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ORIGINAL ARTICLE

Plant Genetic Resources

Conservation of crop wild relative diversity in Northeast Africa: Checklist and prioritization

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Abstract

Crop wild relatives (CWR) are an important source of genetic diversity useful for crop improvement. This study was conducted to create both a checklist and a priority inventory of CWR in Northeast Africa. A partial CWR regional checklist was obtained by combining the floras of Djibouti, Ethiopia and Eritrea, Somalia, South Sudan, and Sudan for priority crop genera. It includes 1020 taxa belonging to 39 families and 130 genera, and about 80% of these taxa are native. The families with the highest number of CWR were the Poaceae (334) and Fabaceae (202). The checklist was then prioritized based on the social and economic value of the related crops using the Food and Agriculture Organization Corporate Statistical Database and the potential use of CWR for crop improvement using the crop gene pool or taxon group concepts. These criteria were applied to the checklist via a serial method to generate a prioritized inventory of 97 CWR taxa belonging to 19 families and 44 genera. Forty-three percent of these taxa occur in more than two countries and additionally 32% in Eritrea and Ethiopia, 18% in Sudan and South Sudan, and 7% in Somalia. For crop improvement, 20% of the taxa have confirmed uses, 23% have recorded potential uses, and 28% have both confirmed and potential uses. This prioritized list includes important CWR taxa related to regionally important food crops such as sorghum and teff, as well as providing a foundation for further conservation studies by conservationists and breeders in this region and worldwide.

Abbreviations: CWR, crop wild relative; FAO, Food and Agriculture Organization; FAOSTAT, Food and Agriculture Organization Corporate Statistical Database; GP1, Primary Gene Pool; GP2, Secondary Gene Pool; GP3, Tertiary Gene Pool; ITPGRFA, International Treaty for Plant Genetic Resources for Food and Agriculture; IUCN, International Union for Conservation of Nature; SADC, Southern African Development Community; TG1a, Taxon Group 1a; TG1b, Taxon Group 1b; TG2, Taxon Group 2; TG3, Taxon Group 3; TG4, Taxon Group 4.

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1 | INTRODUCTION

Crop wild relatives (CWRs) are wild plant taxa that have an indirect use value as gene donors for crop improvement. Their use value is derived from their close genetic relationship to crop plants and therefore the relative ease with which they can contribute traits to their related crops (Maxted et al., 2006). CWRs contain greater breadth of diversity than cultivated crops because they did not pass through the genetic bottleneck of domestication, and their relatively close phylogenetic

relationship to the crop means introgression is often a comparatively straightforward process (Brozynska et al., 2016; Curtin et al., 2021). Most of the crops we have today on our tables were domesticated from their wild relatives in the past 12,000 years (Alseekh et al., 2021).

CWRs provide novel gene/trait sources of resistance to biotic stresses and tolerance to abiotic stresses (Hajjar & Hodgkin, 2007); reduce reliance on agricultural inputs such as fertilizers, pesticides, and water (Maxted & Kell, 2009); and may confer the ability of the crop to produce in marginal climatic conditions (Hilger et al., 2015). However, CWR diversity is threatened by many factors such as encroachment from livestock farming and ranching, tourism and recreation areas, and housing and urban areas, as well as climate change (Kell et al., 2012).

To turn from potential to actual breeding value requires the breeders to be able to access the conserved resources (Fu, 2017; Maxted & Kell, 2009). CWRs may be actively conserved in genebanks (ex situ) and in their natural habitats (in situ) (CBD, 1992; Maxted et al., 1997, 2020). These conserved resources should be made available to breeders to develop new cultivars by incorporating novel traits from the wild to enrich crop diversity (Jarvis et al., 2008; Maxted et al., 2007). However, many breeders have some reluctance to use CWRs because of the linkage drag associated with CWR crosses and the transfer of deleterious weedy traits from CWR to the crop that must be eradicated (Jenczewski et al., 2003). These unwanted traits are removed by a long process that requires backcrossing to crop material and progeny selection, so the progeny ultimately has the beneficial traits of the crop parent combined with desired novel traits from the wild (Shakiba & Eizenga, 2014). Recently, Watson et al. (2018) noted that the time required for developing backcross progeny may be shortened by applying “speed breeding.”

