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Identification of Gaps in Pigeonpea Germplasm from East and Southern Africa Conserved at the ICRISAT Genebank

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The genebank at ICRISAT, Patancheru, India conserves 13,771 accessions of pigeonpea germplasm from 74 countries, including 1,168 accessions from 13 East and Southern African (ESA) countries: Based on availability of georeference data, 916 landraces from seven countries were considered for identifying gaps. Eighty four districts located in four East African countries and 54 districts located in three Southern African countries were identified as geographical gaps in the ICRISAT collection. A total of 25 districts in four countries; six provinces in Tanzania and Zambezia province in Mozambique were identified as gaps in phenotypic diversity for specific traits. Kitui and Machakos in Kenya were found as common districts for geographical as well as trait diversity gaps. Launching collection missions in ESA countries to fill geographical, trait-specific and taxonomical gaps in pigeonpea collection from ESA countries at ICRISAT genebank is recommended.

Key Words: Diversity, Genetic resources, Geographical gap, Germplasm, Landrace

Introduction

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is a versatile food legume of the tropics and subtropics. Because of its multiple uses including food, feed, fuel, fencing, roofing, basket making and as a soil enricher and soil binder, pigeonpea is cultivated in about 82 countries as a field crop or a backyard crop. It has wide adaptability to diverse climates (Nene and Sheila, 1990) and due to high seed protein (up to 31% in the world collection), pigeonpea is an important source of protein for the vegetarian diet especially in the Indian sub-continent. FAO production statistics are available only for 21 countries. During 2010, pigeonpea as a field crop was grown on 4.8 million ha. India has the largest area under pigeonpea cultivation (3.53 m ha) followed by Myanmar (0.58 m ha), Malawi (0.19 m ha), Kenya (0.16 m ha), Uganda (0.10 m ha), Tanzania (0.08 m ha), Dominican Republic (0.02 m ha) and Nepal (0.02 m ha) (FAO, 2010).

Although, East Africa is considered as the secondary center of diversity for pigeonpea (van der Measen, 1990), East and Southern African (ESA) countries, mainly Kenya, Tanzania and Uganda in East Africa and Malawi, Mozambique and Zambia in Southern Africa have been considered as important pigeonpea growing countries (Ramanatha Rao, 1981). Upadhyaya *et al*. (2005) reported high diversity for quantitative traits in accessions from Africa. Over most of Africa, pigeonpea is grown as a vegetable near houses and farm steads, as hedges, and as a crop mostly mixed with cereals and short duration legumes (van der Maesen, 1976; Upadhyaya *et al*., 2010a). Pigeonpea landraces are widely adapted compared to green pea, and can be grown as a vegetable in backyards and on field bunds to support the economies of the landless poor. Because of the perenniality of pigeonpea coupled with the indeterminate flowering habit of most vegetable type accessions, it is possible to extend the harvest of immature pods to sell in local markets for longer period.

Geographic Information Systems (GISs), particularly FloraMap and DIVA_GIS have facilitated a better understanding of species distribution and the gaps in collections (Hijmans and Spooner, 2001; Van Treuren *et al*., 2011). The genebank at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India holds the world's largest collection of pigeonpea germplasm (13,771 accessions), sourcing from

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74 countries including 1,168 accessions from 13 ESA countries. In view of the relatively poor representation of ESA countries in the ICRISAT genebank and the fast erosion of crop diversity due to replacement of landraces, including those of pigeonpea by modern varieties, natural catastrophes such as droughts, floods, fire hazards, urbanization and industrialization and habitat loss due to irrigation projects, overgrazing, mining and climate change (Upadhyaya and Gowda, 2009), there is an urgent need for a critical assessment of the existing world collection of pigeonpea for gaps. Therefore, this study is aimed at summarizing pigeonpea germplasm assembled from East and Southern Africa and conserved at ICRISAT genebank, mapping their geographical distribution, and identifying geographical and trait-specific diversity gaps for possible exploration before potentially valuable germplasm material is lost forever.

Materials and Methods

Passport and characterization databases of the world collection of pigeonpea germplasm conserved at the ICRISAT genebank was used in the present study. Passport data of landraces from ESA countries, including Ethiopia (14), Kenya (343), Rwanda (5), Tanzania (275), Uganda (98) in East Africa and Botswana (3), Madagascar (1), Malawi (249), Mozambique (32), Namibia (5), South Africa (40), Zambia (93) and Zimbabwe (10) in Southern Africa was updated, particularly for information on precise location of collecting site and corresponding geographic coordinates. Using Microsoft Encarta®, an electronic atlas (MS Encarta® Interactive World Atlas, 2000), geographic coordinates were retrieved for landraces having location information. To verify the accuracy of coordinates, the landraces were plotted over a country level map and checked for their presence in the appropriate province/state, district, village or precise location of sampling. Landraces having latitude and longitude information (up to four decimals) were used in the present study to identify gaps in collections from these countries. Landraces from Rwanda (5) and South Africa (4) having georeference data were considered too few, therefore, not considered for identifying gaps in collections from these countries. The final set of 916 landraces from seven countries with geographic coordinates was used to identify gaps in the collections. FloraMap, a software tool developed at Centro Internacional de Agricultura Tropical (CIAT) (Jones and Gladkov, 1999) was used to map the predicted distribution of pigeonpea and DIVA-GIS software was used to identify trait-specific diversity.

