Measuring the state of conservation of crop diversity:

A baseline for marking progress toward biodiversity conservation and sustainable development goals

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Key Messages:

- Urgent biodiversity conservation and sustainable development goals have been set for countries to fully maintain the genetic diversity of cultivated plants and their wild relatives as well as domesticated animals by 2020.
- "Gap analysis" methods are important tools for measuring the current state of conservation of crop and livestock genetic diversity in genebanks, in farmers' fields, and in natural habitats.
- A recent gap analysis study has provided the baseline for the current state of conservation of crop wild relatives in genebanks worldwide, revealing that over 70% of these species require urgent collecting from the wild due to their lack of representation, and over 95% are insufficiently represented with regard to the full range of variation in their native distributions.
- Gap analysis data, methods and results enable measurement of progress as countries work toward meeting their international biodiversity conservation and sustainable development commitments.

Urgent conservation targets for agricultural genetic diversity

New international agreements on sustainable development and biodiversity conservation explicitly prioritize fully safeguarding the genetic diversity of crops and their wild relatives as well as domesticated animals by 2020 **(Table 1)**. These specific targets exist due to an increasing awareness of the value of genetic diversity to food security, improved nutrition, and sustainable agriculture via crop and livestock breeding. At the same time, the priorities recognize the increasing threats to this diversity in natural habitats, farmers' fields and underfunded genebanks, which must be mitigated to ensure that this diversity will be available for use in addressing unforeseen challenges to future food security.

A central challenge in meeting these targets is quantifying the current state of conservation of agricultural genetic diversity, and making it feasible to measure progress in coming years. Data to directly assess levels of genetic diversity in agricultural species is broadly lacking, especially with regard to crop wild relatives. Extensive further collecting of genetic material and major investments in genotyping would be required to directly quantify genetic diversity in these species. While this may become increasingly feasible as relevant technologies continue to advance, a practical, efficient, and rapid methodology is urgently needed to estimate the current state of conservation of diversity in agricultural species. Such an approach should ideally contribute to pinpointing the potential diversity not yet safeguarded, and be capable of re-assessments to measure progress over time.

Table 1: International agreements related to the conservation of agricultural diversity

Agreement	Target	Relevant Text
United Nations Sustainable Development Goals (SDGs)	Goal 2 (End hunger, achieve food security and improved nutrition, and promote sustainable agriculture), Target 2.5	"By 2020 maintain genetic diversity of seeds, cultivated plants, farmed and domesticated animals and their related wild species, including through soundly managed and diversified seed and plant banks at national, regional and international levels, and ensure access to and fair and equitable sharing of benefits arising from the utilization of genetic resources and associated traditional knowledge as internationally agreed."
Convention on Biological Diversity (CBD), Strategic Plan for Biodiversity 2011-2020, Aichi Biodiversity Targets	Target 13	"By 2020, the genetic diversity of cultivated plants and farmed and domesticated animals and of wild relatives, including other socio-economically as well as culturally valuable species, is maintained, and strategies have been developed and implemented for minimizing genetic erosion and safeguarding their genetic diversity."
Convention on Biological Diversity (CBD), Global Strategy for Plant Conservation (GSPC), Updated Strategy 2011-2020	Objective 2 (Plant diversity is urgently and effectively conserved), Target 9	"70 per cent of the genetic diversity of crops including their wild relatives and other socio-economically valuable plant species conserved, while respecting, preserving and maintaining associated indigenous and local knowledge."
United Nations Food and Agriculture Organization (FAO), International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA)	Articles 5, 6, 10 and elsewhere	Text recognizing the need for enhanced conservation *in situ* and *ex situ* of crops and their wild relatives, for minimizing threats to this diversity, and for facilitated access and fair sharing of the benefits arising from the sustainable use of plant genetic resources.
United Nations Food and Agriculture Organization (FAO) Second Global Plan of Action for Plant Genetic Resources for Food and Agriculture	Priority Activities 1.4, 2.5, 2.6, and 3.8	Text recognizing the need for enhanced conservation *in situ* and *ex situ* of crops and their wild relatives.