Conservation planning aims to identify populations for active in situ and ex situ conservation ensuring these represent the maximum CWR diversity (Magos Brehm et al., 2017). An Interactive Toolkit for CWR Conservation Planning (Magos Brehm et al., 2017) was developed to guide researchers and other stakeholders as they plan and implement active CWR conservation. The first step in conservation planning is to prepare a CWR checklist that lists the CWR diversity in a particular geographic region. This checklist provides information about CWR taxa, for instance, taxon names and authorities found in a defined geographical area (Ford-Lloyd et al., 1997; Magos Brehm et al., 2017). Since this checklist is usually too long to assign funds for active conservation, it must be prioritized based on several factors including social and economic values of the related crop and potential use for crop improvement (Kell et al., 2017).

The gene pool (Harlan & de Wet, 1971) and taxon group concepts (Maxted et al., 2006) are used to identify the relat-

Core Ideas

- Both a regional checklist and a priority inventory of crop wild relatives (CWR) for Northeast Africa were developed.
- The final regional CWR checklist includes 1020 taxa belonging to 39 families and 130 taxa genera.
- A priority inventory of 97 CWR taxa were identified belonging to 19 families and 44 genera.

edness of a crop to its wild relatives for crop utilization, since closer relatives are more likely to introgress than distant ones. The gene pool concept is based on crossability and genetic diversity within the specific gene pool, and these gene pools are defined as follows: (a) primary gene pool (GP1) where GP1a includes the cultivated forms and GP1b the wild or weedy forms of the crop; (b) secondary gene pool (GP2) that includes less closely related species from which gene transfer to the crop is possible but difficult using conventional breeding techniques; and (c) more distance tertiary gene pool (GP3) that includes species from which gene transfer to the crop is impossible, or if possible, requires advanced techniques such as genetic engineering, somatic fusion, or embryo rescue. The taxon groups concept is used when information on crossability and diversity is unavailable. These groups are defined as follows: Taxon Group 1a (TG1a) is the crop itself, Taxon Group 1b (TG1b) is the same species as crop, Taxon Group 2 (TG2) is the same series or section as crop, Taxon Group 3 (TG3) is the same subgenus as crop, and Taxon Group 4 (TG4) is the same genus as crop.

Currently, CWR checklists have been developed for several regions including Europe and the Mediterranean (Kell et al., 2008), the Fertile Crescent (Zair et al., 2018), North Africa (Lala et al., 2018), the Southern African Development Community (SADC) (Allen et al., 2019), North America (Khoury et al., 2020), and West Africa (Nduche et al., 2021). In each of these cases, the initial checklist and prioritized inventory have been used as a basis for further CWR conservation planning, such as ex situ and in situ gap analysis in the Fertile Crescent (Zair et al., 2021) and West Africa (Nduche et al., 2021). Additionally, the SADC region has established the first regional network for in situ conservation of CWR (Magos Brehm et al., 2022). Missing from this set of studies is a report of the CWR diversity in Northeast Africa; thus, the objectives of this study are (1) to prepare a Northeast Africa CWR checklist and (2) annotate this checklist to prioritize it for active conservation using the Interactive Toolkit for CWR Conservation Planning (Magos Brehm et al., 2017).

2 | MATERIALS AND METHODS

2.1 | Creation of the CWR checklist of Northeast Africa

No prior digitized floristic checklist was available for Northeast Africa to start building the regional CWR checklist. To produce a partial CWR checklist of Northeast Africa, a digitalized regional floristic checklist was developed by (a) scanning the indexes of the floras in each national flora in the region for the main families containing crops, detailed below; (b) compiling floristic lists into one combined list; (c) matching the genera including crops from the global crop genera list (Kell, 2016) which includes all crop genera in the Annex I of the International Treaty on Plant Genetic Resources for Food and Agriculture (FAO, 2009), the global list of major and minor foods crops (Groombridge et al., 2002), together with the list of those crops from Northeast Africa that have production data included in the Food and Agriculture Organization Corporate Statistical Database FAOSTAT (FAO, 2021); and (d) excluding all taxa from genera that do not contain crops from the combined floristic checklist.