The FloraMap makes precise and detailed maps that eliminate much of the guesswork from the slow, expensive process of finding and recovering species. It takes the absolute minimal data available from germplasm passport database, just latitude and longitude of the collecting site and accession number/identity. The collection sites form a calibration set to construct a climate model. This model is then mapped as a probability surface throughout the world. This has proved its worth in the analyses of a number of important species. Identification of geographical gaps in germplasm collections using FloraMap was considered as the most practical approach. Developed, tested and refined over the past two decades, this Windows based tool relies on climatic data to predict promising collection sites. FloraMap predicts on the idea that climate is a robust indicator of the environmental range of plants and other organisms.

While working with the passport dataset, depending on the country, weights ranging from 1.0 to 1.2 for rainfall and from 0.80 to 1.00 for temperature and diurnal temperature were allocated maintaining the total of the three variables to 3 and an exponential transformation with a power of 0.3 was applied to the monthly rainfall data. More than 91% of total variation was explained by first five principal components (PCs) depending on the country. To achieve higher precision in predicting the probability of pigeonpea occurrence, FloraMap was run for each country separately. Since multiple accessions with identical coordinates were considered as single collection site, the number of actual geographical sites within an area of 18 × 18 km² is less than the number of sampled sites. Collection sites were overlaid on the probability map of each country. Provinces/states (name 1) and districts/administrative units (name 2) with high probability (>50%) and with no collection and/or few collection sites were recorded as gaps. To restrict the area for exploration, the smallest administrative unit (district) was considered as a gap.

Assembled accessions were evaluated for nine quantitative characters in different years at ICRISAT (17° 25'N latitude, 78° 00'E longitude and 545 masl) in vertisols during rainy season. Accessions were sown in 3 rows of 4 m long, with a spacing of 50 cm between plants and 75 cm between rows. The crop was fertilized with 20 kg N and 40 kg P_2O_5 ha^{-1} as basal dose, managed by recommended cultural and plant protection practices, including supplementary irrigation. Observations were recorded as mean of three representative plants from

the middle row for days to 50% flowering, plant height, number of primary and secondary branches/plant, pods/plant, seeds/pod, shelling percentage, 100 seed weight and seed yield/plant, following the descriptors for pigeonpea (IBPGR and ICRISAT, 1993). Using the passport and characterization data of pigeonpea germplasm from ESA countries and DIVA-GIS software (Hijmans *et al*., 2005), gaps in diversity for traits under study were identified. Using DIVA-GIS software, Shannon-Weaver diversity index for different traits was estimated and mapped (Shannon and Weaver, 1949). Districts with high diversity and relatively fewer collection sites were identified as gaps in diversity for each trait and in each country. Due to large number, the diversity maps for important traits do not depict collection sites avoiding the possible clutter. A United States Geological Survey (USGS) land cover map for Africa was used to identify the type of vegetation and land cover in the districts selected and to exclude lakes, forests and other areas where crop cultivation is not known (USGS EROS Center, 2005).

Results

Germplasm Assembled

Initially, the pigeonpea germplasm was assembled by introducing already collected germplasm from various organizations located in different countries and then by launching systematic germplasm collection missions in ESA countries in partnership with national and international institutes, National Agricultural Research Systems (NARS), universities and Non-governmental Organizations (NGOs). The analysis of passport data of the world collection of pigeonpea germplasm assembled at the ICRISAT genebank revealed that a total of 1,168 accessions were assembled from East and Southern African countries (ESA) (Table 1). The collection is from a wide range of latitudes ranging from -26.00° (South Africa) to 8.75° (Ethiopia).

Germplasm Introduced

Eight organizations located in eight countries donated a total of 255 accessions originating in 11 ESA countries (Table 1). Commonwealth Scientific and Industrial Research Organization (CSIRO), Division of Tropical Crops and Pasture, ATFGRC, St. Lucia, Australia (49); Station De Genetique D Amdioration Des Plantes, Versailles, France (2); National Dryland Farming Research Station, Katumani, Kenya (16); Chitedze Agricultural Research Station, Lilongwe, Malawi (3); United States Department of Agriculture (USDA)/Southern Regional Plant Introduction Station, Griffin, USA (1); Agricultural Research and Extension Authority, Agricultural Research Station, Taiz, Yemen (9); Directorate of Plant and Seed Control, Pretoria, South Africa (21) and Msekera Regional Research Station, Chipata, Zambia (61) were the donors of pigeonpea germplasm to ICRISAT genebank (Table 1). ICRISAT regional center at Nairobi has also sent 82 samples