Gap analysis methods provide a global baseline for the state of crop wild relative conservation in genebanks

Recent research by the International Center for Tropical Agriculture (CIAT) in collaboration with the Global Crop Diversity Trust (Crop Trust) and the Royal Botanic Gardens (RBG), Kew assessed the degree of conservation in genebanks of 1,076 species of wild plants closely related to 81 important food and agricultural crops. The analysis initially mapped the distributions of these species in the wild, providing the world's first global atlas of crop wild relatives. The researchers then compared the native distributions of the wild relatives with the geographic locations where these species have already been collected for conservation in genebanks. This comparison was used to prioritize each species for further collecting based upon its degree of conservation with regard to overall number of samples maintained in genebanks, and whether the full geographic and ecological variation (i.e., whether all ecosystems where the species is likely to occur) was represented by samples in genebanks **(Figure 1).**

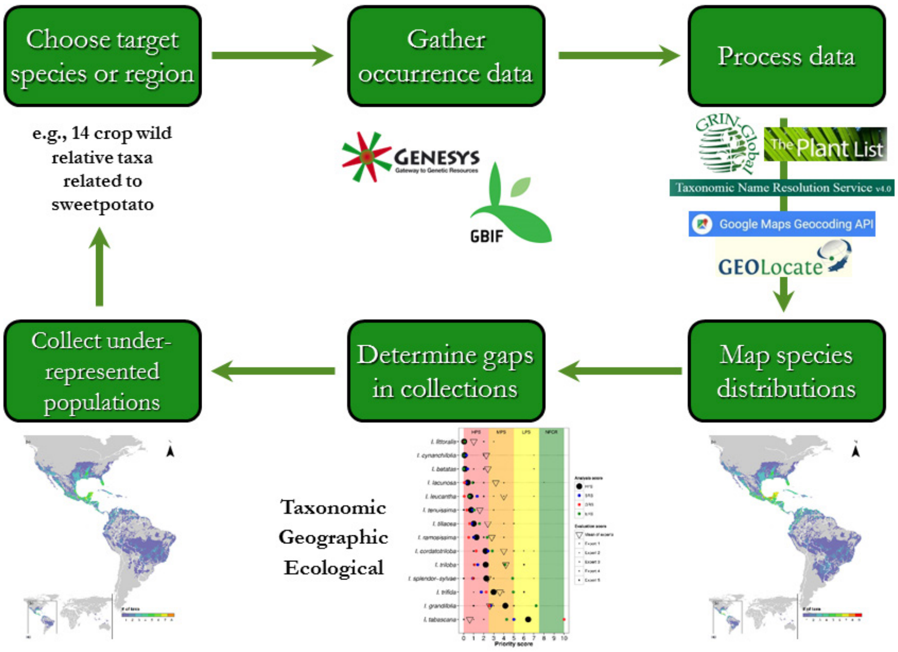

Figure 1: *Conservation gap analysis method, including examples of input data resources and results for the wild relatives of sweetpotato. The analysis is shown as a cycle, demonstrating the potential for iterative assessments to measure progress over time. Gap analysis can be applied at the species or crop genepool scale (as shown here), and subsequently combined to produce national, regional, and global level assessments. For further information see Khoury et al. (2015) and Castañeda-Álvarez et al. (2016).*

The conservation "gap analysis" found that 313 (29%) of wild relative plant species analyzed were completely missing from the world's genebanks, with a further 257 (24%) represented by fewer than 10 samples. Over 70% of all crop wild relative species worldwide were assessed as in urgent need of further collecting to improve their representation in genebanks, and over 95% were found to be insufficiently represented with regard to the full range of geographic and ecological variation in their native distributions. While the most critical priorities for further collecting were found in the Mediterranean and Near East, Western and Southern Europe, Southeast and East Asia, and South America, crop wild relatives that are not sufficiently represented in genebanks were found to occur in almost all countries worldwide **(Figure 2).**

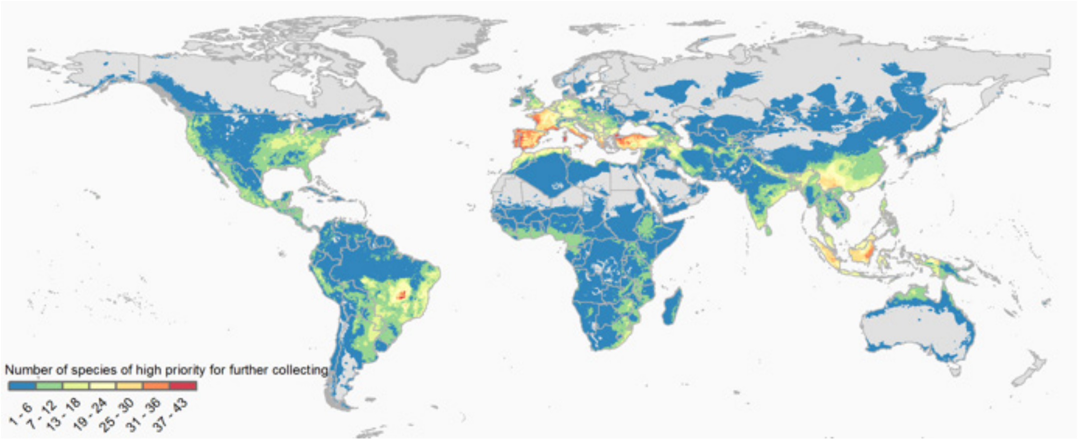

Figure 2: *Global hotspots of distributions of crop wild relative species assessed as in urgent need of further collecting to improve their representation in genebanks. Areas colored yellow, orange, and red possess the highest concentrations of under-represented species. For further information see Castañeda-Álvarez et al. (2016).*