The regional floristic checklist included native and introduced taxa. This was obtained by scanning the indices and compiling the taxon names from the volumes of the floras of the countries in the region containing important CWR families and genera that were previously prioritized by Vincent et al. (2013), such as *Avena* L., *Coffea* L., *Solanum* L., *Sorghum* Moench, and *Vigna* Savi. Two of the initial volumes include the flora of Djibouti (Audru et al., 1993, 1994), and eight out of 10 volumes include the flora of Ethiopia and Eritrea (Edwards et al., 2000, 1995; Hedberg et al., 2003, 1995, 2004; Hedberg et al., 2009, 1989, 2006). (These eight volumes were the only volumes accessible during the COVID-19 lockdown in 2020–2021). In addition, the taxa contained in the four volumes of the flora of Somalia (Thulin, 1993, 1995, 1999, 2006) and the taxa of plants in Sudan and South Sudan (Darbyshire et al., 2015) were added to the floristic checklist and used to identify regional CWR taxa presence.

2.2 | CWR prioritization

Following the recommendations of Kell et al. (2017), two prioritization criteria were applied to the CWR checklist: (a) the economic value of the related crop based on FAOSTAT crop valuation data (FAO, 2021) and (b) the relative utilization potential of the wild relative based on the Gene Pool concept (Harlan & de Wet, 1971) or the Taxon Group concept (Maxted et al., 2006) as a proxy of the CWR breeding potential. The Taxon Group concept was used when the Gene Pool information was not readily available. To this end, the CWR checklist was annotated with the information related to

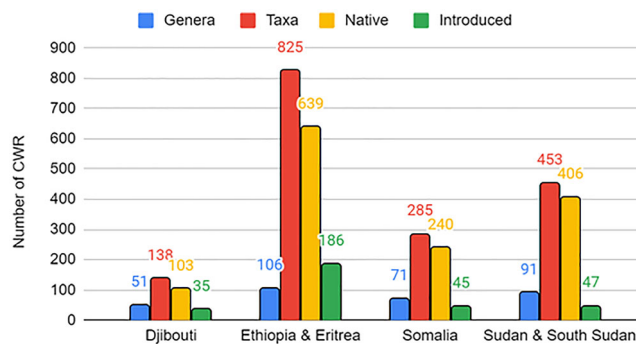


FIGURE 1 The number of genera, taxa, and native and introduced CWR in the CWR checklist in Djibouti, Ethiopia and Eritrea, Somalia, and Sudan and South Sudan.

each prioritization criterion. Priority CWR taxa were those in GP1b, GP2, TG1b, TG2 and GP3, TG3, and TG4, if they had potential or confirmed uses in crop breeding based on the information given in the Harlan and de Wet CWR Catalogue (Vincent et al., 2013) and the Germplasm Resources Information Network Taxonomy (USDA, 2023).

A serial approach was taken to prioritizing all taxa in the CWR checklist, first applying the economic value of the related crop, then secondly, the relative utilization potential of the remaining CWR to produce the prioritized CWR inventory for Northeast Africa. Subsequently, both the CWR checklist and the prioritization inventory were reviewed by local experts from Sudan and Djibouti who agreed to the lists having the highest chance of implementation by policy makers, breeders, conservationists, and geneticists using the limited resources available for regional conservation efforts.

3 | RESULTS

The CWR regional checklist of Northeast Africa includes 1020 taxa belonging to 39 families and 130 genera (Table S1). The families with the highest number of CWR taxa were the Poaceae (334 taxa) and the Fabaceae (202 taxa), representing 33% and 20%, respectively, of all families included in the checklist. Eighty percent (814 taxa) of CWR diversity is native to the region, with the highest percentage of native taxa found in Sudan and South Sudan where 90% of the taxa were native taxa (Figure 1). The highest number of CWR concentration per unit area is found in Djibouti with 0.006% CWR/km², followed by Ethiopia and Eritrea (0.0007% CWR/km²), Somalia (0.00045% CWR/km²), and Sudan and South Sudan (0.000177% CWR/km²).

Ninety-seven CWR taxa, belonging to 19 families and 44 genera, were identified as priorities for active conservation in the region; of these 68 (70%) are native to the region and 29 (30%) are introduced (Table S2). The families with the highest

TABLE 1 The total number of families, genera, related crops, and number of CWR in each genus in the Northeast Africa crop wild relative (CWR) priority inventory.