Table 1. Pigeonpea germplasm from East and Southern Africa assembled at ICRISAT genebank

Region/Country	Total accs.	Introductions	Collections		Biological status of collection			Landraces with geo-reference data
			Year of collection	No. of accs. collected	Breeding material	Wild	Landraces	
East Africa								
Ethiopia	14	-	1984	14	-	-	14	14
Kenya	343	31	1976	63	26	5	312	311
			1982	249				
Rwanda	5	-	1982	5	-	-	5	5
Tanzania	275	58	1981	217	3	13	259	257
Uganda	98	15	1991	24	1	-	97	90
			1993	34				
			1993	25				
Southern Africa								
Madagascar	1	1	-	-	1	-	-	-
Malawi	249	5	1979	21	1	4	244	133
			1983	223				
Botswana	3	3	-	-	-	3	-	-
Mozambique	32	22	1981	10	-	1	31	31
Namibia	5	5	-	-	-	5	-	-
South Africa	40	37	1982	3	21	15	4	3
Zambia	93	68	1980	20	-	7	86	80
Zimbabwe	10	10	-	-	-	10	-	-
Total	1168	255		913	53	63	1052	924

originating in Kenya (6), Mozambique (21), Tanzania (41) and Uganda (14). All accessions from Botswana (3), Madagascar (1), Namibia (5) and Zimbabwe (10) are introductions in the ICRISAT genebank in India.

Germplasm Collected

During 1976-93, ICRISAT and its partners have launched 14 collection missions in nine ESA countries (eight in East Africa and six in Southern Africa) and collected a total of 913 samples (Table 1). Maximum samples were collected in Kenya (312) followed by Malawi (244) and Tanzania (217). ICRISAT had collaboration with 15 organizations for collecting pigeonpea germplasm in nine ESA countries. Important collaborators in East Africa include, Haile Sellassie I University, Debre Zeit and Plant Genetic Resources Centre (PGRC), Addis Ababa in Ethiopia; University of Nairobi, Nairobi, Kenya and Food and Agriculture Organization (FAO)/National Dryland Farming Research Station, Katumani in Kenya (van der Maesen, 1976; Remanandan *et al*., 1982); Institut Des Sciences Agronomiques Du Rwanda (ISAR), Butare in Rwanda (Prasada Rao and Mengesha, 1982); International Institute of Tropical Agriculture (IITA)/ United States Agency for International Development (USAID), Dar-Es-Salaam/Ministry of Agriculture, Zanzibar in Tanzania (Remanandan and Mengesha, 1981) and Makerere University, Kampala in Uganda (Singh *et al*., 1991; Reddy *et al*., 1993). The collaborators in Southern Africa includes IBPGR, Italy/Ministry of Agriculture and Natural Resources in Malawi; IBPGR, Rome/University of Eduardo Mondlane, Maputo in Mozambique (Ramanatha Rao, 1981); Grain Crops Research Institute, Potchefstroom in South Africa (van der Maesen, 1982); IBPGR, Rome/Ministry of Agricultural and Water Development in Zambia.

Past collections revealed that Shewa (12) in Ethiopia; Central (20), Coast (38), Eastern (242) and Nyanza (12) in Kenya; Southern (104) in Malawi; Nampula (17) and Zambezia (13) in Mozambique; Arusha (22), Dodoma (63), Lindi (16), Morogoro (56), Mtwara (26), Pwani (15) and Ruvuma (18) in Tanzania; Northern (35) in Uganda and Eastern (61) and Northern (16) in Zambia are the important source provinces resulting in more than 10 accessions.

Biological Status of Collection

Analysis of the passport data for biological status of the collection from ESA includes 1,052 landraces, 53 breeding materials and 63 wild accessions belonging to 14 species of three genera (Table 1). Landraces were from Ethiopia (14), Kenya (312), Rwanda (5), Tanzania (259), Uganda (97), Malawi (244), Mozambique (31), South Africa (4) and Zambia (86). All accessions from Botswana (3), Namibia (5) and Zimbabwe (10) belong to genus *Rhynchosia*.

Wild Relatives

The 14 species of genus *Dunbaria, Eriosema* and *Rhynchosia* assembled from nine ESA countries includes 59 introductions and four collections. The wild species assembled from ESA countries include *Dunbaria ferruginea* (1), *Eriosema ellipticum* (1), *Rhynchosia aurea* (1), *R. cyamosperma* (1), *R. densiflora* (3), *R. edulis* (1), *R. micrantha* (5), *R. minima* (22), *R. rothii* (1), *R. sublobata* (9), *R. totta* (11), *R. velutina* (1), *R. venulosa* (1) and *R. verdcourtii* (3). Species name is not available for two accessions of genus Eriosema. All wild species assembled from ESA countries belong to the quaternary genepool (Bohra *et al*., 2010). None of them are crossable with cultivated pigeonpea.

