically valuable root and tuber crop, only ranked behind potatoes. It is predominantly used as food, providing proteins and micronutrients such as vitamin C and potassium. Yams are also processed into flour or starch for domestic and industrial purposes (Wanasundera and Ravindran, 1994). They contain active chemical constituents for pharmaceutical products, while bitter yam [*Dioscorea dumetorum* (Kunth) (Pax)] is used for the treatment of diabetes, due to its blood sugar lowering ability (Andres et al., 2017).

Yams (*Dioscorea* spp.) belongs to the family Dioscoraceae, and include both wild and cultivated species, with over 600 recognizable species (The Plant List, 2013; Cao et al., 2021). Edible forms have been selected by farmers, users and by breeding programmes that have occurred over the past centuries and are cultivated from among the wild relatives. Their vigorous herbaceous forms that were first domesticated in the Niger River Basin of the region and are currently cultivated in Africa, Asia, South America and Oceania (POWO, 2021). Yams are the most economically valuable crop in West Africa and different species of yam have different centres of origin; *D. rotundata* Poir, *D. alata* L. and *D. trifida* L.f. were domesticated in West Africa, Southeast Asia and tropical America, respectively (Harlan, 1992; Andres et al., 2017). Edible yam species are vegetatively propagated using the tubers, sections of tuber or the corms. Current threats from habitat destruction, intensive land management, drought, competition from invasive species and climate change are causing genetic erosion and even extinction (Vincent et al., 2013a; Magos Brehm et al., 2017), intensify the need for collection missions and more active conservation of the genepool. (Vincent et al., 2013b; IUCN, 2021).

Crop wild relatives (CWR) are wild plant taxa closely related to crops with an indirect use as novel gene or allele donors to their related crops (Maxted et al., 2006). They are a vital subset of plant genetic resources that provide profitable genetic diversity for crop improvement. CWR are socioeconomic valuable resources that are needed to maintain future food, nutrient and economic security (Magos Brehm et al., 2017). Yam CWR such as *Dioscorea bulbifera* L. has been used to confer genes for high yield in White Guinea yam (Saini et al., 2016), *Dioscorea abyssinica* Hochst. ex Kunth has been used to transfer yam mosaic virus resistance in *Dioscorea rotundata* Poir (White Guinea yam), *Dioscorea alata* (Greater yam/Water yam) and *Dioscorea cayenensis* Lam (Yellow Guinea yam) (Kikuno et al., 2011b; Lopez- Montes et al., 2012). *Dioscorea praehensilis* Benth has confirmed use for breeding anthracnose resistance in White Guinea yam (Lopez- Montes et al., 2012). Maxted and Kell (2009) reported the transfer of novel traits from 185 CWR to their related crops. Pimentel et al. (1997) estimated the global monetary value of CWR contribution to improved crop yield at about USD 115 billion per annum (USD 207 billion in 2023).

Entire genepool conservation is important to maintain the breath of genes and alleles in a crop and its wild relatives to prevent genetic erosion and make adaptive diversity available to breeders. Conservation strategies involve both *in situ* and *ex situ* techniques. *In situ* conservation involves the recognition, designation, management and monitoring of a population in its natural habitat, where its intrinsic features resides (Maxted et al., 1997c). *In situ* conservation is the major conservation technique, while *ex situ* conservation is a complementary method, acting as a backup and provision of access to the conserved resource (FAO, 2001; Heywood and Dulloo, 2005; Stolton et al., 2006). *Ex situ* conservation involves the safeguarding of biological diversity outside their intrinsic habitat. It requires the identification, sampling, transfer, management and monitoring of target plant samples outside their natural habitat (Maxted et al., 1997c). Although, some edible yam species have received priority for *ex situ* collection, conservation and documentation in recent years, the wild relatives of yams are inadequately represented in *ex situ* collections (GBIF.org, 2020; Genesys, 2020). Similarly, whilst there are hand full of *in situ* conservation of edible yam species (Scarcelli et al., 2019; Sharif et al., 2020; Sugihara et al., 2020), *in situ* conservation of wild relatives are scarcely documented (Chair et al., 2010)

The aim of this work was to develop a global genepool conservation and sustainable use strategies for wild yam through: (a) Identifying existing gaps in *ex situ* collection of yams and developing strategies to fill the gaps (b) Recommending a network of sites for active *in situ* conservation of the global yam priority wild relatives (c) Supporting the sustainable utilization of global yam priority CWR to enhance global food provision.

Methods

1 Compilation of the CWR Checklist and Prioritization

The wild yam checklist was compiled using the CWR checklist and inventory template (Magos Brehm, 2017) and based on the World Checklist of Selected Plant Families (WCSP) (<https://powo.science.kew.org/>), The Plant List <http://www.plantlist.org>, the Germplasm Resources Information Network (GRIN) <https://npgsweb.ars-grin.gov/gringlobal/taxon/taxonomysearchcwr>, Harlan de Wet CWR diversity (<https://www.cwrdiversity.org/checklist/>). The use of genepool concept as the only criterion in the prioritization

was to ensure the use of the priority CWR for the improvement of their related crops. It will facilitate the use of the priority CWR as resources for breeders in the modification of crops to produce desirable cultivars.

The CWR checklist was annotated to aid prioritization and yam wild relatives were prioritized based on the closeness of the wild relatives to their related crops, via the use of the genepool concept (Harlan, 1971). The yam CWR checklist was prioritized based on a point scoring procedure and the level of scores was directly proportional to the degree of closeness to the crop species. GP1b species were given the highest point (9) because of the ease of crossability of CWR with related crops. Conversely, GP3 were given a lower score due to the difficulty in gene transfer, without the application of sophisticated techniques. Tertiary genepool (GP3) with proven use in crop improvement, were selected for prioritization (Ford-Lloyd et al., 2008; Maxted, 2013) and given a score of three. Both the yam CWR checklist and priority list were sent for validation to experts from the International Institute of Tropical Agriculture, Ibadan in Nigeria, the Michael Okpara University of Agriculture, Umudike in Nigeria and *Dioscorea* genus experts from the University of Abomey – Calavi, Cotonou in Benin.

The inventory of the priority yam wild relatives was completed with information on taxonomy, genepool, uses, distribution, socioeconomic value of crops, threat status, biology and conservation status in the CWR checklist and data inventory template (Thormann et al., 2017). The information was retrieved from the Germplasm Resources Information Network (GRIN) <https://npgsweb.ars-grin.gov/gringlobal/taxon/taxonomysearchcwr>, International Union for Conservation of Nature and Natural Resources (IUCN) <https://www.iucnredlist.org/>, RainBio (<http://rainbio.cesab.org/>), Royal Botanical Garden Kew worldwide specimen data, World Checklist of Selected Plant Families (WCSP) <http://wcsp.science.kew.org/cite.do>. The Plant List <http://www.plantlist.org>, Global Portal on Plant Genetic Resources (GENESYS) <https://www.genesys-pgr.org/>, National Plant Germplasm System (NPGS) (<https://data.nal.usda.gov/dataset/national-plantgermplasm-system>), Kew Herbarium Catalogue (<http://apps.kew.org/hercat/gootlomepage.do>), JSTOR Global Plants (<http://plants.jstor.org/>), Missouri Botanical Garden worldwide specimen data, TROPICOS (<http://www.tropicos.org/Home.aspx>), African Plant Database (<http://www.ville-ge.ch/musinfo/bd/cjb/africa/recherche.php?langue=an>), New York Botanical Gardens (NYBG) Steere Herbarium <https://sweetgum.nybg.org/science/ih/>, Board of Trustees, Royal Botanical Gardens Kew (<http://www.powo.science.kew.org>), International Institute of Tropical Agriculture (IITA).

2. Diversity Analysis of Priority CWR

2.1 Occurrence Data Collection, Quality Verification, Control and Overview

The occurrence data of the yam priority CWR were collated using the 'Occurrence data collation template v.1' (Magos Brehm et al., 2017b) from the Global Biodiversity Information Facility (GBIF), Global Portal on Plant Genetic Resources (GENESYS) <https://www.genesys-pgr.org/>, RainBio (<http://rainbio.cesab.org/>), International Union for Conservation of Nature and Natural Resources (IUCN) <https://www.iucnredlist.org/>, the New York Botanical Garden (NYBG) Steere Herbarium <https://sweetgum.nybg.org/science/ih/>, The herbarium of Royal Botanical Garden, and via contacting *Dioscorea* genus experts.

Records without geographic coordinates but with collection site information were georeferenced with Google map (<https://www.mapsgoogle.com>). Occurrence records with geographic coordinates not expressed in

decimal degrees were converted using Canadensys (<https://data.canadensys.net/tools/coordinates>). Duplicate records were removed, (i.e, records with the same information but different sources or documented twice from the same source (Magos Brehm et al., 2017), while records that lied abnormally in erroneous locations were reviewed and georeferenced wherever possible. Occurrence records were further checked for spelling errors, and formatted and standardized to be used in the CAPFITOGEN 3 tool (Parra - Quijano et al., 2021), i.e, based on the FAO- Bioversity Multi-Crop descriptors (FAO-BIOVERSITY, 2015). The occurrence records were verified using the 'TesTable' tool of CAPFITOGEN 3 to ensure it meets the required standard for other CAPFITOGEN3 tools analyses followed by the GEOQUAL tool to evaluate the quality of the geographic coordinates and accuracy of collection sites of the records. Only records with Totalqual of 60 to 100 were included in the analyses to exclude accession with unreliable data and include accessions with scores records (Parra - Quijano et al., 2021)

2.2 Distribution, Hotspots and complementary analyses

The species richness and species richness rarefaction maps were created in DIVA – GIS 7.5 (Hijmans et al., 2012), at resolution of 10 X 10 km (approximately 5 arc minutes) The rarefaction technique evaluates species richness for a particular number of samples, based on a systematic plot of the number of species against samples; a rarefaction curve is generated by re-sampling at random and plotting the number of taxa observed per sample. Rarefaction analysis perceives that individuals in a habitat are genetically close and evenly distributed and those samplings are similar. If all these presumptions are not reached, the outcome is biased.

Predicted distribution models were developed for the priority CWR with more than 10 occurrence records using the Maximum Entropy Algorithm (MaxEnt) (Table S1) (Phillips et al., 2006), and circular buffer of 50 km(CA50) (Hijmans and Spooner, 2001) around each occurrence for those taxa with less than 10 records, following the approach suggested by Magos Brehm et al. (2022) Model calibration was carried out by dividing the taxa distribution records of the priority CWR into training set (75% of total occurrence records) and test set (25%). Bioclimatic variable raster files were sourced from WorldClim2.1 (<https://www.worldclim.org/bioclim>), edaphic variable raster files, from ISRIC- World Soil Information (<https://files.isric.org/soilgrids/>), geophysical data were obtained as Digital Elevation Map (DEM) files from the National Aeronautic Space Administration (NASA) (<https://www.nasa.gov>). By using the Spatial Analyst Tools of the ArcMap 10.4.1 (ESRI, 2015), the ecogeographic variable raster files were re-sampled to equal cell size of 0.41666666667 m, clipped to the same extent, reprojected to the same grid (WGS – 84), and formatted to ASCII grid format. At the resolution of 10 X 10 km (approximately 5 arc minutes at Equator), variables of each ecogeographic component (bioclimatic, edaphic and geophysical) were selected for each taxon, using the Random Forest, followed by bivariate correlation analysis integrated in the SelecVar tool of CAPFITOGEN 3 (Parra - Quijano et al., 2021). Only variables with weak correlation ($p > \text{value} \leq 0.34$) or not correlated variables ($p\text{-value} = 0$) were used to produced the species distribution model for each taxon (Table S1). As recommended by Liu et al. (2005) maximum training sensitivity plus specificity threshold was applied. The validity of the models were assessed using three criteria; (a) average area under the test receiver operating characteristics curve [(ATAUC) > 0.7] (b) standard deviation of ATAUC (STAUC) < 0.15 and (c) the section of potential distribution area with a STAUC > 0.15, being < 10% were secured and used for assessing taxa predicted distribution as recommended by Ramírez-Villegas et al. (2010) and applied by other authors (Ramirez-Romero et al., 2019; Mponya et al., 2020; Magos Brehm et al., 2022). For a model to be valid, all three criteria had to be met. Alternatively, as

recommended by Hijmans and Spooner (2001) predicted distribution were produced by circular buffer method, using a radius of 50 km (CA50) around each present point. In this case, intersecting locations were not considered more than once.