Family	Genus	Related crop	Number of CWR taxa
Poaceae	<i>Avena</i>	Oat	4
	<i>Digitaria</i>	Fonio millet/white fonio	2
	<i>Echinochloa</i>	White millet/Siberian millet	1
	<i>Eleusine</i>	Finer millet	4
	<i>Elymus</i>	Wheat	1
	<i>Eragrostis</i>	Teff	2
	<i>Oryza</i>	Rice	4
	<i>Pennisetum</i>	Pearl millet	3
	<i>Saccharum</i>	Sugarcane	4
	<i>Setaria</i>	Foxtail millet	2
	<i>Sorghum</i>	Sorghum	2
Fabaceae	<i>Cicer</i>	Chickpea	1
	<i>Lablab</i>	Hyacinth bean	1
	<i>Lens</i>	Lentil	1
	<i>Lupinus</i>	Lupin	2
	<i>Medicago</i>	Alfalfa	1
	<i>Phaseolus</i>	Scarlet runner bean	1
	<i>Vicia</i>	Common vetch	1
Brassicaceae	<i>Vigna</i>	Mung bean/cowpea	6
	<i>Brassica</i>	Cabbage/mustard	1
	<i>Diplotaxis</i>	Mustard	2
	<i>Raphanus</i>	Radish	1
Asteraceae	<i>Sinapis</i>	Ethiopian cabbage, mustard, rape, black mustard Cabbage, Turnip, Radish	1
	<i>Carthamus</i>	Safflower seed	2
Cucurbitaceae	<i>Lactuca</i>	Lettuce	1
	<i>Citrullus</i>	Watermelon	1
Rutaceae	<i>Cucumis</i>	Melon/cucumber	3
	<i>Citrus</i>	Citron/key lime	2
Rubiaceae	<i>Coffea</i>	Coffee	3
Rosaceae	<i>Fragaria</i>	Strawberry	3
	<i>Malus</i>	Apple	1
Dioscoreaceae	<i>Dioscorea</i>	Yam	4
Areaceae	<i>Elaeis</i>	Oil palm	1
	<i>Phoenix</i>	Date palm	2
Euphorbiaceae	<i>Manihot</i>	Cassava	1
Oleaceae	<i>Olea</i>	Olive	2
Solanaceae	<i>Solanum</i>	Eggplant, aubergine	11

number of the priority CWR taxa are the Poaceae (29 CWR taxa), Fabaceae (14), and Solanaceae (11), with CWR taxa representing ~29%, 14%, and 11% of the family, respectively. The most CWR species were found in the *Solanum* (11 CWR species) and *Vigna* (6) genera representing 11% and 6% of the species respectively (Table 1).

The geographical distribution of the priority CWR inventory varies across the region: 43% of the taxa occur in more

than two countries, 32% in Eritrea and Ethiopia, 18% in Sudan and South Sudan, and 7% in Somalia. The closest wild relatives to the crop (GP1b and TG1b) represent 31% of priority CWR (Figure 2). Across the CWR found in Northeast Africa, 42% (41 taxa) are considered to be regional priorities because the CWR has at least one documented trait which could be introgressed for crop improvement (Table 2). Additional details of the related crop(s), gene pool/taxon group

TABLE 2 Relatedness of crop wild relative (CWR) taxa and their confirmed use in crop improvement in the priority inventory in Djibouti, Eritrea, Ethiopia, Somalia, Sudan, and South Sudan.