Intensity of Collection

Accessions with geo-reference data represent 336 geographical sites of germplasm collection in Ethiopia (10), Kenya (66), Malawi (35), Mozambique (29), Rwanda (2), South Africa (3), Tanzania (88), Uganda (58) and Zambia (45). The average number of samples per collection site was three in the collection from ESA; one in Ethiopia, Mozambique and South Africa; two in Uganda and Zambia; three in Rwanda and Tanzania; four in Malawi and five in Kenya indicating the intensity of germplasm collection in these countries. FAO statistics for area of cultivation in different countries and the number of accessions in genebank from those countries indicated the representation of one accession per 463 ha in Kenya, per 275 ha in Tanzania, per 249 ha in Malawi and per 98 ha in Uganda (FAO, 2010).

Geographical Gaps

A total of 84 districts located in 35 provinces of four East African countries and 54 districts located in 18 provinces of three Southern African countries were found as the important geographical gaps (Fig. 1, Table 2 and 3). Five districts of three provinces in Ethiopia, 12 districts of three provinces in Kenya, 37 districts of 14 provinces in Tanzania, 30 districts of 15 provinces in Uganda, six districts of three provinces in Malawi, 28 districts of eight provinces in Mozambique and 20 districts of seven provinces in Zambia were identified

as the geographical gaps in the collections from ESA countries (Fig. 1, Table 2 and 3). Maximum districts (37) were identified as gaps in Tanzania. Districts of Welo in Ethiopia; Kagera, Kigoma, Mara, Mwanza, Rukwa, Shinyanga and Singida in Tanzania; Kamuli, Kibaale, Kitgum, Kotido, Moroto, Pallisa in Uganda; Central and Northern in Malawi; Inambane, Manica, Maputo, Nassa, Sofala and Tete in Mozambique and Central, Copper belt, Lusaka and Southern in Zambia were not explored during the past collection missions launched by ICRISAT.

Gaps in Trait-specific Diversity

Eight districts in Eastern, Central and Coast provinces in Kenya were identified as gaps in phenotypic diversity for all traits (Fig. 2 and Table 4). Mubende district in South Buganda province for days to 50% flowering; Hoima and Msindi districts in Western province for seeds/pod, shelling percentage and seed yield/plant and Apec and Gulu districts in Northern province for primary and secondary branches/plant and shelling percentage were the trait diversity gaps in Uganda. Coast, Dodoma, Mtwara and Tanga provinces for all traits except pods/plant, Arusha and Dodoma provinces for pods/plant were identified as gaps in Tanzania. Zambezia province in Mozambique was identified as gap for diversity of all traits. Nsanje and Thyolo for days to 50% flowering, Balantyre, Chickwawa, Chiradzulu, Machinga, Mulanje, Mwanza Nsanje, Thyolo and Zomba districts in Southern province in Malawi were identified as gaps in diversity for all traits except days to 50% flowering. Chipata district in Eastern province of Zambia was identified as gap in diversity for primary branches/plant, shelling percentage and seed yield/plant.

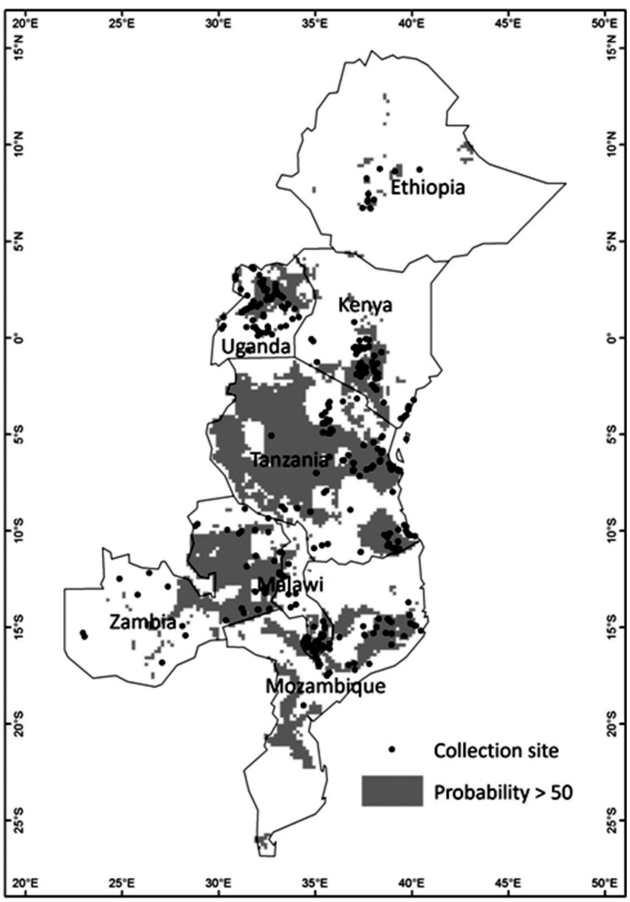

Fig. 1. Geographical distribution and the gaps (districts shaded) identified in the pigeonpea landraces collection from East and Southern African countries at ICRISAT genebank