Complementary analysis was undertaken to identify potential locations for *in situ* conservation of the priority CWR using DIVA – GIS 7.5 (Hijmans et al., 2012), at resolution of 10 X 10 km (approximately 5 arc minutes). The World PA map was obtained from UNEP-WCMC (2019) and overlapped with the taxon richness map and complementary genetic reserve site map to assess the degree of passive *in situ* conservation of the priority CWR in the existing network of PA, to effectively preserve and maintain their genetic diversity and protect them from diseases, pest, grazing, exploitation, degradation, fragmentation and fluctuation (Vincent et al., 2019). The maps generated were processed in DIVA- GIS 7.5, QGIS 3.16.8 (QGIS-Development Team, 2021) and ArcMap 10.4.1 (ESRI, 2015).

2.3 Ecogeographic Land Characterization (ELC) map

In order to ascertain suitable locations for the *in situ* and *ex situ* safeguarding of the diversity of priority taxa, ecogeographic land characterization maps (ELC) were prepared (Parra - Quijano et al., 2021; Magos Brehm et al., 2022). Ecogeographic diversity is used as a proxy for genetic diversity (Parra-Quijano et al., 2012a; Magos Brehm et al., 2022). To generate the species specific ELC maps, ecogeographic layers were created for each taxon by cropping the global ecogeographic layers to the actual size of the native spatial distribution range, using the rLayer tool of CAPFITOGEN3 (Parra - Quijano et al., 2021). The global ecogeographic layers were sources from WorldClim 2.1 (<https://www.worldclim.org/bioclimate>). This was done by inputting the taxon occurrence data in rLayer tool and using a buffer cropway of 300 km at a resolution of 10 X 10 km approximately (5 arc – minutes). SelecVar tool of CAPFITOGEN3 was then used to identify the most important variable for each taxon amongst the 29 ecogeographic variables (comprising of 13 bioclimatic, 12 edaphic and 4 geophysical) (Tables S5 and S6). The species specific ELC maps were produced using the ELC maps tool of CAPFITOGEN3, to ensure a more specific adaptive scenario for each of the priority CWR. The species specific ELC maps were generated using the cropped ecogeographic layers for each taxon with the kmeanbic method (Parra - Quijano et al., 2021), at a cell size of 10 km X 10 km (approximately 5 arc – minutes). The kmeanbic method was used because the function in R, evaluates the clustering process used in the univariate analysis of major components. It involves the analysis of progressive clusters by using the major components filtered from the raw data as variables. For each cluster, the information measure is determined as a criterion of goodness of fit, used to calculate the ideal number of clusters.

3. Gap Analysis of Priority CWR

3.1 In situ gap analysis

The method described by Maxted et al. (2008); Scheldeman and van Zonneveld (2010) and Parra-Quijano et al. (2012b) were adopted in this study. *In situ* gap analysis involves the evaluation of the best combination of sites for *in situ* conservation at both taxon and genetic levels. At taxon level, the world PA map was overlapped with the occurrence data of priority yam CWR, using QGIS 3.16.8. Similarly, the world PA map was intersected with the passport data, using the 'join attribute by location' in the 'data management tool' of QGIS 3.16.8, to identify records within and outside PA network. The *in situ* conservation gaps were determined by evaluating the relative number of populations of taxa in PA compared to those outside PA (Contreras-Toledo et al., 2019;

Mponya et al., 2020). At the ecogeographic level, to determine the level of representativeness of wild yam' diversity in PA, the Representa of CAPFITOGEN 3 (Parra - Quijano et al., 2021) was used to identify the ELC categories represented in the network of PA based on the ELC map (Ramírez-Villegas et al., 2010 ; Zair et al., 2021)

3.2 Ex situ gap analysis

Gap analysis of *ex situ* conservation was also assessed at taxon and ecogeographic levels. At the taxon level, the map of observed *ex situ* collection was subtracted from the map of potential distribution to determine the current *ex situ* conservation gap. The Representa tool' of CAPFITOGEN3 was then used to determine the level of representativeness of the ELC categories in the germplasm collection assess (Parra - Quijano et al., 2021). The map was processed in ArcMap 10.7 (ESRI, 2015), QGIS 3.16.8 (QGIS-Development Team, 2021) and DIVA-GIS 7.5 (Hijmans et al., 2012) at a cell size of 10 X 10 km (approximately 5 arc minutes). The ELC map was classified into quartiles, based on the frequencies of the ELC map, using the ELC zones in the ELC map. The frequency categories were low, mid- low, mid- high and high. 'Null' was used to classify zones where occurrence data were absent. The gaps in *ex situ* conservation were obtained by comparing the diversity present in *ex situ* accessions with that diversity that occurs in the wild (Contreras-Toledo et al., 2019).

Results

CWR Checklist Compilation and Overview

A total of 27 CWR were prioritized out of the 38 CWR taxa. The number of CWR related to edible yam species are 17 for the Greater/water yam (*D. alata* L.), 5 for Aerial yam (*D. bulbifera* L.), 25 for Yellow Guinea yam (*D. cayanensis* Lam), 5 for Bitter yam [*D. dumetorum* (Kunth) (Pax.)], 5 for Lesser/ Asiatic yam (*D. esculenta* (Lour) Burkill), 12 for White Guinea yam (*D. rotundata* Poir.) and one for *D. trifida* L. (Fig. 1). Three CWR are nationally endemic to Madagascar and include *D. antaly* Jum. & H. Perrier, *D. inopinata* Prain & Burkill and *D. transversa* R. Br. Twenty eight CWR (73.7%) are regionally endemic – 15 are endemic to Africa, 13 are endemic to Asia, while 7 are cosmopolitan (Fig. 2).

Priority taxa

Based on the opinion of the experts consulted, a consensus was reached to prioritize 27 out of the 38 CWR taxa. Regarding the global threat status of the priority CWR, thirteen are Least Concern, two (*D. hamitonii* Hook. F. and *D. nummularia* Lam) are Near Threatened, one; *D. brevipetiolata* Prain & Burkill is Vulnerable, one (*D. pynaertii* De Wild) is Data Deficient, while ten are Not Evaluated (IUCN, 2023). Twenty four of the priority CWR belong to the secondary genepool (GP2), *D. baya* De Wild and *D. burkillana* J. Miegé belong to the tertiary genepool (GP3), and *D. hispida* Dennst belongs to the primary genepool (GP1b) (Table 1)

Table 1

Thirty eight Priority CWR, their related crops, genepool concept level and previous known uses in Crop Improvement

S/N	Crop	Priority CWR	Concept Level	Uses in Crop Improvement
1	Greater yam/Water yam (<i>D. alata</i> L.)	<i>Dioscorea brevipetiolata</i> Prain & Burkill	Secondary	
		<i>Dioscorea calcicola</i> Prain & Burkill	Secondary	
		<i>Dioscorea cirrhosa</i> Lour.	Secondary	
		<i>Dioscorea decipiens</i> Hook. f.	Secondary	
		<i>Dioscorea glabra</i> Roxb.	Secondary	
		<i>Dioscorea hamiltonii</i> Hook. f.	Secondary	
		<i>Dioscorea inopinata</i> Prain & Burkill	Secondary	
		<i>Dioscorea lanata</i> Bail	Secondary	
		<i>Dioscorea nummularia</i> Lam.	Secondary	Disease resistance (USDA, 2023)
		<i>Dioscorea oryzetorum</i> Prain & Burkill	Secondary	
		<i>Dioscorea schimperiana</i> Hochst. ex Kunth	Secondary	
		<i>Dioscorea transversa</i> R. Br.	Secondary	
<i>Dioscorea wallichii</i> Hook.f.	Secondary			
2	Aerial yam (<i>D. bulbifera</i> L.)	<i>Dioscorea arachidna</i> Prain & Burkill	Secondary	
		<i>Dioscorea pentaphylla</i> L.	Secondary	
3	Yellow Guinea yam (<i>D. cayanensis</i> Lam)	<i>Dioscorea baya</i> De Wild	Tertiary	
		<i>Dioscorea burkilliana</i> J.Miege	Tertiary	

S/N	Crop	Priority CWR	Concept Level	Uses in Crop Improvement
		<i>Dioscorea praezensilis</i> Benth.	Secondary	
		<i>Dioscorea sagittifolia</i> Pax	Secondary	
4	Bitter yam [<i>D. dumetorum</i> (Kunth) (Pax.)]	<i>Dioscorea antaly</i> Jum. & H.Perrier	Secondary	
		<i>Dioscorea hispida</i> Dennst	Primary	
5	White Guinea yam (<i>D. rotundata</i> Poir.)	<i>Dioscorea abyssinica</i> Hochst. ex Kunth	Secondary	Yam mosaic virus and anthracnose resistance (Lopez- Montes et al., 2012; USDA, 2023)
		<i>Dioscorea burkilliana</i> J.Miege	Secondary	Growth habit and gene transfer (fertility) (USDA, 2023)
		<i>Dioscorea mangelotiana</i> J. Miege	Secondary	
		<i>Dioscorea minutiflora</i> Engl.	Secondary	
		<i>Dioscorea praezensilis</i> Benth.	Secondary	Crop quality and Disease resistance (USDA, 2023)
		<i>Dioscorea pynaetii</i> De Wild	Secondary	
		<i>Dioscorea smilacifolia</i> De Wild. & T. Durand	Secondary	
		<i>Dioscorea togoensis</i> R. Knuth	Secondary	

Diversity Analysis of Priority CWR

A total of 18,577 occurrence records were collated for the 27 global yam priority CWR, however, 8,812 records were retained after data verification and quality check was carried out. 6446 occurrence records were collated from GBIF, 2,116 from IUCN, 27 from GENESYS, 200 from RainBio, 20 from The Herbarium Catalogue, Royal Botanic Gardens, Kew, while two records were sourced from New York Botanical Garden (NYBG). The number of occurrence records for each priority CWR ranged from two to 2896. *D. transversa* R. Br., *D. praezensilis* Benth and *D. pentaphylla* L. have the highest number of records (1229), while *D. calcicola* Prain & Burkill, *D. inopinata* Prain & Burkill and *D. lanata* Bail have the least, two, six and eight, respectively (Table S1). Of the 8,812 occurrence records, 626 (7.10%) were genebank accessions (Table S2). These accessions were mainly sourced from the Thailand Institute of Scientific and Technological Research, Dodo Creek Research station (Solomon Island), Southern Regional Centre Laloki (NARI) (Papua New Guinea), International Crop Research Institute for the Semi- Arid Tropics (India), and Faculte des Sciences et Techniques (Benin).