Taxon	Relatedness to CWR	Confirmed use of CWR to broaden crop improvement	References
<i>Avena abyssinica</i> Hochst	GP3	Crown rust resistance and drought tolerance	Gnanesh et al. (2014)
<i>Avena fatua</i> L.	GP1b	Drought tolerance	Leggett (1992); Suneson (1967)
<i>Avena sterilis</i> L.	GP1b	Cold tolerance, yield improvement crown rust resistance, stem rust resistance	Forsberg and Reeves (1992); Gnanesh et al. (2014); Hoffman et al. (2006); Jellen and Leggett (2006); Rothman (1984); Sánchez-Martín et al. (2012); Takeda and Frey (1976)
<i>Brassica nigra</i> (L.) Koch	GP2	Blackleg resistance, clubroot resistance	Gerdemann-Kncorck et al. (1994)
<i>Carthamus lanatus</i> L.	GP3	Alternaria leaf spot resistance, bacterial blight resistance, fusarium wilt resistance, gene transfer	Heaton and Klisiewicz (1981); Mayerhofer et al. (2011); Prasad and Anjani (2005)
<i>Citrus maxima</i> (Burm.) Osbeck	GP2b	Gene transfer	Grosser et al. (2007)
<i>Coffea canephora</i> Pierre ex A. Froehner var. <i>gossweileri</i> A. Chev.	GP2b	Coffee berry disease resistance, coffee rust resistance, root knot nematode resistance	Anthony et al. (2011); Levi et al. (2005); Noir et al. (2003); Prescott-Allen and Prescott-Allen (1988)
<i>Coffea liberica</i> Hiern	GP2b	Coffee rust resistance	Anthony et al. (2011); Prakash et al. (2004); Prescott-Allen and Prescott-Allen (1988)
<i>Fragaria chiloensis</i> (L.) Duchesne.	GP1b	Fruit size, fruit quality	Ahmadi and Bringham (1992)
<i>Fragaria vesca</i> L.	GP3	Anthraxnose resistance, powdery mildew resistance, improved aroma	Ahmadi and Bringham (1992); Scott (1951)
<i>Fragaria virginiana</i> Duchesne.	GP1b	Fruit number, fruit size, powdery mildew resistance, scorch resistance, day neutral	Ahmadi and Bringham (1992); Hancock et al. (2002)
<i>Diplotaxis eruroides</i> (L.) DC.	GP3	Alternaria blight resistance, blackleg resistance, cytoplasmic male sterility	Klewer et al. (2003); Prakash et al. (2009); Siemens (2002)
<i>Diplotaxis harra</i> (Forssk.) Boiss.	GP3	Gene transfer	Begum et al. (1995)
<i>Eleusine africana</i> K. OByrne	GP1b	Fertility trait	Dida and Devos (2006)
<i>Eleusine kigeziensis</i> S.M.	GP1b	Fertility trait	Dida and Devos (2006)
<i>Thinopyrum junceum</i> (L.) Á. Löve	GP3	Soil salinity tolerance	Nevo and Chen (2010)
<i>Gossypium longicalyx</i> Hutch. & B.J.S. Lee.	GP2	Reniform nematode resistance	Robinson et al. (2007)
<i>Ipomoea purpurea</i> (L.) Roth.	GP3	Gene transfer	Cao et al. (2009)
<i>Lens ervoides</i> (Brign.) Grande	GP2	Seed size, yield improvement, anthracnose resistance, <i>Ascochyta</i> blight resistance, <i>Stemphylium</i> blight resistance	Ahmad et al. (1997); Kumar et al. (2014); Tullu et al. (2011)

(Continues)

TABLE 2 (Continued)