Table 2. Geographical gaps (districts) identified in pigeonpea germplasm from East Africa, assembled at ICRISAT genebank

Country	Province	District
Ethiopia	Hararge	Dire Dawa-Isa-Gurgur, Jijiga
	Shewa	Haykoch & Butajira, Yerer & Kereyu,
	Welo	Wag
Kenya	Coast	Taita-Taveta
	Eastern	Isiolo, Kitui, Machakos, Meru, Nithi
	Rift Valley	Kajiado, Laikipia, Narok, Samburu, Turkana, West Pokot
Tanzania	Arusha	Kiteto
	Iringa	Iringa, Njombe
	Kagera	Biharamulo, Muleba, Ngara
	Kigoma	Kasulu, Kibondo, Kigoma
	Lindi	Kilwa, Lindi, Liwale, Nachingwea
	Mara	Bunda, Magu, Musoma, Serengeti
	Mbeya	Chunya, Mbeya, Mbozi
	Morogoro	Morogoro
	Mwanza	Geita, Kwimba, Sengerema
	Pwani	Kisarawe
	Rukwa	Mpanda, Nkasi, Sumbawanga
	Shinyanga	Kahama, Maswa, Shinyanga,
	Singida	Iramba, Manyoni, Singida,
	Tabora	Igunga, Nzega, Tabora
Uganda	Apac	Kwania
	Arua	Koboka, Madi-okollo,
	Gulu	Ajwa, Nwoya,
	Kamuli	Budiope, Bulamogi
	Kibaale	Bugangaizi
	Kiboga	Kiboga
	Kitgum	Agago, Aruu, Chua, Lamwo
	Kotido	Jie, Labwor,
	Kumi	Bukedea, Ngora
	Lira	Dokolo, Kiyoga, Moroto, Otuke
	Luwero	Buruli, Nakaseke
	Masandi	Kibanda
	Moroto	Bokora
	Pallisa	Pallisa
	Soroti	Amuria, Kaberamaido, Kapelebyong, Usuk

Table 3. Geographical gaps identified in pigeonpea germplasm from Southern Africa assembled at ICRISAT genebank

Country	Province	District
Malawi	Central	Ntcheu
	Northern	Karonga, Mzimba, Nkata-Bay, Rumphi
	Southern	Mangochi
Mozambique	Inambane	Govuro, Inchassaro, Mabote
	Manica	Gondola, Guro, Machaze, Macossa, Mussarize, Sussumdenga
	Maputo	Boane, Namacha,
	Nampula	Muecate
	Nassa	Cuamba, Matarica, Maua, Mecanhelas, Nipepe
	Sofala	Buzi, Chibabava, Gorongosa, Machanga, Muamza
	Tete	Chifunde, Chiuta, Moatize
	Zambezia	Gile, Ile, Morrumbal
Zambia	Central	Kabwe-rural, Mkushi, Mumbwa, Serenje
	Copper belt	Kalulishi, Kitwe, Luanshya, Ndola-rural
	Lauapula	Mansa, Mwense, Samfiya
	Lusaka	Luangwe, Lusaka-rural
	Northern	Chilubi, Chinsali, Empika, Luwingu
	North-western	Mufumbwe
	Southern	Kalomo, Namwala

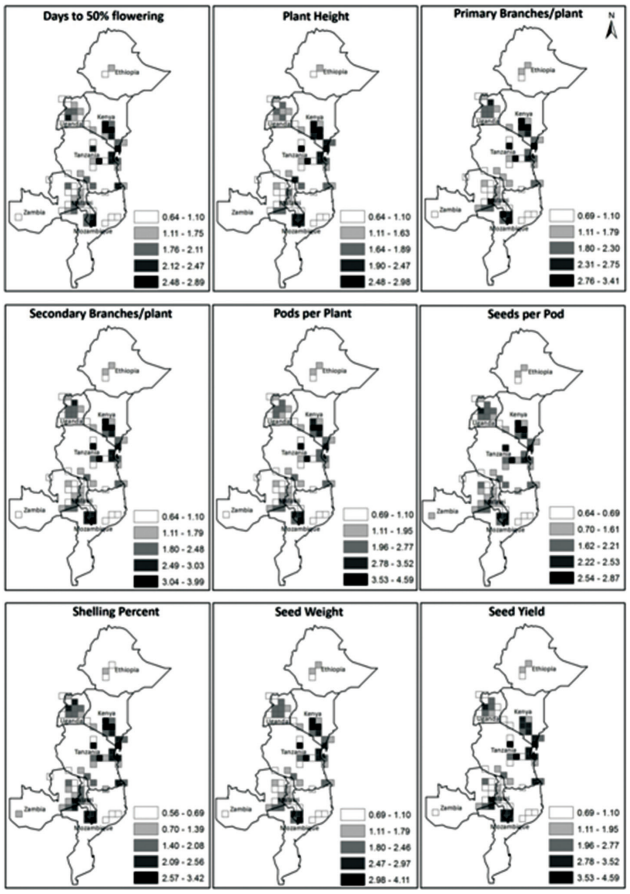

Fig. 2. High diversity areas (grids) for different agronomic traits of pigeonpea landraces from East and Southern Africa