Diversity, hotspots and complementary analyses

Hotspots were found in Nzerekore region of Guinea, Nimba and Grand Gedeh regions of Liberia, Montagnes, Sassandra- Marahouse, and Bas – Sassandra regions of Cote d'Ivoire, Volta, Greater Accra and Eastern regions of Ghana, Centrale and Plateau regions of Togo, Donga, Oueme, Atlantique, Littoral and Plateau provinces of Benin, South West zone of Nigeria, Es region of Cameroon, Sangha- Mbaere region of Central Africa Republic, Likouala and Sangha regions of Congo, and Shan province of Myanmar and Thailand (Fig. 4). Species richness was highest in Thailand (Fig. 5). Apart from Thailand in Asia, all the areas of hotspots diversity were in West and Central Africa, this is because these regions have more occurrence records and more priority CWR are native to the regions (Fig. 4). **Fig. 4** Species richness of the 27 global yam priority CWR

The number of ecogeographic variables used in the SDM ranged from 11 in *D. pynaertii* De Wild to 35 in *D. nummularia* Lam (Table S4 and S5). Areas of highest potential diversity were found in Bas – Sassandra, Goh-Djiboua, Lagunes, Lacs, Comoe, Montagnes, Sassandra and Abidjan districts of Cote d' Ivoire, Western, Western North, Ashanti, Central, Eastern, Volta, Brong Ahafo, Ahafo, Bono Eas, Oti West and Greater Accra regions of Ghana, Mono, Oueme, Atlantique and Plateau provinces of Benin, South West, South- South and South East zones of Nigeria, Ogooue- Maritime, Moyen Ogooue and Ngounie regions of Gabon (Fig. 6), Thailand and Cambodia (Figs. 7 and 8). Most areas of predicted richness also corresponds to the area of observed hotspots diversity such as Lacs, Bas – Sassandra, Montagnes and Sassandra districts of Cote d'Ivoire, Volta, Accra and Eastern (Koforidue) regions of Ghana, Mono, Oueme, Littoral, Atlantique provinces of Benin (Figs. 4 and 6).

A total of 13 complementary sites were identified to conserve all priority CWR. Out of these 13, four are located within existing network of PA, two in Asia, one in Africa and one in Oceania (Table 2, Figs. 9 and 10). Eight priority CWR were found in the complementary sites. The complementary sites not located in existing network of PA were found each in Ethiopia, Nigeria, Democratic Republic of Congo and Madagascar in Africa (Fig. 9), two each in India and Thailand and one in Malaysia in Asia (Fig. 10)

Table 2
Complementary sites in PA and the number of CWR and occurrence data recorded

Number in maps	Protected area	Designation	Country	Number of CWR	Number of occurrence records	Priority CWR
1	Sangha Trinational	World Heritage site (natural or mixed)	Central Africa Republic	6	35	<i>D. baya</i> , <i>D. burkilliana</i> , <i>D. mangenotiana</i> , <i>D. praehensilis</i> , <i>D. schimperiana</i> , <i>D. smilacifolia</i>
2	Socotra Archipelago	World Heritage site (natural or mixed)	Yemen	1	6	<i>D. lanata</i>
10	Blue Fig Creek	Nature Refuge	Australia	1	1	<i>D. transversa</i>
11	Namtok Ched Sao Noi	Natural Park	Thailand	0	0	-

Ecogeographic Land Characterization (ELC) map

The number of ecogeographic variables used in the generation of the ELC maps ranged from 10 to 11 among 13 of the global yam priority CWR where ecogeographic diversity were possible (Table S6). The number of ecogeographic categories ranged from 18 in *D. cirrhosa* Lour to 27 in *D. abyssinica* Hochst. ex. Kunth, *D. antaly* Jum. & H.Perrier and *D. baya* De Wild (Table S6). Based on the species specific ELC maps, the *ex situ* gap analysis showed that the average of 14.09% of the ecogeographic diversity of 13 of the global yam priority CWR for which ecogeographic diversity analysis was possible, is not conserved *ex situ* (Figs. S1 to S13, Table S7, S8 and S9). Similarly, 79% of the ecogeographic diversity of 13 of the 27 global yam priority taxa is not conserved *in situ* (Table S10). *Dioscorea schimperiana*, *D. praehensilis* and *D. hispida* have the highest frequencies of ELC categories in PA, while ELC categories 8, 7 and 11 have the highest total frequencies in PAs (Table S10). Similarly, *D. transversa*, *D. praehensilis* and *D. abyssinica* have the highest frequencies of ELC categories in *ex situ* collections, while ELC categories 11, 18 and 4 have the highest total frequencies *ex situ* (Table S8)

In situ gap analysis

Analysis of the occurrence data showed that 4.87% (430) of the total occurrence records were found in PA (Table S2). Taxa populations were present only in three complementary sites in PA; Sangha Trinational, Socotra Archipelago and Blu Fig Creek (Table 3). The CWR present in the complementary sites in PA are *D. baya*, *D. burkilliana*, *D. mangenotiana*, *D. praehensilis*, *D. schimperiana*, *D. smilacifolia*, *D. lanata* and *D. transversa*. The CWR not found in PA are *D. antaly*, *D. calcicola*, *D. inopinata*, *D. pynaertii* and *D. sagittifolia* (Table 11). Two complementary sites in PA are found in Asia, while one each were in Africa and Oceania, respectively. Protected areas with the highest number of populations are Sugarloaf (77), Yanganmbi (54) and Great Sandy (42). Dong Phayayen Khao Yai Forest Complex (7), Sangha Trinational (6) and Lamto Scientific

Reserve (5) had the highest number of CWR (Table S11). Although six priority CWR did not occur in any PA, 10.8% (4) of the taxa were present in ≥ 5 PA, while the remaining 85.2% (23) were found in less than five different PA (Table S11). Similarly, 37.04% (10) of the taxa had < 5 populations in network of PA (Table S2). *Dioscorea transversa*, *D. smilacifolia* and *D. minutiflora* had the highest number of populations in PA, with 427, 42 and 30 records, respectively (Table S11). Similarly, *D. transversa*, *D. smilacifolia* and *D. minutiflora* occurred in more PA, occurring in 37, 6 and 5 PA, respectively. Protected areas with yam wild relatives were found in 17 countries. Countries with the highest number of PA with taxa are Australia, with 37 PA, followed by Thailand, Guinea and DR Congo, with three PA each. Population of priority wild yams were found in 60 PA. Australia, Congo (the Democratic Republic of) and Congo (the) had the highest number of population in PA, with 247, 56 and 38, respectively (Table S12).

Ex situ gap analysis

The SDM of 23 priority CWR passed the validation criteria, however, for the other 3 taxa *D. inopinata* Prain & Burkill, *D. lanata* Bail and *D. pynaertii* De Wild, a CA50 buffer area was created around each presence point (Table S1). 14.8% (4) of priority taxa have at least 50 accessions in genebank, while 62.963% (17) were underrepresented in genebanks, with less than 50 accessions conserved *ex situ*. *Dioscorea praeheensis* Benth, *D. minutiflora* Engl. and *D. pentaphylla* L. have the highest number of accessions in genebanks, with 112, 70 and 60 accessions, respectively. Among all the countries with occurrence data, 34 countries have genebank accessions conserved *ex situ*. However, 18.5% (5) of the taxa are not represented in *ex situ* collections. These are *D. calcicola*, *D. inopinata*, *D. lanata*, *D. pynaertii* and *D. transversa*. Areas of further *ex situ* collection were identified in Mali, Liberia, Cote d' Ivoire, Ghana, Togo, Cameroon, Angola, Ethiopia, Madagascar in Africa (Fig. 11), India, Thailand, Lao People's Democratic Republic, Vietnam and Cambodia (Figs. 12 and 13). Only five taxa do not require further *ex situ* collection and include *D. glabra*, *D. hispida*, *D. minutiflora*, *D. pentaphylla* and *D. praeheensis*, because they have at least 50 accessions represented in genebanks (Table S2). 81% (22) of the priority taxa were conserved *ex situ*, however, only 7.10% (626) accessions from 81% (22) of the priority CWR were represented in *ex situ* collections (Table S2)

Discussion

The global yam genepool diversity comprises yam CWR endemic to Africa, Asia, Oceania and Cosmopolitan taxa. This study focuses on the development of a conservation strategy for global yam wild relatives. Our findings suggest there existing *ex situ* conservation of global yam wild relatives, but major gaps still exist in *ex situ* collections and there virtually no active *in situ* conservation. Therefore, the global yam genepool requires urgent active safeguarding to ensure its maintenance and availability for crop improvement. (Maxted et al., 2015; Mburu et al., 2016). The highest number of observations and number of occurrences are found in Australia and Benin and this is attributed to high level of sampling in recent years in the two countries. However, the least number of records were found in Eritrea, Niger, Chad and South Sudan. Field survey should be conducted in these countries with few occurrence records to ensure adequate data are available for enhanced conservation planning.

The high priority CWR observed diversity, identified in some areas such as Montagnes, Sassandra – Marahouse, and Bas- Sassandra regions of Cote d' Ivoire, Volta, Greater Accra and Eastern regions of Ghana,

Donga, Oueme, Atlantique, Littoral and Plateau provinces of Benin, South West zones of Nigeria, Est region of Cameroon, Likouala and Sangha regions of Congo, Thailand is due to the relatively high number occurrence data associated with those areas. The areas of observed hotspot diversity are in congruence with the biodiversity hotspots of the world (Conservation International, 2008). The observed hotspot diversity areas in West Africa are within the Guinean forest, while the areas in Thailand corresponds with the Indo-Burma, India and Myanmar biodiversity hotspots. These two diversity hotspots are among 36 biodiversity hotspots and agricultural centres of origin of the world (Conservation International, 2007). The Guinean forest extends from Guinea, Sierra Leone, Liberia, Cote d' Ivoire, Ghana, Togo and Nigeria, while the Indo-Burma, India and Myanmar biodiversity hotspot spans from Myanmar, Thailand, Cambodia, Vietnam, India and China. To qualify as a biodiversity hotspot, an area must have at least 1500 endemic vascular plants and loss at least < 70% of its original vegetation (Hoffman et al., 2016). Most areas of predicted distribution also correspond with the areas of hotspot diversity such as Lacs, Bas – Sassandra and Montagnes districts of Cote d' Ivoire, Volta, Accra and Eastern (Koforidue) regions of Ghana, Mono, Oueme, Littoral and Atlantique provinces of Benin (Figs. 4 and 6). For a comprehensive conservation of priority CWR, complementary analysis is required (Fielder et al., 2015; Contreras-Toledo et al., 2019). Similarly, Namtok Ched Sao Noi, Natural Park, Thailand, a reserve sites in PA is located within the Indo-Burma, India and Myanmar biodiversity hotspots (Conservation International, 2007). Complementary analysis has been used to identify priority locations in regions such as Southern Africa Development Commission (SADC) (Magos Brehm et al., 2022) and Middle East (Zair et al., 2021). Establishment of the four complementary sites in PA and the other 9 outside PA will help strengthen the *in situ* conservation of the global yam priority CWR.

The identification of conservation gaps in the ecogeographic diversity of the global yam priority CWR will initiate and facilitate the germplasm collection *and ex situ* conservation of taxa with ecogeographic diversity gaps to ensure their effective representation in *in situ* and *ex situ* conservation (Magos Brehm et al., 2022). *Ex situ* collection should be prioritized for *D. arachidna* Prain & Burkill, *D. cirrhosa* Lour, *D. schimperiana* Hochst. ex. Kunth found in few ELC categories and that of the 14 priority CWR where ELC map analysis were not possible. Similarly, the ecogeographic diversity of *D. hispida* Dennst. *and D. minutiflora* Engl. found in few ELC categories and that of the 14 priority CWR where ELC map analysis were not possible should be given priority for *in situ* conservation.

Complementary analysis was used to identify priority sites within existing PA for *in situ* conservation of priority CWR in regions such as; Southern Africa (Magos Brehm et al., 2022), Middle East (Zair et al., 2021) and West Africa (Nduche et al., 2022). However, for yam CWR, the number of CWR not conserved in PA *in situ* is large (95.5%) (Table S11). This is inconsistent with the report by Magos Brehm et al. (2022) and Nduche et al. (2022), where only 19% and 37.3% of the regional priority CWR occurred outside the PA network. For the taxa not represented in PA, 23 taxa that had less than five populations in PA and the five priority CWR that did not occur in any PA, further field survey should be conducted to discover if this is a true reflection of yam CWR occurrence. The taxa absent in PA include *D. antaly*, *D. calcicola*, *D. inopinata*, *D. pynaertii* and *D. sagittifolia*. Also, for the countries with occurrence data but had no taxa in PA, more collection programmes should be implemented as this is likely to increase the number of taxa in PA. Among the priority CWR found in PA are *D. abyssinica* and *D. praezensilis*, with confirmed uses in the improvement of White Guinea yam against resistance for yam mosaic virus (Lopez- Montes et al., 2012) and potential use for adapting White Guinea yam and yellow yam to biotic stress (Kikuno et al., 2011a).