Taxon	Relatedness to CWR	Confirmed use of CWR to broaden crop improvement	References
<i>Lupinus mexicanus</i> Cerv. er Lag.	GP3	Gene transfer	Busmann-Loock et al. (1992); Clements et al. (2005)
<i>Malus sylvestris</i> Miller	GP1b	Agronomic trait	Volk et al. (2015)
<i>Manihot carthagenensis</i> (Jacq.) Müll. Arg. subsp. <i>glaziovii</i> (Müll. Arg.) Allem	GP2	Cassava bacterial blight; resistance, cassava mealy bug resistance, cassava mosaic virus resistance	Hahn et al. (1980); Hajjar and Hodgkin (2007); Nair and Unnikrishnan (2006); Prescott-Allen and Prescott-Allen (1988)
<i>Medicago arborea</i> L.	GP3	Anthracnose resistance	Armour et al. (2008); Quiros and Bauchan (1988)
<i>Olea europaea</i> subsp. <i>cuspidata</i> (Wall. ex G. Don) Cif.	GP2	(a) Crop ontology trait	Hannachi et al. (2009)
<i>Oryza brachyantha</i> A. Chev. & Roehr.	GP2	Bacterial blight resistance	Brar and Singh (2011)
<i>Oryza longisteminata</i> A. Chev. & Roehr.	GP1b	Drought tolerance, yield improvement, bacterial blight resistance, grassy stunt resistance	Brar and Singh (2011); Hajjar and Hodgkin (2007); Jena (2010)
<i>Pistacia khinjuk</i> Stocks.	GP2	Rootstock	Hormaza and Wunsch (2007)
<i>Pennisetum purpureum</i> Schumach.	GP2	Cytoplasmic male sterility, fertility restoration genes, panicle length, days to maturity, yield improvement	Dujardin and Hanna (1989); Hajjar and Hodgkin (2007); Hanna (1997); Palit et al. (2014)
<i>Pennisetum squamulatum</i> Fresen.	GP2	Fertility restoration genes	Dujardin and Hanna (1989)
<i>Phaseolus coccineus</i> L.	GP2	Aluminum tolerance, yield improvement, angular leaf spot resistance, anthracnose resistance, bean stem maggot resistance, bean yellow mosaic virus resistance, common bacterial blight resistance, fusarium root rot resistance, white mold resistance	De Ron et al. (2015); Freytag et al. (1982); Loskutov and Rines (2011); Mahuku et al. (2003); Miklas et al. (1999); Porch et al. (2013); Schwartz and Singh (2013); S. P. Singh (2001); R. Singh et al. (2008); Wilkinson (1983); Zapata et al. (2004)
<i>Saccharum spontaneum</i> L.	GP2	Cold tolerance, red rot resistance, smut resistance, sugarcane mosaic virus, early maturing	Cordeiro et al. (2003); Prescott-Allen and Prescott-Allen (1986)
<i>Setaria viridis</i> (L.) P. Beauv.	GP1b	Triazine resistance	Darmency and Pernes (1985)
<i>Sinapis arvensis</i> L.	GP2	Blackleg resistance, sclerotinia resistance, cytoplasmic male sterility	Hu et al. (2002); Snowdon et al. (2000); Wei et al. (2010)
<i>Solanum aethiopicum</i> solan L.	GP3	Rootstock, yield improvement, bacterial wilt resistance, fusarium wilt resistance	Collonnier et al. (2001); Daunay (2008); Frary et al. (2007); Rotino et al. (2014); USDA (2011)
<i>Solanum incanum</i> L.	GP2	Drought tolerance, rootstock, verticillium wilt resistance	Frary et al. (2007); Knapp et al. (2013); (USDA, 2011)
<i>Solanum linnaeanum</i> Hopper & Jaeger	GP2	Fungal wilt resistance	Frary et al. (2007); Rotino et al. (2014); Yin et al. (2015)

(Continues)

TABLE 2 (Continued)

Taxon	Relatedness to CWR	Confirmed use of CWR to broaden crop improvement	References
<i>Solanum macrocarpon</i> L.	GP3	Rootstock	USDA (2011)
<i>Solanum marginatum</i> L. f.	GP3	Gene transfer	Borgato et al. (2007)
<i>Sorghum purpureosericeum</i> (Hochst. ex A. Rich.) Schweinf. & Asch.	GP3	Sorghum shoot fly resistance	Nwanze et al. (1990)
<i>Vigna radiata</i> var. <i>sublobata</i> (Roxb.) Verdc.	GP1b	Bruchid resistance	Konarev et al. (2002)
<i>Vigna vexillata</i> (L.) A. Rich	GP3	Gene transfer	Gomathinayagam et al. (1998)

Note: Additional details are provided in Table S3.

Abbreviations: GP1b, Primary Gene Pool; GP2, Secondary Gene Pool; GP3, Tertiary Gene Pool. TG1b, Taxon Group 1b; TG2, Taxon Group 2; TG3, Taxon Group 3; TG4, Taxon Group 4.