Discussion

Success of gap analysis depends on the quality of input data. In many genebanks, most of the older germplasm collections do not have complete passport information, particularly, the georeference data (latitude and longitude) of the collection sites, which poses a problem in assessing the geographical completeness of collections (Upadhyaya *et al*., 2010b). Inaccuracy of georeference data is an additional constraint. Updating passport data for location information and geo-reference data and their validation is essential for the identification of gaps using GIS software such as FloraMap and DIVA-GIS. The gaps are more evident in legume crops including wild relatives (Khoury *et al*., 2010). The geographical gaps identified here using FloraMap and the gaps identified

Table 4. Gaps identified (districts) in diversity for different traits of pigeonpea germplasm from East and Southern Africa assembled at ICRISAT genebank

Country	Province/State	Districts	Traits*
Kenya	Coast	Kwale	DFL, PHT, PRBR, SCBR, PDPL, SDPD, SHP, SDWT, SDYLD
	Central	Kirinyaga, Muranga, Nyeri, Thika	DFL, PHT, PRBR, SCBR, PDPL, SDPD, SHP, SDWT, SDYLD
	Eastern	Imbu, Kitui, Machakos	DFL, PHT, PRBR, SCBR, PDPL, SDPD, SHP, SDWT, SDYLD
Uganda	North	Apac, Gulu	PRBR, SCBR, SHP
	South Buganda	Mubende	DFL
	Western	Hoima, Masindi	SDPD, SHP, SDYLD
Tanzania	Coast, Dodoma, Mtwara, Tanga		DFL, PHT, PRBR, SCBR, SDPD, SHP, SDWT, SDYLD
	Arusha, Dodoma		PDPL
Mozambique	Zambezia		DFL, PHT, PDPL, SDPD, SDYLD, SHP, PRBR, SCBR, SDWT
Malawi	Southern	Nsanje and Thyolo	DFL
		Balantyre, Chikwawa, Chiradzulu, Machinga, Mulanje, Mwanza, Nsanje, Thyolo, Zomba	PHT, PRBR, SCBR, PDPL, SDPD, SHP, SDWT, SDYLD
Zambia	Eastern	Chipata	PRBR, SDYLD, SHP

*DFL=Days to 50% flowering, PHT=Plant height, PDPL=Pods/plant, SDPD=Seeds/pod, PRBR=Primary branches/plant, SCBR=Secondary branches/plant, SHP=Shelling percentage, SDWT=100 seed weight, SDYLD=Seed yield/plant (g).

in trait-specific diversity using DIVA-GIS will provide valuable information such as geographical distribution of species and related traits (Marilia *et al*., 2003; Upadhyaya *et al*., 2010b).

The genetic potential of crop wild relatives (CWR) in crop improvement is now well demonstrated and are likely to contain some traits of interest including climate change adaptation (FAO, 2008). For example, *Dunbaria ferruginea* Wight and Ann. for salinity tolerance (Singh *et al*., 1990), *D. heynei* Wight & Ann as a green manure (Arora and Chandel, 1972), *Eriosema ellipticum* Wel. Ex Beker (Abbot and Lowore, 1995), *Rhynchosia minima* (L.) DC as medicinal use (Morris, 1999) and *R. rothii* Benth. Ex. Aitch, as a source for high seed protein content (>30%) (Remanandan, 1981).

When the levels of resistance to various biotic and abiotic stresses in cultivated germplasm are low or the range of genetic variability is narrow and selection pressure results in virulent biotypes of the pests and diseases, the discovery and incorporation of additional genes for resistance from wild species becomes key to sustaining crop productivity. ICRISAT had launched only a few collection missions exclusively for wild relatives and conserves only a fraction of total genetic variability that exists in wild relatives (Jarvis *et al*., 2008; Upadhyaya *et al*., 2010b). Out of 555 wild accessions belonging to 66 species of six genera conserved at ICRISAT genebank, 63 accessions of 14 species belonging to three genera are from ESA countries. Out of 33 species of *Rhynchosia*, 12 are from ESA countries indicating ESA as good source region for *Rhynchosia*. Therefore, there is a need for launching collection missions exclusively for wild relatives of pigeonpea to fill taxonomical gaps in the collection at ICRISAT genebank.

Wide variation for latitude (from -26 00^{o} in South Africa to 8.75^{o} in Ethiopia) and longitude (from 23.06^{o} in Zambia to 44.48^{o} in Mozambique) of collection sites indicates that the landraces from ESA countries are from diverse climates and show wide adaptation. Nene and Sheila (1990) reported the adaptation of pigeonpea landraces up to 32^{o} latitudes on both sides of equator. Remanandan and Mengesha (1981) reported that the main land in Tanzania has been adequately covered and fairly represented in the pigeonpea collection and the island of Zanzibar needs to be considered for collection in future. Remanandan and Mengesha (1981) reported that the collection from Tanzania is from altitudes ranging between 1000-1500 m and may be a good source for cold tolerance. Remanandan (1990) reported gaps in collection from Uganda. Collections from Tanzania and Kenya are mostly large seeded, perennial type and suitable for use as vegetable and agroforestry (Remanandan and Mengesha, 1981; Remanandan *et al*., 1982).