The number of CWR not already conserved *ex situ* is 5 (19%), relatively low, compared to the number of germplasm represented in genebanks. This is inconsistent with the findings by Zair et al. (2021); Magos Brehm et al. (2022) and (Nduche et al., 2022) where 30%, 50% and 71.6% of priority CWR were not represented in *ex situ* collections. Similarly, FAO (2010a) reported that about 15,903 accessions of yams and their wild relatives are conserved in 99 facilities of 57 countries. However, 81.4% (22) of the priority taxa requires further *ex situ* collection, because of their low representation (< 5 populations) in genebanks. This entails an active collaborative collection programme from stakeholders such as genebank curators, plant breeders, protected area managers, conservation park rangers, farmers and herbarium curators to ensure effective representation of the underrepresented taxa in genebanks. Priority should be given to those taxa not conserved *ex situ*, which are *D. calcicola*, *D. inopinata*, *D. lanata*, *D. pynaertii* and *D. transversa*, where *ex situ* conservation gaps were identified at the taxon and ecogeographic diversity levels.

Based on the result of this work, the recommendations for the global genepool conservation strategy for yam are:

1. Conduct field work in the PA predicted to have suitable habitat for species but for which occurrence data were not found (Table S3).
2. Verify the suitability and accessibility of the recommended genetic reserves, including the soil fertility, topography and location of the sites. Establish four new genetic reserves within PA in the four countries, (Sangha Trinational, Central Africa Republic; Socotra Archipelago, Yemen; Namtok Ched Sao Noi, Thailand; and Blue Fig Creek, Australia), to actively conserve the priority CWR. Also, establish genetic reserve outside existing PA for the nine sites in seven countries (Ethiopia, Nigeria, Democratic Republic of Congo, Madagascar, India, Thailand and Malaysia), for active *in situ* conservation of the global yam priority CWR. Improve the population management quality of the four reserves in PA for optimal and active safeguarding of the priority taxa.
3. Conduct field survey for the six taxa (*Dioscorea antaly* Jum. & H. Perrier, *Dioscorea calcicola* Prain & Burkill, *D. inopinata*, *D. nummularia* Lam., *D. pynaertii* and *D. sagittifolia*) absent in the network of PA and 10 taxa with < 5 populations in PA (*D. arachidna* Prain & Burkill, *D. brevipetiolata* Prain & Burkill, *D. cirrhosa* Lour, *D. decipiens* Hook. f., *D. hamiltonii* Hook. f., *D. hispida* Dennst., *D. mangelotiana*, *D. oryzetorum* Prain & Burkill, *D. togoensis* R. Knuth and *D. wallichii* Hook. f.) to ensure their *in situ* and *ex situ* conservation.
4. Prioritize the germplasm collection of the five taxa not represented *ex situ* (*D. cirrhosa*, *D. inopinata*, *D. lanata*, *D. pynaertii* and *D. transversa*), 17 taxa underrepresented in genebanks (*D. abyssinica*, *D. antaly*, *D. arachidna*, *D. baya*, *D. brevipetiolata*, *D. burkilliana*, *D. cirrhosa*, *D. decipiens*, *D. hamiltonii*, *D. mangelotiana*, *D. nummularia*, *D. oryzetorum*, *D. sagittifolia*, *D. schimperiana*, *D. smilacifolia*, *D. togoensis* and *D. wallichii*) to enhance their effective *ex situ* representativeness. Also, more *ex situ* techniques such as cryopreservation, and *in vitro* storage should be used in the preservation of CWR accessions.
5. Identify and prioritize taxa in ELC zones with low frequencies (Tables S8 and S10) through ELC map tool analysis to ensure that all ELC categories are conserved both *in situ* and *ex situ* (Parra - Quijano et al., 2021).
6. Periodically, review and update the results of this study and the recommendations, especially if there are new goals in the conservation priorities, more occurrence data, recent species distribution modelling techniques and advanced ecogeographic analysis tools.

Conclusion

The bases for a global genepool conservation strategy for yam was developed in this study. The six taxa absent in the existing network of PA and the 10 taxa with < 5 populations were prioritized for urgent *in situ* and *ex situ* conservation. Similarly, the four priority CWR with less than ten occurrence data, the five taxa not represented *ex situ*, and 17 taxa under-represented in genebanks should be prioritized for germplasm collection and preservation. Establishment of the 13 proposed reserve sites will deepen then global conservation effort and priorities for the 27 yam CWR. Also, filling the identified gaps in the conservation of the yam taxa, and implementing the proposed recommendations will facilitate the utilization of the CWR in the modification of their related crops to ensure food security and mitigate climate change. This study will help to guide and consolidate the conservation efforts on the yam genepool *ex situ* collection and predefine the standard for active *in situ* conservation of the crop genepool. The priority CWR can be used as important genetic sources in the improvement of their related crop species.

Declarations

The authors declare that they have no known competing financial or personal interest that could have influenced the reporting of the work.

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References

1. Andres C, AdeOluwa OO, Bhullar GS (2017) Yam (*Dioscorea* spp.). In Brian Thomas, Brian G Murray and Denis J Murphy (Editors in Chief), Encyclopedia of Applied Plant Sciences, Vol 3, Waltham, MA: Academic Press, 2017, pp. 435–441
2. Cao T, Sun J, Shan N, Chen X, Wang P, Zhu Q, Xiao Y, Zhang H, Zhou Q, Huang Y (2021) Uncovering the genetic diversity of yams (*Dioscorea* spp.) in China by combining phenotypic trait and molecular marker analyses. *Ecol Evol* 16(11):9970–9986. 10.1002/ece3.7727 PMID: 34367553; PMCID: PMC8328405
3. Chair H, Cornet D, Deu M, Baco MN, Agbangla A, Duval MF, Noyer JL (2010) Impact of farmer selection on yam genetic diversity. *Conserv Genet* 11(6):2255–2265. <https://doi.org/10.1007/s10592-010-0110-z>

4. Conservation International (2007) Guinean Forests of West Africa. In Biodiversity Hotspots. Accessed June 21, 2022
5. Conservation International (2008) Guinean Forests of West Africa Biodiversity Hotspot Program for Consolidation <https://www.cepf.net/sites/default/files/gfwa-program-for-consolidation-2008>
6. 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 Genetic Resources* 1–11. 10.1017/S1479262118000540
7. Danquah EO, Danquah FO, Frimpong F, Dankwa KO, Weebadde CK, Ennin SA, Asante MO, Brempong MB, Dwamena HA, Addo-Danso A, Nyamekye DR, Akom M, Opoku AY (2022) Sustainable Intensification and Climate-Smart Yam Production for Improved Food Security in West Africa: A Review. *Front. Agron.* 4, <https://doi.org/10.3389/fagro.2022.858114>
8. ESRI (2015) Arcmap for desktop release version 10.4.1. Environmental Systems Research Institute, Redlands, California
9. 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
10. FAO (2001) International Treaty on Plant Genetic Resources for Food and Agriculture. Food and Agriculture Organization of the United Nations, Rome, Italy
11. 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: <http://www.fao.org/agriculture/seed/sow2/en/> Accessed 25 July 2021
12. FAOSTAT (2021) FAOSTAT. URL: <http://www.fao.org/faostat/en/#home> (Accessed March, 2023)
13. 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)
14. Ford-Lloyd BV, Maxted N, Kell SP (2008) Establishing conservation priorities for crop wild relatives. In: Maxted, N., Ford-Lloyd, B.V., Kell, S. P, Iriondo, J., Dulloo, E. & Turok, J.(eds) *Crop Wild Relative Conservation and Use*. CAB International Wallingford, UK pp110- 119
15. GBIF.org, (2020) GBIF Occurrence Download <https://www.gbif.org/occurrence/search> Accessed 24 October 2020
16. Genesys (2020) Global Portal on Plant Genetic Resources, Genesys. <https://www.genesys-pgr.org/welcome>. Accessed 20 November 2020
17. Harlan J (1971) Agricultural origins centers and noncenters. *Science* 174:468–474
18. Harlan JR (1992) *Crops and Man*. American Society of Agronomy, p 2
19. Heywood VH, Dulloo ME (2005) *Situ Conservation of Wild Plant Species – A Critical Global Review of Good Practices*. IPGRI Technical Bulletin No. 11. IPGRI, Rome
20. Hijmans R, Guarino L, Mathur P (2012) DIVA-GIS.7.5.0. <https://www.diva-gis.org/documentation>. Accessed 26 July 2021
21. Hijmans R, Spooner D (2001) Geographic distribution of wild potato species. *Am J Bot* 88:2101–2112
22. Hijmans R, Spooner D (2001) Geographic distribution of wild potato species. *Am J Bot* 88:2101–2112

23. Hoffman M, Koenig K, Bunting G, Costanza J, Williams K (2016) Biodiversity Hotspots (version 2016.1) (Version 2016.1) [Data set]. Zenodo. <http://doi.org/10.5281/zenodo.3261807>
24. IUCN (2021) The IUCN Red List of Threatened Species. Version 2021-3. <https://www.iucnredlist.org>. Accessed on 20 May 2022.
25. IUCN (2023) The IUCN Red List of Threatened Species. Version 2022-2. Accessed February 2023 <https://www.iucnredlist.org>
26. Kikuno H, Kumar PL, Asiedu R, Bhattacharjee R, Gedil M, Sartie A, Otoo E, Dumet D (2011a) Dioscorea. Wild Crop Relatives: Genomic and Breeding Resources Industrial Crops. Springer, Berlin Heidelberg, pp 71–96
27. Kikuno H, Kumar PL, Asiedu RR, Gedil M, Sartie A, Otoo E, Dumet D (2011b) Dioscorea. Wild Crop Relatives: Genomic and Breeding Resources Industrial Crops. Springer, Berlin Heidelberg, pp 71–96
28. Liu C, Berry PM, Dawson TP, Pearson RG (2005) Selecting thresholds of occurrence in the prediction of species distributions. *Ecography* 28:385–393
29. Lopez- Montes A, Bhattacharjee R, Tessema G (2012) Yam breeding at IITA: achievements, challenges and prospects. <http://r4dreview.iita.org/index.php/tag/yam-breeding/>
30. 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. *Divers Distrib*. <https://doi.org/10.1111/ddi.13512>
31. Magos Brehm J, Kell S, Thormann I, Gaisberger H, Dulloo ME, Maxted N (2017) Interactive Toolkit for Crop Wild Relative Conservation Planning. University of Birmingham, Birmingham, UK and Bioversity International, Rome, Italy <http://www.cropwildrelatives.org/conservation-toolkit>
32. 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 Dataverse, V1.
33. Magos Brehm J, Kell S, Thormann I, Maxted N, Dulloo ME (2017) Template for the preparation of a technical background document for a National Strategic Action Plan for the conservation and sustainable use of crop wild relatives. *Univ Birm Bioversity Int*. 10.7910/DVN/VQV
34. Maxted N (2013) *In Situ, Ex Situ* Conservation. *Encyclopedia of Biodiversity (Second Edition)*, Academic Press, pp 313–323, <https://doi.org/10.1016/B978-0-12-384719-5.00049-6>
35. Maxted N, Avagyan A, Frese L, Iriondo J, P KS, Brehm JM, Singer A, E, D (2015) Conservation planning for crop wild relative diversity. In: Redden R, Yadav SS, Maxted N, Dulloo ME, Guarino L, Smith P, Hoboken (eds) *Crop Wild Relatives and Climate Change*. John Wiley & Sons, Inc, NJ., USA, pp 88–108
36. Maxted N, Ford- Lloyd BV, Jury S, Kell SP, Scholten MA (2006) Towards a definition of crop wild relative. *Biodivers Conserv* 15:2673–2685
37. Maxted N, Ford-Lloyd BV, Hawkes JG (1997c) Complementary conservation strategies. In: Maxted N, Ford-Lloyd BV, Hawkes JG (eds) *Plant Genetic Conservation: The In-situ Approach*. Chapman & Hall, London, pp 20–55
38. Maxted N, Ford-Lloyd BV, Kell SP (2008) Crop wild relatives: establishing the context. In: Maxted N, Ford-Lloyd BV, Kell SP, Iriondo J, Dulloo E, Turok J (eds) *Crop Wild Relative Conservation and Use*. CAB International, Wallingford, pp 3–30