The research is part of the project Adapting Agriculture to Climate Change, a global 10-year effort to collect, conserve and promote the use of the wild relatives of 29 major crops. The project is funded by the Norwegian government and managed by the Crop Trust in partnership with the Millennium Seed Bank of RBG, Kew. The project is being implemented with national and international organizations involved in crop conservation and breeding efforts, and directly contributes to improving the degree of conservation and availability for breeding of crop wild relatives at national and global levels. The initiative is projected to support crop wild relative collecting in 20 to 25 countries. Further details on the global baseline for the state of conservation of crop wild relatives is available at www.cwrdiversity.org.

A case study for measuring change in conservation status of a wild relative species over time

The gap analysis method quantifies the state of conservation of crop wild relatives maintained at a certain point in time in genebanks. The approach can be applied iteratively to assess progress after conservation actions have taken place. To illustrate this use, we performed a historical gap analysis for *Solanum acaule* Bitter, an important potato wild relative native to the Peruvian, Bolivian, and Argentine Andes that has contributed to frost tolerance and late blight (*Phytophthora infestans* (Mont.) de Bary) resistance (Castañeda-Álvarez et al. 2015).

We used historical records to assess the change in conservation status over time by analyzing the representation of the species in genebanks in decade intervals from 1950 to the present **(Figure 3)**. As the earliest genebank samples were collected from the field in the 1950's, the gap analysis results prior to that decade mark the species at the highest priority for collecting. Substantial collecting efforts particularly in the 1950's and 1970's reduced the level of priority for further collecting evident in the gap analysis results. The species is now considered to be sufficiently represented in genebanks. Unfortunately most other crop wild relatives have not received such conservation attention.

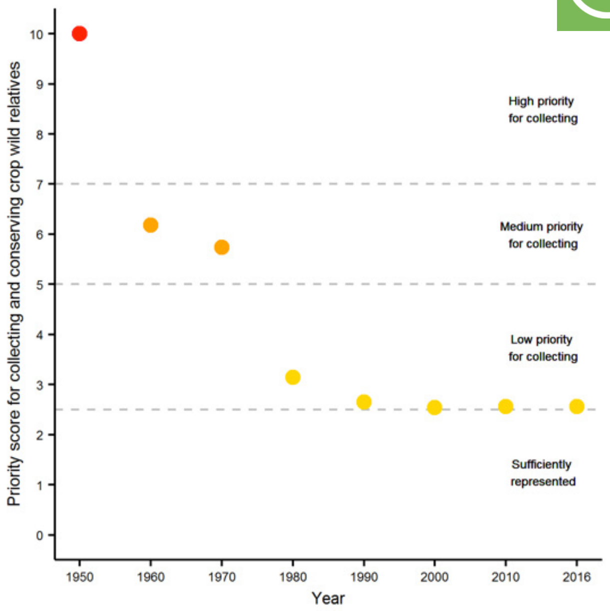

Figure 3: *Changes in priority for further collecting and conserving of Solanum acaule Bitter over time. The species was not represented in genebanks before the 1950's, and therefore was assessed at the highest priority for further collecting (priority score of 10). Collecting efforts in subsequent decades lowered the gap analysis priority result score, until in recent decades the species has come to be considered sufficiently represented in genebanks. For further information see Castañeda-Álvarez et al. (2015) and Castañeda-Álvarez et al. (2016).*

Application of the gap analysis method to other types of agricultural diversity

While the current gap analysis methodology and results can be immediately used as the baseline for the degree of conservation of wild species in genebanks related to most of our globally important food crops, the method can be modified to assess conservation in other organisms and conservation formats as well, including:

- ***Ex situ* and *in situ* conservation of cultivated crop diversity.** The gap analysis method can be applied to analyses of the degree of conservation in genebanks and farmers' fields of crop landraces and varieties. However, as the distribution of a cultivated species is also driven by cultural and socio-economic factors, modeling crop distributions will require adaptation and further refinement of existing methods, with the participation of social scientists, crop modelers, and other experts.