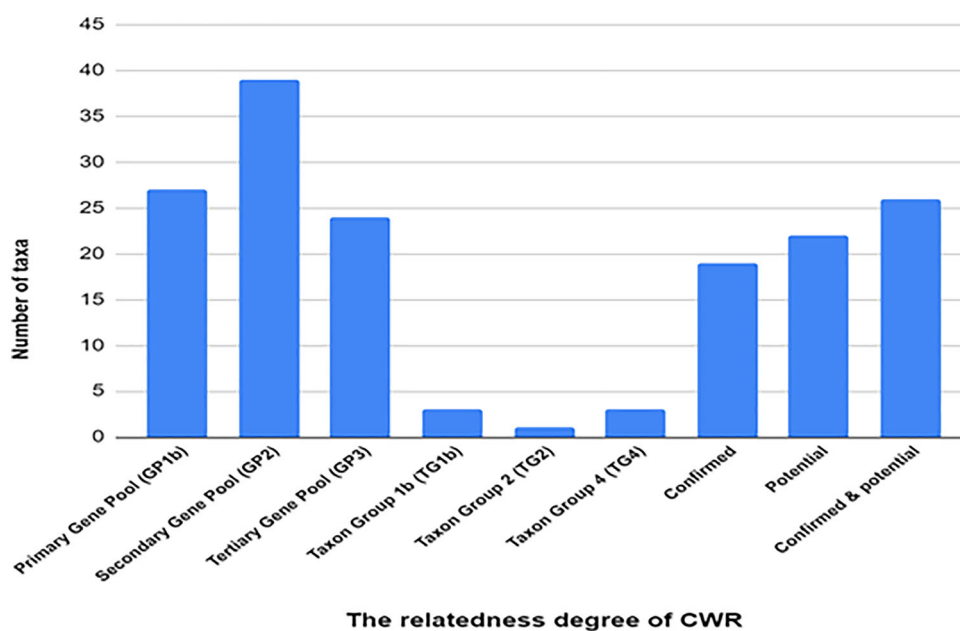


FIGURE 2 Degree of relatedness for a priority crop wild relative (CWR) using gene pool and taxon group concepts in the Northeast Africa. (GP1b, Primary Gene Pool; GP2, Secondary Gene Pool; GP3, Tertiary Gene Pool. TG1b, Taxon Group 1b; TG2, Taxon Group 2; TG3, Taxon Group 3; TG4, Taxon Group 4; confirmed, confirmed for crop breeding; potential, potential for crop breeding).

assignment and the suggested trait(s) to target for introgression are shown in Table S3.

4 | DISCUSSION

The Northeast African CWR checklist (1020 taxa) has fewer CWR taxa than those found in North Africa (5780 taxa) (Lala et al., 2018), Southern African Development Community (SADC) region (1900 taxa) (Allen et al., 2019), and West Africa (1651 taxa) (Nduche et al., 2021). Vincent et al. (2013) noted that CWR per unit area is a more accurate estimation of CWR concentration because it considers the size of the

country or region. Also, the method used for developing this checklist fits the required conservation needs of this region and is not the same as the method used to develop checklists for other regions. For example, the CWR checklist in Northeast Africa only focused on food crops, while CWR in North Africa considered food and fodder crops (Lala et al., 2018).

The importance of CWR is recognized by the Food and Agriculture Organization of the United Nations' Second Global Plan of Action for Plant Genetic Resources (FAO, 2011) and Convention of Biological Diversity (CBD, 2022). Therefore, the regional approach of conservation of CWR identifies the value of the CWR, the most important CWR taxa exist in a specific region, and recognize populations or

areas within the region that need immediate conservation (Kell et al., 2017).

The CWR priority inventory contains several food crops that are economically important both regionally and globally that were identified by Vincent et al. (2013). The exploitation value of CWR is annually about \$115 billion per year worldwide (Hossain et al., 2022). Cash crops such as cotton (*Gossypium hirsutum* L.) and coffee (both *Coffea arabica* L. and *Coffea canephora* Pierre ex A. Froehner) make a vital contribution to the overall gross domestic product in Sub-Saharan Africa (Coleman & Thigpen, 1993; Gilbert et al., 2013). For example, *Coffea liberica* Hiern and *C. canephora* Pierre ex A. Froehner var. *gossweileri* A. Chev, in the GP2 for cultivated coffee, are confirmed sources of disease and insect resistance (Table 2), while a GP3 of eggplant/aubergine, *Solanum macrocarpon* L., has documented potential as a source of drought tolerance (Table S3).

The Northeast Africa priority checklist fits to other international priority checklists. For instance, the Global Crop Diversity Trust prioritized 29 crops for the world's future food security under the project "Adapting Agriculture to Climate Change: Collecting, Protecting, and Preparing Crop Wild Relatives" (Dempewolf et al., 2014). The Northeast Africa CWR priority inventory includes 37 taxa related to 13 crops out of these are 29 prioritized crops. These matched crops are alfalfa (*Medicago sativa* L.), African rice (*Oryza longistaminata* A. Chev. & Roehr), beans, chickpea (*Cicer arietinum* L.), cowpea [*Vigna unguiculata* (L.) Walp], eggplant (*Solanum melongena* L.), finger millet [*Eleusine coracana* (L.) Gaertn], lentil (*Lens culinaris* Medik), oat (*Avena sativa* L.), sorghum [*Sorghum bicolor* (L.) Moench], pearl millet [*Pennisetum glaucum* (L.) R. Br], sweet potato [*Ipomoea batatas* (L.) Poir], and vetch (*Vicia sativa* L.) (Table S3). This CWR inventory is not an end in itself but should be available online for regular taxonomic and assessment updates to include the most important CWR taxa in the region (Rubio Teso et al., 2018).