39. 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
40. Mburu SW, Koskey G, Kimiti JM, Ombori O, Maingi JM, Njeru EM (2016) Agrobiodiversity conservation enhances food security in subsistence-based farming systems of Eastern Kenya. *Agric & Food Secur* 5:19. <https://doi.org/10.1186/s40066-016-0068-2>
41. Mponya NK, Chanyenga T, Brehm JM, Maxted N (2020) In situ and ex situ conservation gap analyses of crop wild relatives from Malawi. *Genet Resour Crop Evol* 68:759–771
42. Nduche M, Brehm JM, Parra - Quijano M, Maxted N (2022) In-situ and ex-situ conservation gap analyses of West African priority crop wild relative. *Genetic Resour Crop evolution* 70:333–351
43. Parra-Quijano M, Iriondo JM, Torres E (2012a) Ecogeographical land characterization maps as a tool for assessing plant adaptation and their implications in agrobiodiversity studies. *Genet Resour Crop Evol* 59:205–217
44. Parra-Quijano M, Iriondo JM, Torres E (2012b) Improving representativeness of genebank collections through species distribution models, gap analysis, and ecogeographical maps. *Biodivers Conserv* 21:79–96
45. Parra - Quijano M, Iriondo JM, Torres M, López E, Maxted F, Kell N (2021) S.P., CAPFITOGEN3: A toolbox for the conservation and promotion of the use of agricultural biodiversity. Bogotá, Colombia, pp 45–194 <http://www.capfitogen.net/en/>. Accessed 23 December 2021
46. Phillips S, Anderson R, Schapire R (2006) Maximum entropy modelling of species geographic distributions. *Ecol Model* 190(3–4):23
47. Pimentel D, Wilson C, McCullum C, Huang R, Dwen P, Flack J, Tran Q, Saltman T, Cliff B (1997) Economic and environmental benefits of biodiversity. *Bioscience* 47:747–757
48. POWO (2021) Plants of the World Online. Facilitated by the Royal Botanic Gardens, Kew. Published on the Internet; <http://www.plantsoftheworldonline.org/> Retrieved 17 October 2021
49. QGIS-Development Team (2021) QGIS 3.16. 8 Geographic Information System Open Source Geospatial Foundation Project. <http://qgis.osgeo.org>
50. Ramirez-Romero R, Garibay-Benitez D, Vargas-Ponce O, Joyce A, Bernal JS (2019) Do assortative mating and immigrant inviability help maintain population genetic structuring of an herbivore on a crop and a wild relative? *Insect Sci* 26:283–296
51. Ramírez-Villegas J, Khoury K, Jarvis A, Debouck DG, L G (2010) A gap analysis methodology for collecting crop genepools: a case study with Phaseolus beans. *PLoS ONE* 5:e13497
52. Ramírez-Villegas J, Khoury K, Jarvis A, Dg D, Guarino L (2010) A gap analysis methodology for collecting crop genepools: a case study with phaseolus beans. *PLoS ONE* 5:E13497
53. Saini H, Kashihara Y, Lopez- Montes AJ, 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
54. Scarcelli N, Cubry P, Akakpo R, Thuillet AC, Obidiegwu J, Baco MN, Otoo E, Sonké B, Dansi 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. *Sci Adv* 5(5):eaaw1947.
<https://doi.org/10.1126/sciadv.aaw1947>
55. 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
Accessed 18 June 2022
 56. Sharif BM, Burgarella C, Cormier F, Mournet P, Causse S, Van KN, Kaoh J, Rajaonah MT, Lakshan SR, Waki J, Bhattacharjee R, Badara G, Pachakkil B, Arnau G, Chair H (2020) Genome-wide genotyping elucidates the geographical diversification and dispersal of the polyploid and clonally propagated yam (*Dioscorea alata*). *Ann Botany* 126(6):1029–1038. <https://doi.org/10.1093/aob/mcaa122>
 57. Stolton S, Maxted N, Ford-Lloyd B, Kell SP, Dudley N (2006) Food stores: using protected areas to secure crop genetic diversity. WWF Arguments for protection series. WWF, Gland, Switzerland
 58. Sugihara Y, Darkwa K, Yaegashi H, Natsume S, Shimizu M, Abe A, Hirabuchi A, Ito K, Oikawa K, Tamiru-Oli M, Ohta A, Matsumoto R, Agre P, Koeyer DD, Pachakkil B, Yamanaka S, Muranaka S, Takagi H, White B, Asiedu R, Innan H, Asfaw A, Adebola P, Terauchi R (2020) Genome analyses reveal the hybrid origin of the staple crop white Guinea yam (*Dioscorea rotundata*). *PNAS* 117(50):31987–31992.
<https://doi.org/10.1073/pnas.2015830117>
 59. The Plant List (2013) Version 1.1. Published on the Internet; <http://www.theplantlist.org/> (Accessed 08 May 2023)
 60. Thormann I, Kell S, Magos Brehm J, Dulloo E, N M (2017) CWR checklist and inventory data template, v1. Harvard Dataverse, v 4.
 61. UNEP-WCMC, (2019) The World Database on Protected Areas (WDPA), Cambridge, UK.
<https://www.protectedplanet.net/>. Accessed 9 Jan 2022
 62. USDA (2023) Agricultural Research Service, National Plant Germplasm System. Germplasm Resources Information Network (GRIN Taxonomy). National Germplasm Resources Laboratory, Beltsville, Maryland. URL: <https://npgsweb.ars-grin.gov/gringlobal/taxon/taxonomysearchcwr>. Accessed 14 July 2023
 63. Vincent H, Amri A, Castaneda-Alvarez NP, 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
 64. Vincent H, Wiersema J, Kell S, Fielder H, Dobbie S, Castañeda-Álvarez NP, Guarino L, Eastwood R, León B, Maxted N (2013a) A prioritized crop wild relative inventory to help underpin global food security. *Biology Conserv* 167:265–275
 65. Vincent H, Wiersema J, Kell S, Fielder H, Dobbie S, Castañeda-Álvarez NP, Guarino L, Eastwood R, León B, Maxted N (2013b) A prioritized crop wild relative inventory to help underpin global food security. *Biology Conserv* 167:265–275
 66. Wanasundera J, Ravindran G (1994) Nutritional assessment of yam (*Dioscorea alata*) tubers. *Plant Foods Hum Nutr.* Jul;46(1):33 – 9. 10.1007/BF01088459. PMID: 7971785
 67. Zair W, Maxted N, Brehm M, Amri J, A (2021) Ex-situ and in situ conservation gap analysis of crop wild relative diversity in the Fertile Crescent of the Middle East Genetic Resources and Crop Evolution. 68:693–709

