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Hans H. Ruthenberg Award for Graduates 2009

Anne Rysavy “GIS based Gap Analysis as a Tool for Biodiversity Conservation Optimization: The IITA Cowpea Collection”

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Summary

Cowpea (*Vigna unguiculata* (L.) Walp.) is an important grain legume cultivated in most tropical and some temperate regions. It is one of the most widely adapted, versatile grain legumes of high nutritious value. Cowpea production across Africa accounts for approx. 91% of world output. Cowpea has an impact on nutrition as a valuable protein source and livelihoods of small scale farmers and plays a key role in the life of many people, especially in developing countries. The International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria, maintains the world collection of cowpea in trust for the international community. But besides conservation, multiplication, regeneration and characterization of germplasm collections another central function of a genebank is the expansion of germplasm collections to cover as much agrobiodiversity as possible.

Many literature sources cite that biodiversity is constantly diminishing. Today only 150 of originally 270,000 species are cultivated and 80% of agricultural production relies on only 12 species. Rice (*Oryza sativa*), wheat (*Triticum spp*), maize [*Zea mays*] and potato [*Solanum tuberosum*] provide approx. 50% of human's energy requirements. As biodiversity is exposed to different natural, biological and anthropogenic hazards, accelerating the speed of loss and leading to irreplaceable losses of agricultural biodiversity, it is of high importance to stop and reverse this trend.

Aware of the fact that IITA's cowpea collection displays some gaps cowpea is an obvious target crop for a GIS based gap analysis to avoid future losses of cowpea genetic diversity. Therefore, it is of high importance to assess the cowpea accession collection at IITA to get an overview about the current conservation status and to guide future sampling. A gap analysis is an evaluation technique to estimate the degree of coverage of already sampled regions, to identify regions in Africa where the probability of finding more and diverse cowpea accessions is the highest and hence, additional sampling is needed and those where no collections have been performed yet.

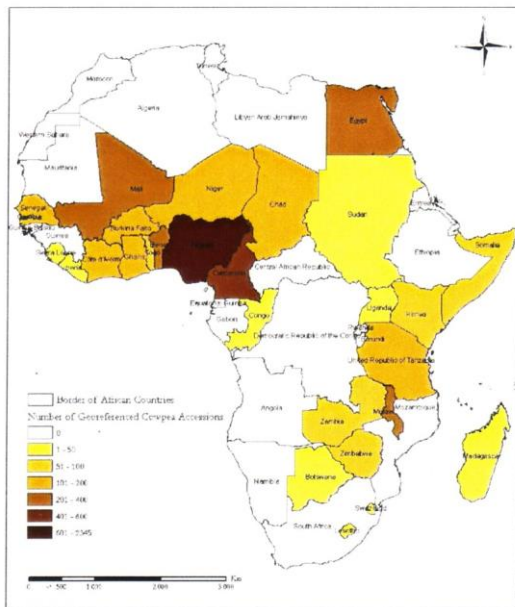


Fig. 1 Country-wise distribution of georeferenced cowpea accessions.

The original database reported 10,814 cowpea accessions of African origin, approx. 50% with geographical coordinates available. As only accessions with location data in coordinate form can be used in GIS the first aim of this study was to complement the location information of as many accessions as possible. This was done with World Wind 1.4 which allowed georeferencing an additional 677 accessions. A final crosscheck to validate the spatial accuracy of the data was performed using ArcMap a commercial application part of ArcGIS™.

The final database for analysis counted 5,717 accessions with the correct geographical coordinates (Fig. 1). This represents 53% of the African cowpea accessions available within the IITA genebank.

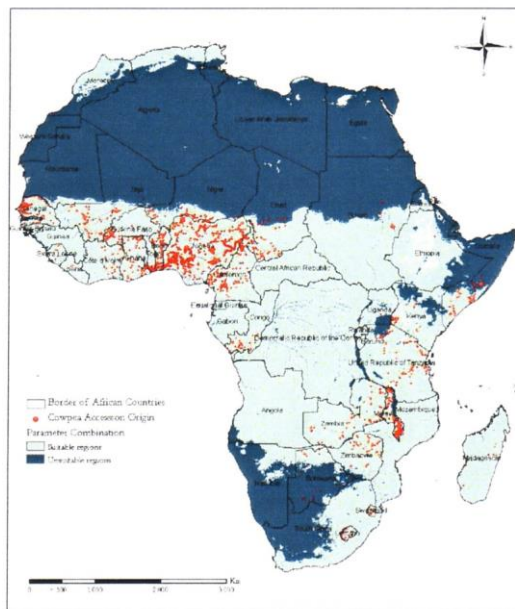


Fig. 2 Geographic origin of African cowpea germplasm maintained in IITA genebank and the regions suitable and unsuitable for cowpea growth derived by the parameter combination.

In the next step ecogeographical site descriptors: temperature, precipitation, length of growing period and altitude, were extracted to determine areas with environmental conditions favored by cowpea. Therefore regions with similar environmental conditions were identified using GIS techniques to predict areas where the possibility of filling gaps in the collection is most likely.

As shown in Fig. 2 regions with similar environmental conditions cover approx. all of sub-Saharan Africa except some regions located in East Africa (Rwenzori Mountains and Ethiopian Highlands), as well as in South Africa, where the Kalahari Desert extends. This study used the spatial analysis tools FloraMap™, Homologue™ and DIVA-CIS to identify potential areas for future conservation activities of cowpea.

FloraMap™ extracts climatic variables for every pixel an accession is located in. These are 12 monthly averages for temperature, rainfall totals and mean diurnal temperature ranges. Afterwards a Principle Component Analysis was applied.

Homologue™ is an advancement of FloraMap™, hence uses the same central algorithm for climate. Additionally the software takes variable soil conditions into account. DIVA-GIS is a varied computer tool that can be used for many different purposes such as mapping biological diversity distribution, identifying complementary areas in terms of diversity or extract climate data using BIOCLIM and DOMAIN algorithms.

The geographical scope of the present study was focused on sub-Saharan Africa. Results of all three software applications indicated that cowpea can be found between 15°N and 20°S. With respect to new collections main focus should be put on countries where so far no collections have been done, but where the spatial analysis showed high probability of encountering cowpea — Burundi, Eritrea, Equatorial-Guinea, Guinea-Bissau, Namibia and Rwanda respectively. In countries with only few georeferenced accessions, existing non-georeferenced passport data of cowpea accessions need to be complemented or new sampling should be carried out. The ecogeographic distribution of cowpea showed that cowpea occurs over a large range of climates - temperature as well as precipitation. However, it occurs most likely in subtropical to tropical conditions characterized by warm temperatures and relatively high precipitation. It was demonstrated that the software applications FloraMap™, Homologue™ and DIVA-GIS, including the predictive models EcoCrop, BIOCLIM and DOMAIN could be useful tools to perform a gap analysis for the existing cowpea germplasm collection. Generally speaking, all methodologies were successfully applied and it was possible to predict the continent wide potential distribution of cowpea and prioritize future sampling areas. In conclusion, the greatest benefit of this study may be the fact that it was possible to get an overview about the distribution of collected cowpea accessions in Africa and guide or limit future conservation activities. Furthermore it can be concluded that predictive models should only help and complement expert knowledge rather than replace it. AU methodologies described are useful approaches in conserving genetic diversity of useful species.

Key words: Biodiversity - Cowpea (*Vigna unguiculata* (L.) Walp.) - Distribution — DIVA-GIS -FloraMap™ — Gap Analysis — Genetic Conservation — Homologue™