Three crops—rice, maize, and wheat—provide about 50% of the plant calories consumption in the world (FAO, 2016). For example, drought-tolerant genes of *O. longistaminata* A. Chev. & Roehr. a GP1b of rice (Brar & Singh, 2011) were introgressed into cultivated rice and allowed cultivation in new areas in the Philippines (Hajjar & Hodgkin, 2007). Moreover, introduced taxa such as *Citrus maxima* (Bur.) Osbeck and *Malus sylvestris* (L.) Mill are included on this list because of their potentially evolved genes since being introduced that are useful for crop improvement (Maxted et al., 2007).

The Northeast African region also includes CWR of staple food crops like sorghum *S. bicolor* (L.) Moench and teff *Eragrostis tef* (Zuccagni) Trotter that provide food for millions. Sorghum is the fifth largest grain crop in terms of world production, and 46% of the world's consumption occurs in sub-Saharan Africa, both as food for people and feed for ani-

mals (Raubach et al., 2021; Sanders et al., 2019). In Sudan, sorghum is the main staple crop, accounting for about 80% of the total cereal production. In contrast, in Ethiopia and Eritrea, teff is the most stable crop, and this area is considered its center of origin and diversity. Recently, teff has received increased attention globally because it is naturally gluten free; thus, teff flour can be utilized in foods as gluten free in comparison to other cereals particularly wheat (Araya et al., 2010; Baye, 2014; Weich, 2005; Yumbya et al., 2014). Furthermore, the close CWR of teff *Eragrostis pilosa* (L.) P. Beauv can potentially be used as a parent for developing improved teff cultivars with enhanced drought tolerance through breeding (Table S3).

5 | CONCLUSION

The Northeast Africa region is a rich source of crop and CWR diversity. It includes globally important crops, some of which are probably restricted to this region (i.e., eggplant, finger millet, teff, pearl millet, rice, sorghum, and coffee). The inherent CWR diversity is largely untapped for crop improvement and sustainable food production at the local, regional, and international levels. The aim of this study was to develop a CWR checklist and identify a priority checklist of CWR for active conservation in the region as the first step towards securing this gene pool for current and future utilization in crop improvement programs. Both a checklist of 1020 CWR taxa and a priority inventory of 97 taxa were identified. These lists can now be used to facilitate targeted in situ and ex situ conservation actions at both the national and regional levels. Consequently, this will facilitate medium- and long-term maintenance of food security in this region where food insecurity is an apparent and growing concern in the face of climate change, population growth, and civil unrest. This study highlights the value of CWR in the region as a source of confirmed and/or potential use for crop improvement especially for biotic and abiotic stress tolerance (Table 2). In addition, this study provides an essential baseline of information for questions such as which trait and specific populations of CWR are important to meet food security needs. This study could be leveraged to implement the following initiatives:

- a. Establishing a regional CWR conservation network for national genebanks, protected areas, breeders, universities, and researchers to raise awareness about CWR; increasing conservation and sustainable use of CWR in the region; creating links with other international institutions such as the International Union for Conservation of Nature (IUCN) and FAO.
- b. Conducting "gap analyses" by utilizing various methods to detect in situ and ex situ conservation gaps in the regional CWR priority checklist.

- c. Climate change modeling to understand the likely impact of climate change on the identified regional CWR priority diversity which will assist in targeting taxon selection for active conservation.
- d. Threat assessment of the regional priority CWR using IUCN Red Listing Categories and Criteria to further facilitate identifying which taxon to select for active conservation.
- e. Including a plant breeder (agronomist) who can review the CWR inventory taxa and provide guidance regarding which taxa will be most useful for crop improvement, thus further refining the list of priority taxa for conservation planning.

AUTHOR CONTRIBUTIONS

Ahmed Aldow: Conceptualization; data curation; formal analysis; investigation; methodology; resources; validation; visualization, writing—original draft; writing—review & editing. **Joana Magos Brehm:** Supervision. **Maha Kordofani:** Resources; validation. **Fatouma Abdoul-latif:** Resources; validation. **Nigel Maxted:** Supervision.

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CONFLICT OF INTEREST STATEMENT

The authors declare no conflict of interest.

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

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