Figures

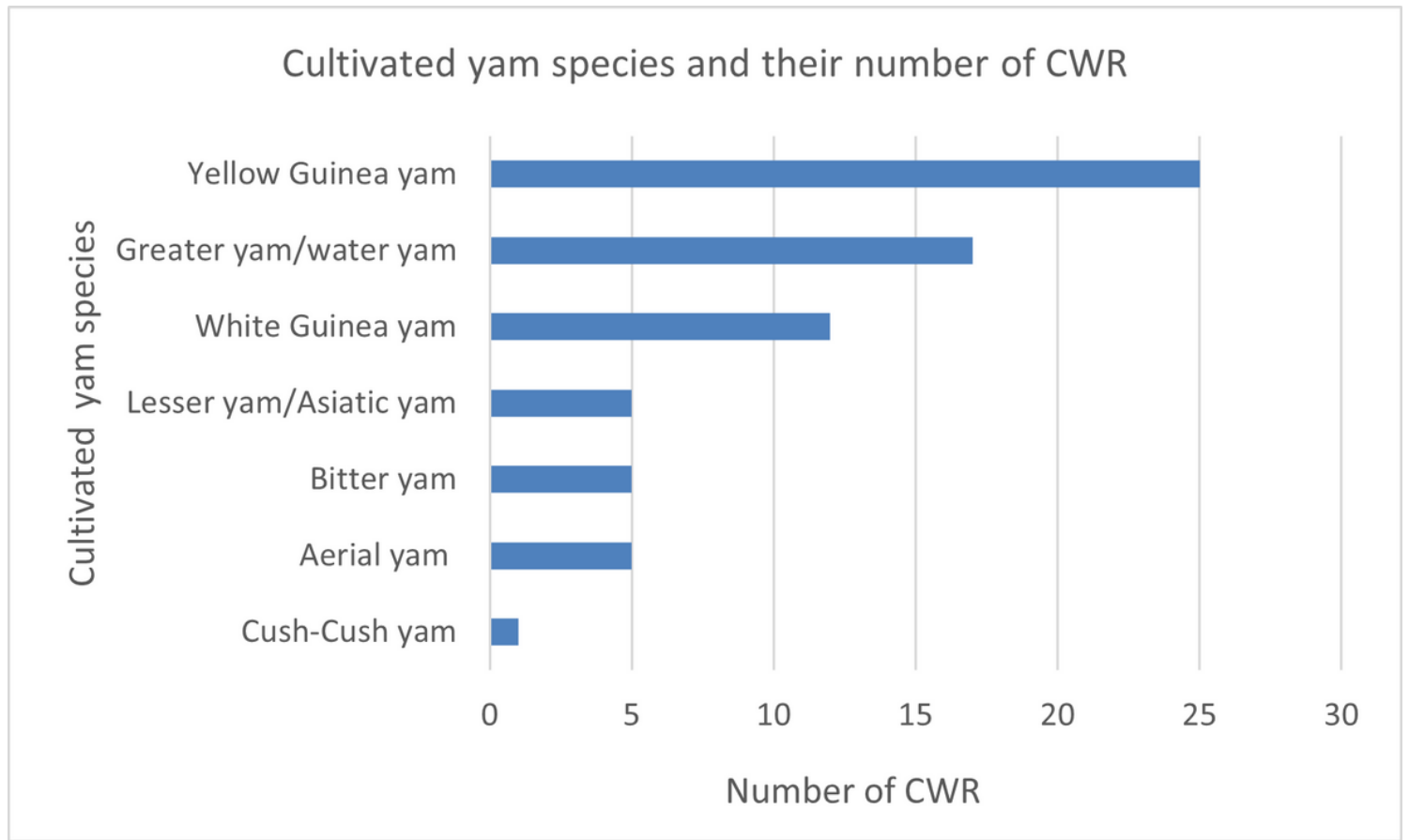


Figure 1

Cultivated yam species and number of their priority CWR

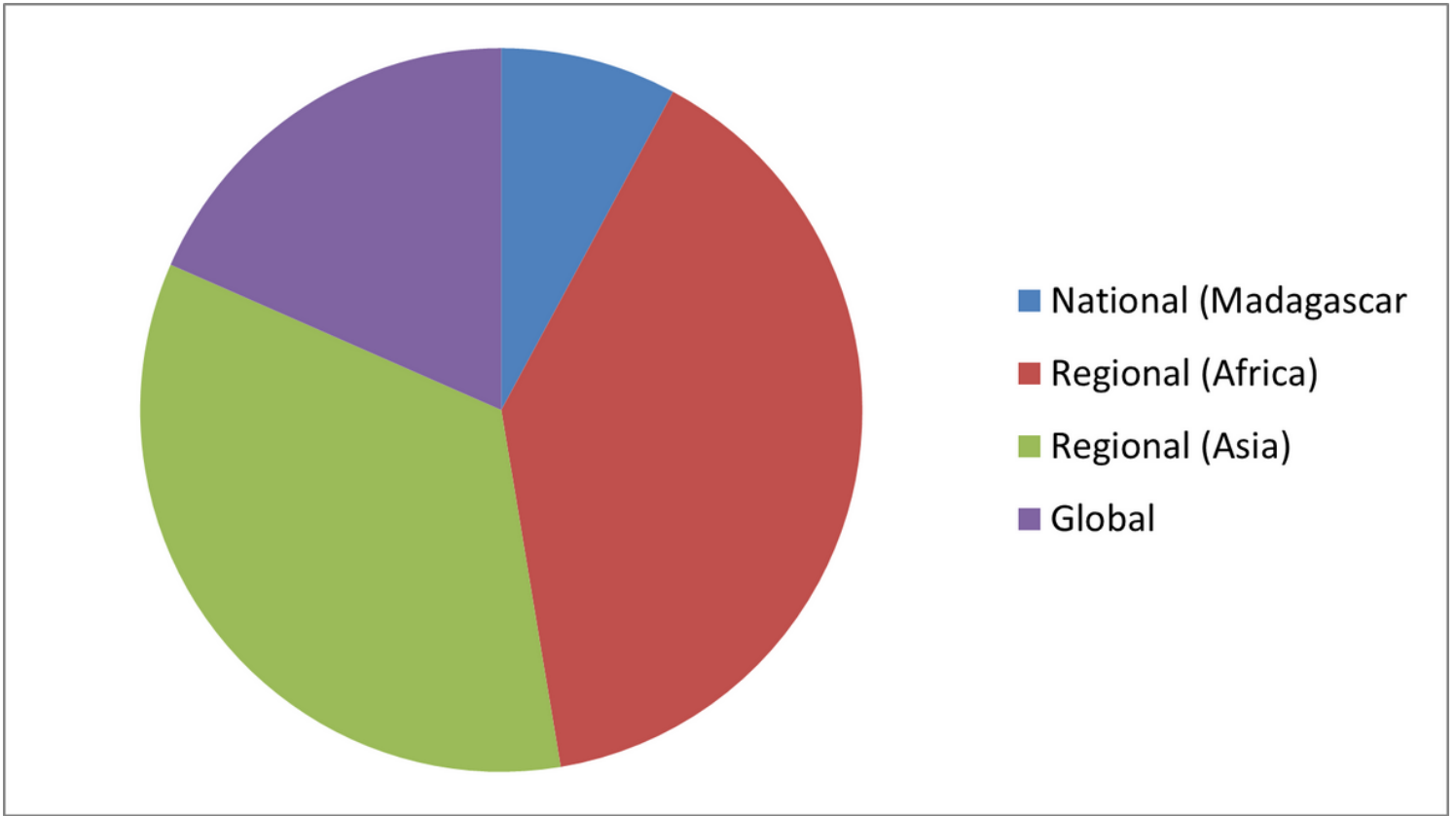


Figure 2

Percentage of endemism of global yam priority CWR

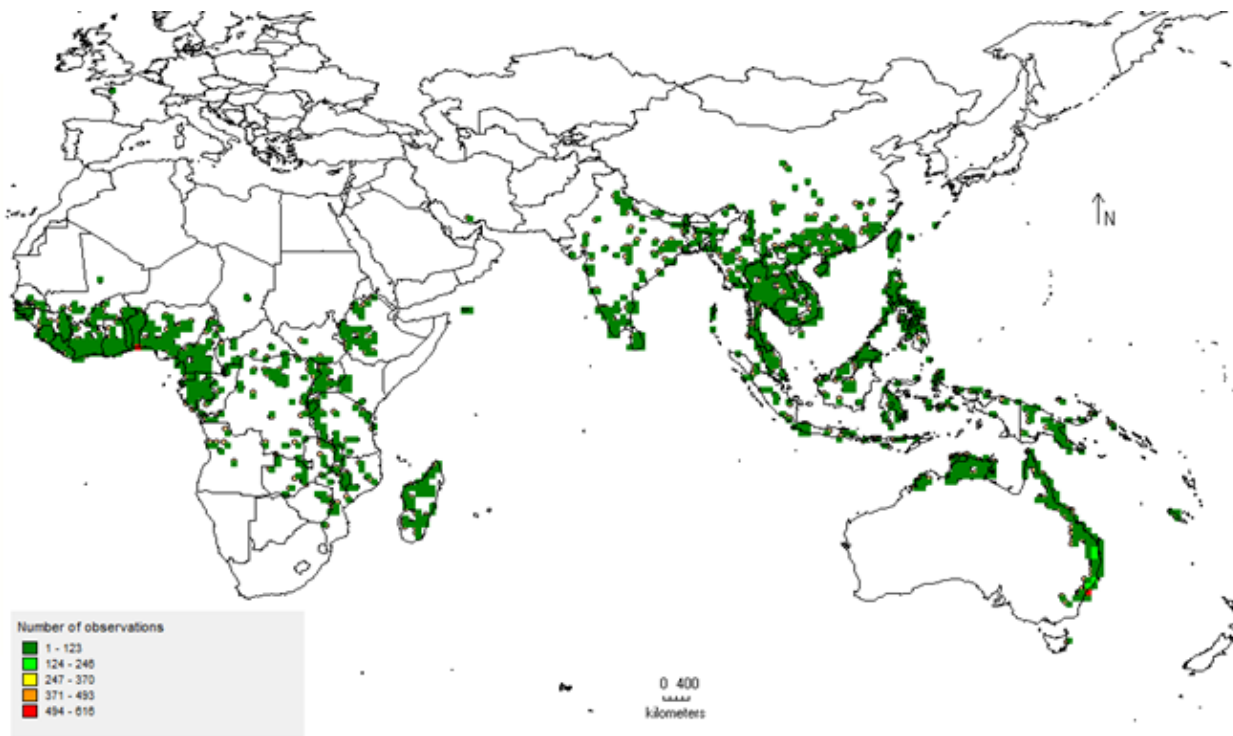


Figure 3

Number of observations of the 27 priority CWR in Africa, Asia and Oceania

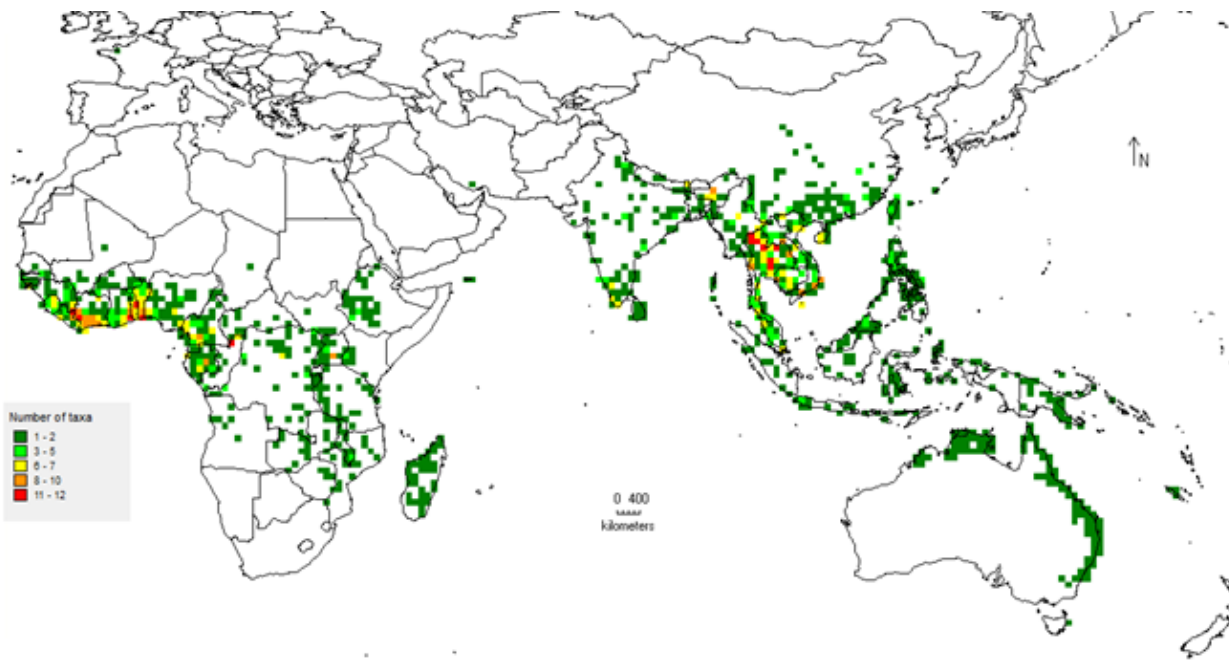


Figure 4

Species richness of the 27 global yam priority CWR

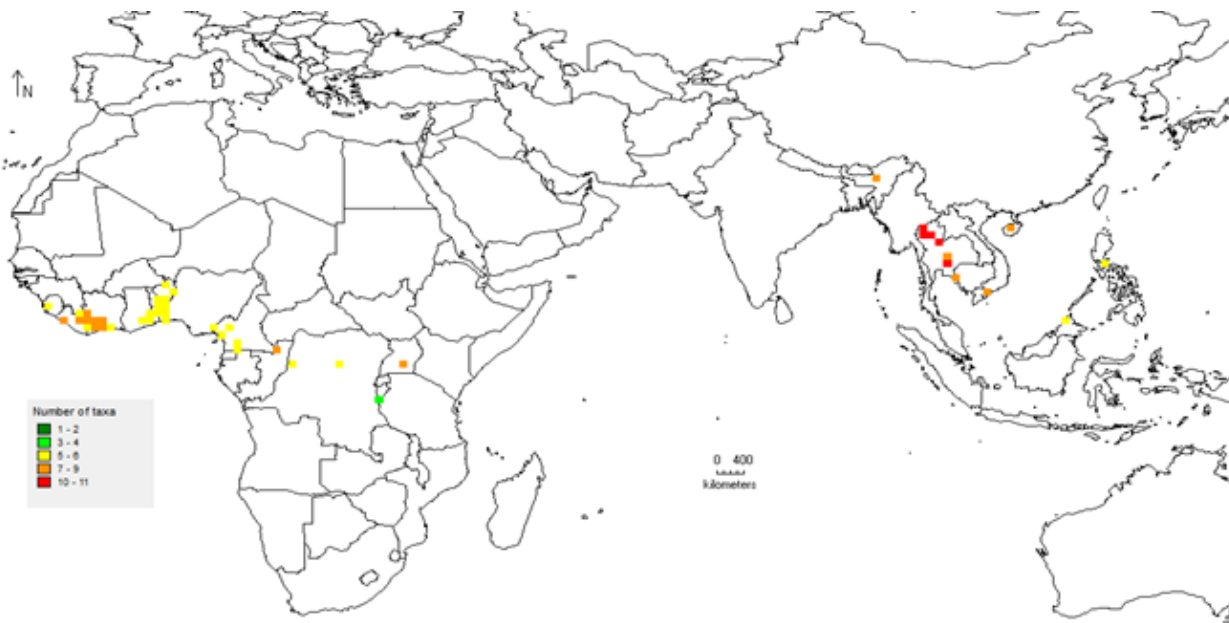


Figure 5

Species richness rarefaction of the 27 global yam priority CWR

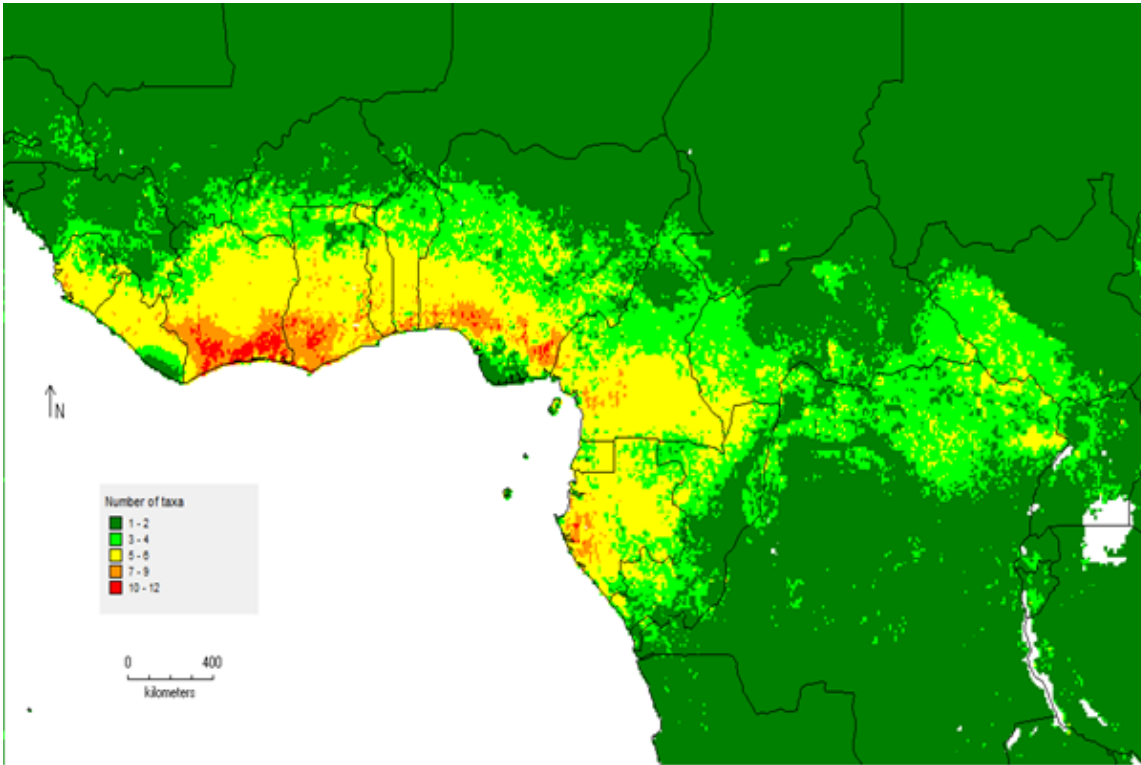