Pigeonpea originated in India spread around 2200-2000 BC to Africa where a secondary center of diversity developed (van der Maesen, 1980). With the slave trade, the pigeonpea was carried from Africa to the Americas. ESA being the secondary center of diversity for pigeonpea, the geographical, diversity and taxonomical gaps (all wild relatives of cultivated pigeonpea) identified in the study may be considered as the potential areas for exploration (van der Maesen, 1990) (Table 2, 3 and 4).

The gaps identified in the present study can be prioritized (Table 2, 3 and 4). Generally, prioritization will be done by the collecting team at the time of actual launch of the collection mission depending upon the threat to diversity, availability of resources and accessibility to the target region. The districts, which were found as gaps in diversity for almost all traits and those common for geographic area and diversity may be explored on priority to increase the variability in the collection. It is suggested to increase the variability not only for important agronomic traits but for new and adaptive traits also by filling gaps in the pigeonpea collection from ESA countries. Districts/provinces, the area under pigeonpea cultivation is high and per ha representation in ICRISAT genebank is low, thus require further exploration to have good representation and more variability in the world collection of pigeonpea (FAO, 2010). Uganda was under represented in the world collection of pigeonpea at ICRISAT (Upadhyaya *et al*., 2005). Because of habitat loss, changing cropping patterns and food habits in different parts of ESA, it is suggested that the area for exploration in the districts identified may be decided prior to the launch of the collection mission in consultation with local government officials, NARS scientists, extension officers and non-governmental organizations, who will have the knowledge of pigeonpea cultivation in the districts. All reports and other publications on past collections should be considered while preparing route maps for districts identified as gaps. It is especially important to collect complete passport information, including georeference data while collecting germplasm samples in order to facilitate future mapping efforts.

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References

Abbot P and J Lowore (1995) *Livestock grazing in Chimaliro Forest Reserve*: Preliminary results and implications for the management of browse resources, 25p.

Arora RK and SPS Chandel (1972) Botanical source areas of wild herbage legumes in India. *Trop. Grasslands*. **6**: 213-221.

Bohra Abhishek, Nalini Mallikarjuna, Kulbhusan Saxena, Hari Upadhyaya, Isabel Vales and Rajeev Varshney (2010) Harnessing the potential of crop wild relatives through genomics tools for pigeonpea improvement. *Plant Biol*. **37**: 85-100.

Food and Agriculture Organization (2010) http://www/FAO. ORG/FAOSTAT database.

Food and Agriculture Organization of the United Nations (2008) *Climate Change and Biodiversity for Food and Agriculture*. Rome: FAO, Rome, Italy.

Hijmans RJ, L Gaurino and E Rojas (2005) DIVA-GIS, version 5.0. *A geographic information system for the analysis of biodiversity data-Manual*. International Potato Center, Lima, Peru.

Hijmans RJ and DM Spooner (2001) Geographic distribution of wild potato species. *American J. Bot.* **88**: 2101-2112. Available online (accessed 6 October 2011): www.amjbot. org/content/88/11/2101.full.

IBPGR and ICRISAT (1993) *Descriptors for Pigeonpea* [*Cajanus cajan* (L.) Millsp.]. International Board for plant Genetic Resources, Rome, Italy. International Crops Research Institute for the Semi-Arid Tropics, Patancheru, India.

Jarvis A, A Lane and RJ Hijmans (2008) The effect of climate change on crop wild relatives. *Agri. Ecosystems Env.* **126**: 13-23.

Jones PG and A Gladkov (1999) *FloraMap*: a Computer tool for predicting the distribution of plants and other organisms in the wild. Version 1. Edited by Annie L. Jones, CIAT, CD-ROM series, Cali, Colombia; Centro Internacional de Agricultura Tropical.

Khoury C, B Laliberte and L Guarino (2010) Trends in *ex situ* conservation of plant genetic resources: a review of global crop and regional conservation strategies. *Genet. Resour. Crop Evol.* **57**: 625-639. Doi:10.1007/s10722-010-9534-z.

Marilia Lobo Burle, Celia Maria Torres Cordeiro, Jaime Roberto Fonseca, M Palhares de Melo, Rosa de Belem das Neves Alves and Tabare Abadie (2003) Characterization of germplasm according to environmental conditions at the collecting site using GIS-two case studies from Brazil. *Plant Genet. Resour. Newslett.* **135**: 1-11.

Morris JB (1999) Legume genetic resources with novel "value added" industrial and pharmaceutical use. *In:* Janick J (ed.), *Perspectives on New Crops and New Uses*. ASHS Press, Alexandria, VA. pp. 196–201.