Figure 6

Taxa richness based on predicted distribution of the 27 global yam priority CWR for Africa

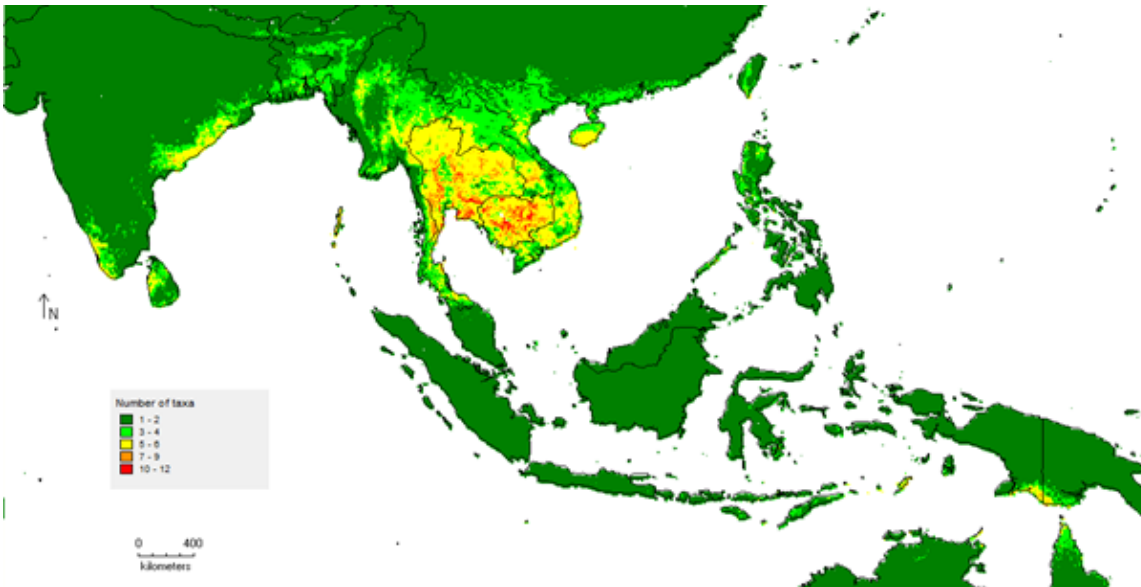


Figure 7

Taxa richness based on predicted distribution of the 27 global yam priority CWR for Asia and Oceania

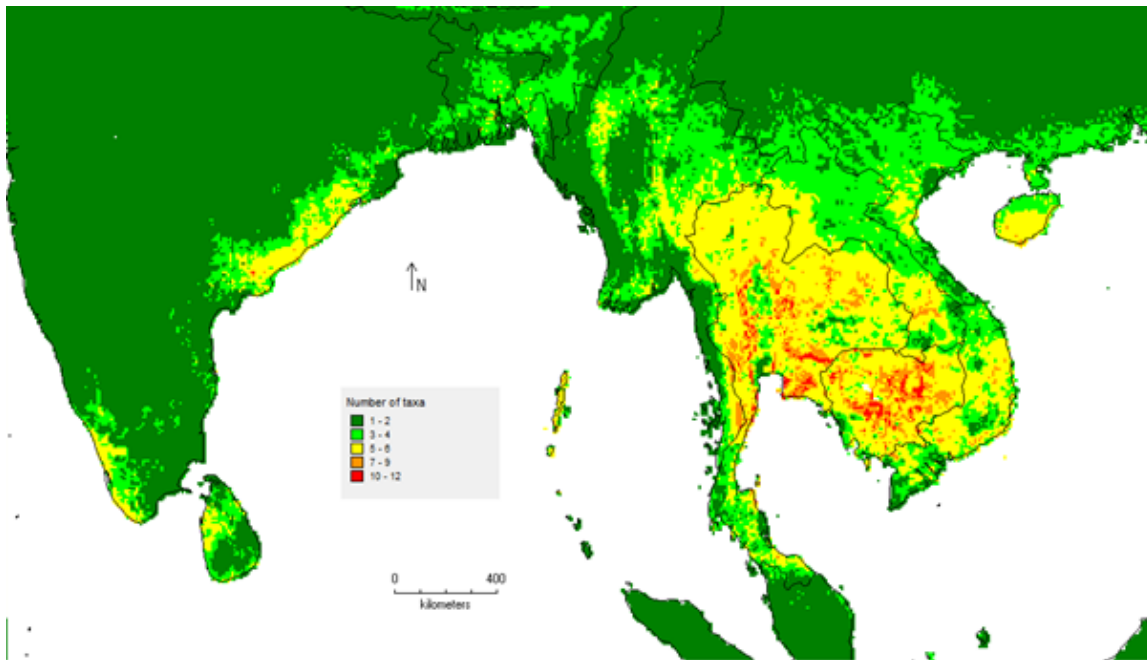


Figure 8

Taxa richness based on predicted distribution of the 27 global yam priority CWR for Asia

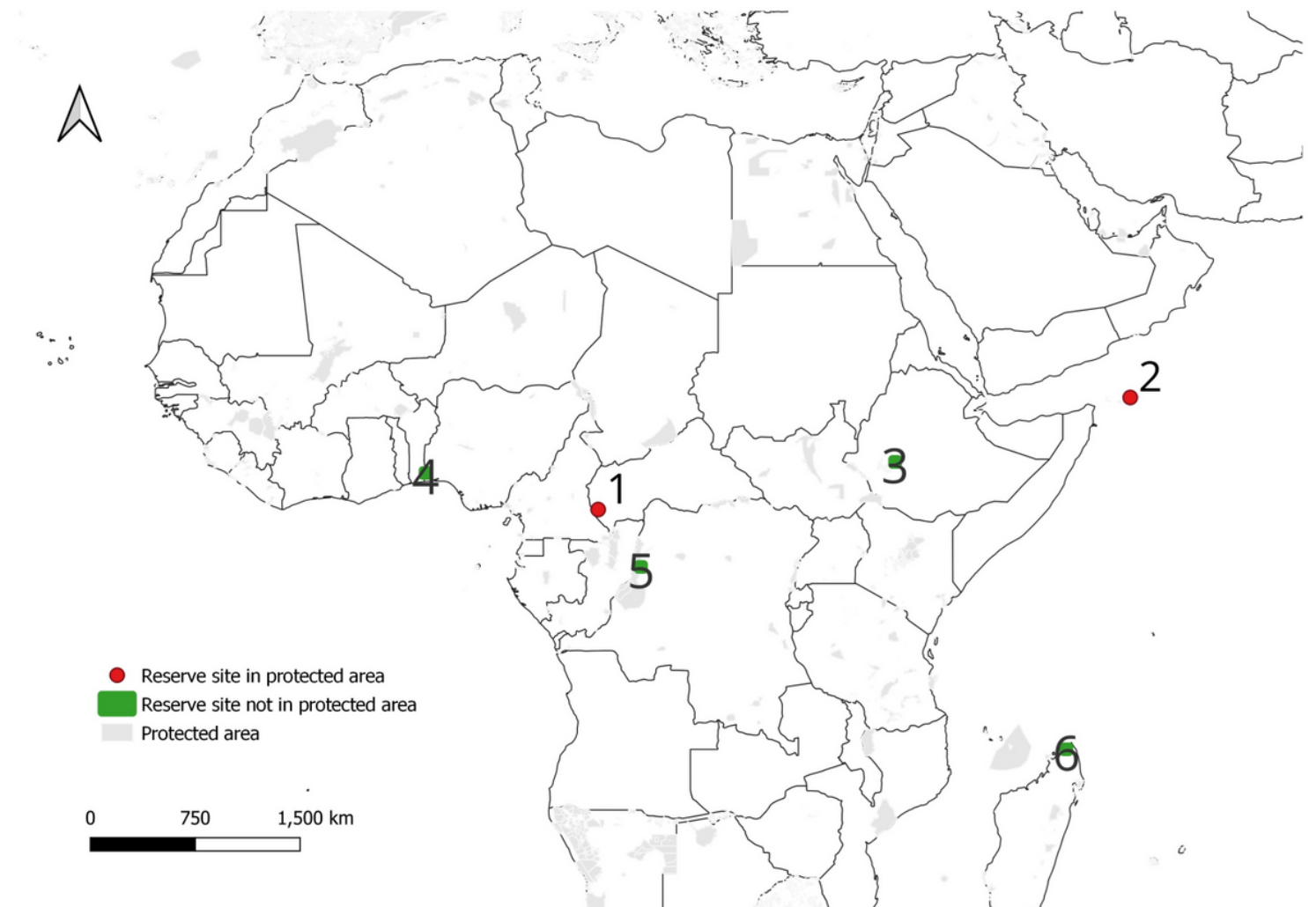


Figure 9

Complementary analysis showing six potential sites for implementing genetic reserve for active conservation of global yam priority CWR in Africa. Grid cell is 50 X 50 km