MS Encarta^{R} Interactive World Atlas (2000) 1995-1999 Microsoft Corporation. One Microsoft way, Redmond, WA 98052-6399.

Nene YL and VK Sheila (1990) Pigeonpea: Geography and importance. *In:* Nene YL, SD Hall and VK Sheila (ed) *The pigeonpea*, CAB International, Wallingford, Oxon OX 10 8DE, UK, pp 1-14.

Prasada Rao KE and MH Mengesha (1982) Sorghum germplasm collection in Rwanda. *Genetic Resources Progress Report 46*. ICRISAT, Patancheru, Andhra Pradesh, India.

Ramanatha Rao V (1981) Germplasm collection mission to Mozambique. *Genetic Resources Progress Report 35*. ICRISAT, Patancheru, Andhra Pradesh, India.

Reddy VG, P Remanandan, EN Sabiiti and MH Mengesha (1993) Sorghum, finger millet and pigeonpea germplasm collection in Uganda. *Genetic Resources Progress Report 77*. ICRISAT, Patancheru, Andhra Pradesh, India.

Remanandan P (1981) The wild gene pool of *Cajanus* at ICRISAT, present and future. *In: Proceedings of the International Workshop on Pigeonpea*, Volume 2, 15-19 December 1980, ICRISAT, Patancheru, Andhra Pradesh, India, pp 29-38.

Remanandan P (1990) Pigeonpea Genetic Resources. *In:* Nene YL, SD Hall and VK Sheila (ed.), *The Pigeonpea*. CAB International, Wallingford, OXM OX10 8DE, UK, pp 1-14.

Remanandan P and MH Mengesha (1981) Pigeonpea germplasm collection mission in Tanzania. *Genetic Resources Progress Report 38*. ICRISAT, Patancheru, Andhra Pradesh, India.

Remanandan P, A Shakoor and ECK Ngugi (1982) Pigeonpea germplasm collection mission in Kenya. *Genetic Resources Progress Report 48*. ICRISAT, Patancheru, Andhra Pradesh, India.

Shannon CE and W Weaver (1949) *The mathematical theory of communication*. Univ. Illinois Press, Urbana.

Singh L, SC Gupta and DG Faris (1990) Pigeonpea Breeding. *In:* Nene YL, SD Hall and VK Shiela (ed) *The Pigeonpea*. CAB International, Wallingford, Oxon OX 10 8DE, UK, pp 89-115.

Singh AK, DG Rusoke, MWO Latigo, SZ Mukuru and S Appa Rao (1991) Legumes germplasm collection in Uganda. *Genetic Resources Progress Report 66*. ICRISAT, Patancheru, Telangana, India.

Upadhyaya HD and CLL Gowda (2009) *Managing and enhancing the use of germplasm-strategies and methodologies*. Technical Manual no.10. ICRISAT, Patancheru, Andhra Pradesh, India, 236 p.

Upadhyaya HD, RPS Pundir, CLL Gowda, KN Reddy and Sube Singh (2005) Geographical patterns of diversity for qualitative and quantitative traits in the pigeonpea germplasm collection. *Plant Genetic Resources: Characterization Utilization* **3**: 331-352.

Upadhyaya HD, KN Reddy, CLL Gowda and Sube Singh (2010a) Identification and evaluation of vegetable type pigeonpea

(*Cajanus cajan* (L.) Millsp.) in the world germplasm collection at ICRISAT genebank. *Plant Genetic Resources: Characterization Utilization* **8**: 162-170.

Upadhyaya HD, KN Reddy, M Irshad Ahmed and CLL Gowda (2010b) Identification of gaps in pearl millet germplasm from Asia conserved at the ICRISAT genebank. *Plant Genetic Resources: Characterization Utilization* **8**: 267-276.

USGS EROS Center (2005) Africa land cover characteristics database.

van der Maesen LJG (1976) Pigeonpea collection trip in Kenya. *Genetic Resources Progress Report 18*. ICRISAT, Patancheru, Andhra Pradesh, India.

van der Maesen LJG (1980) India is the native home of the pigeonpea. Liber gratulatorius in honoreum HCD de Wit, Miscellaneous papers 19, Landbouwhoge school Wageningen, pp 257-262.

van der Maesen LJG (1982) Germplasm collection in South Africa. *Genetic Resources Progress Report 43*. ICRISAT, Patancheru, Andhra Pradesh, India.

van der Maesen LJG (1990) Pigeonpea: Origin, history, evolution and taxonomy. *In:* Nene YL, Hall SD, Sheila VK (ed.), *The pigeonpea*. CAB International, Wallingford, Oxon OX 10 8DE, UK, pp 44-87.

van Treuren R, P Coquin and U Lohwasser (2011) Genetic resources collections of leafy vegetables (lettuce, spinach, chicory, artichoke, asparagus, lamb's lettuce, rhubarb and rocket salad): composition and gaps. *Genet. Resour. Crop Evol.* DOI 10.1007/s10722-011-9738-x.