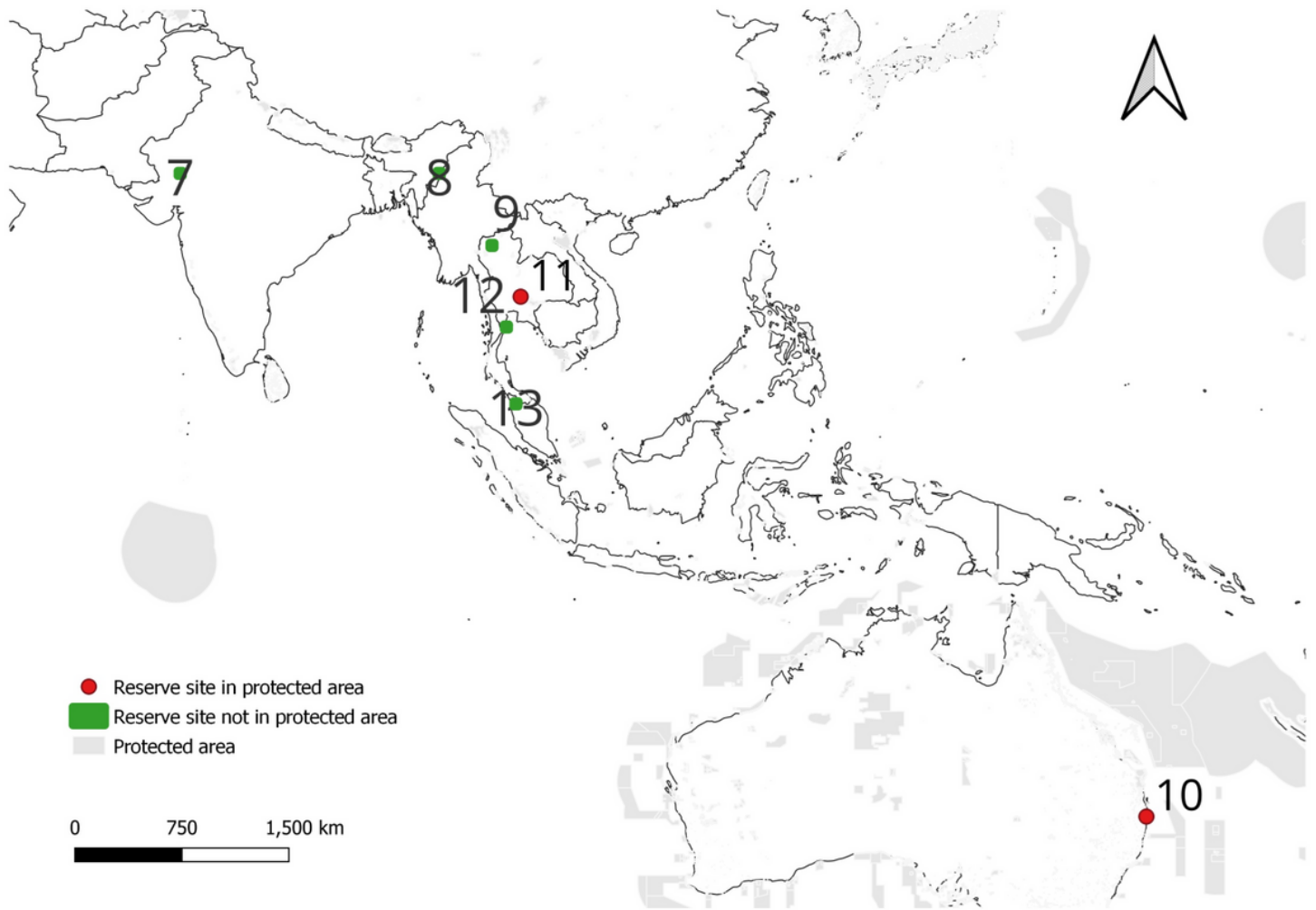


Figure 10

Complementary analysis showing potential sites for implementing genetic reserves for active conservation of global yam priority CWR in Asia and Oceania. Grid cell is 50 X 50 km

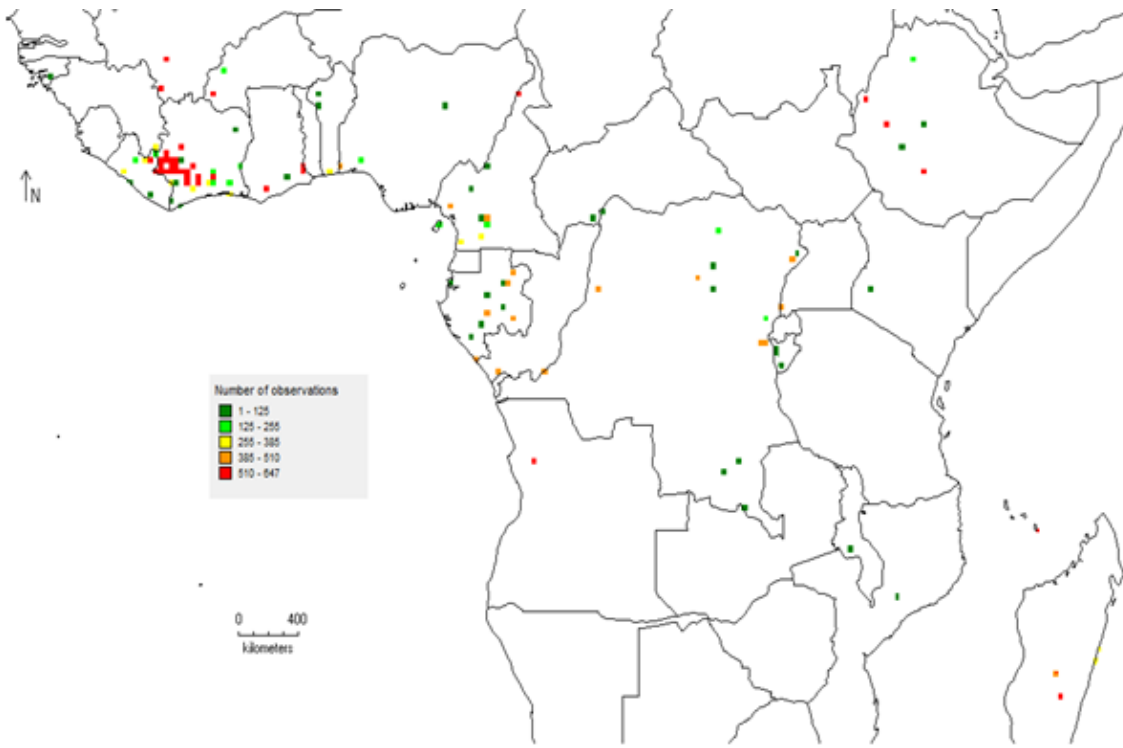


Figure 11

Priority areas in Africa for further *ex situ* collection of the 27 global priority yam wild relatives, based of species distribution models

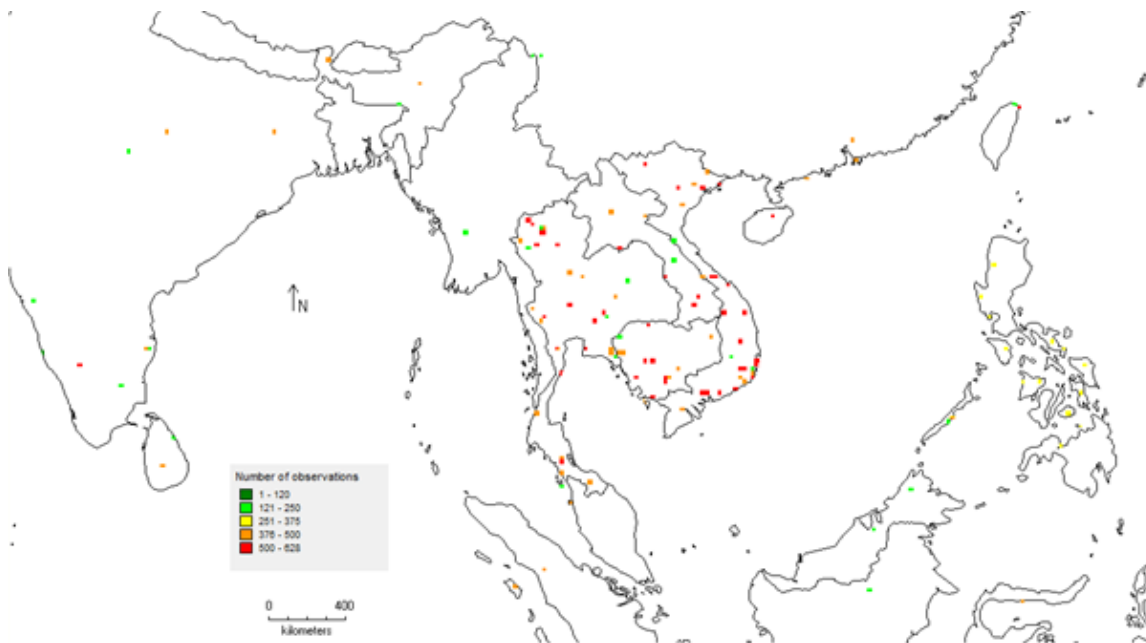


Figure 12

Priority areas in Asia and Oceania for further *ex situ* collection of the 27 global priority yam wild relatives, based of species distribution models

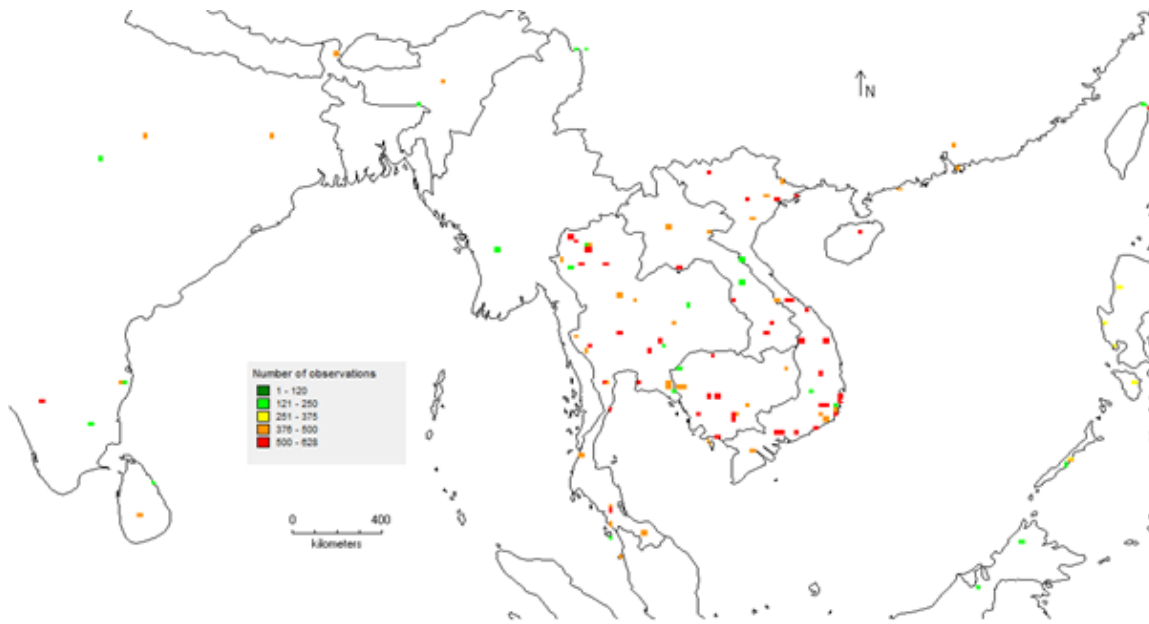


Figure 13

Priority areas in Asia for further *ex situ* collection of the 27 global priority yam wild relatives, based of species distribution models

Supplementary Files

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- [SupplementaryfileforglobalyampriorityCWR1a.xlsx](#)