- *In situ* **conservation of wild relative species.** The gap analysis methodology can easily be applied to assessing the state of coverage of crop wild relative diversity in protected areas. Species distribution maps can be combined with maps of formally protected areas and analyzed with regard to the intensity of different threats to natural habitats. Distribution maps can also be used to prioritize new land areas for protection based upon high species richness or unique features worthy of conservation. Appropriate thresholds for the adequacy of conservation of such species *in situ* need further development.

- *Ex situ* **and** *in situ* **conservation of domesticated animal genetic diversity.** The known distributions of diverse livestock breeds can be compared to the locations where that diversity has previously been collected for conservation in genebanks, as well as where that diversity is actively maintained by farmers. This comparison can likewise aid in the identification of collecting priorities and of *in situ* conservation targets. Useful microbial, insect pollinator, and other biodiversity associated with food security can also be assessed through similar methods.

Beyond conservation, meeting Sustainable Development Goal 2.5 and other targets requires metrics for assessing progress in access to, and sharing of benefits arising from the use of, agricultural genetic diversity. Indicators measuring progress of compliance with the Multilateral System of Access and Benefit Sharing of the International Treaty on Plant Genetic Resources for Food and Agriculture, and the Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization of the Convention on Biological Diversity, are recommended.

Policy recommendations

Agricultural genetic diversity occurring in the wild, in farmers' fields, and in genebanks represents the global food system's raw material for further crop and livestock improvement and a safety net against hunger. We present a gap analysis method which provides the baseline for the degree of conservation of this diversity at national, regional, and global levels. The method can then be applied iteratively to measure progress over time in achieving conservation and sustainable development goals.

In order to meet impending conservation targets, such gap analysis methods should be urgently employed to assess the current degree of conservation of the broader wealth of agricultural biodiversity, and the results used to prioritize and implement specific actions aimed at conserving crop and wild relative and domesticated animal diversity *in situ* and *ex situ*. Follow-up gap analyses should be used to measure progress by countries and internationally toward the comprehensive conservation of this diversity. Ongoing global efforts to improve conservation of agricultural biodiversity are critically important, but these efforts must be expanded to include all countries and all important crops and their wild relatives, as well as livestock and other useful species, in order to truly achieve the comprehensive maintenance of genetic diversity in agriculture.

Further efforts beyond safeguarding of agricultural genetic diversity are also required by the different international agreements. Critical activities include ensuring that traditional knowledge associated with these resources is respected and preserved, protecting farmers' rights to practice conservation and exchange, ensuring that germplasm repositories are adequately equipped to conserve and distribute these genetic resources over the long term, and enhancing access and benefit-sharing with regard to this diversity worldwide.

The window of opportunity for taking steps to secure and make accessible the world's agricultural diversity threatened *in situ* and in underfunded genebanks will not remain open indefinitely, and concerted immediate efforts are clearly needed to reach the goals agreed upon by 2020.

Further Reading

Castañeda-Álvarez NP, Khoury CK, Achicanoy HA, Bernau V, Dempewolf H, Eastwood RJ, Guarino L, Harker RH, Jarvis A, Maxted N, Mueller JV, Ramírez-Villegas J, Sosa CC, Struik PC, Vincent H, and Toll J (2016). Global conservation priorities for crop wild relatives. *Nature Plants* 2(4): 16022.

This new research provides a global baseline for the state of conservation of 1076 crop wild relatives related to 81 of our most important food and agricultural *crops in genebanks. The data used in the analysis, the methods and the results can be applied at national, regional, and global levels to measure progress toward our shared conservation and development goals. All of the taxonomic and geographic data, methods and results are freely available under open source licenses in order to maximize their use. For more information, see the project website at www.cwrdiversity.org.*

Examples of gap analysis applied at the crop genepool level, referenced in this Brief:

- Castañeda-Álvarez NP, de Haan S, Juarez H, Khoury CK, Achicanoy HA, Sosa CC, Bernau V, Salas A, Heider B, Simon R, Maxted N, and Spooner DM (2015). *Ex situ* conservation priorities for the wild relatives of potato (*Solanum* L. section *Petota*). *PLoS One* 10(4): e0122599.

- Khoury CK, Heider B, Castañeda-Álvarez NP, Achicanoy HA, Sosa CC, Miller RE, Scotland RW, Wood JRI, Rossel G, Eserman LA, Jarret RL, Yencho GC, Bernau V, Juarez H, Sotelo S, de Haan S, and Struik PC (2015). Distributions, *ex situ* conservation priorities, and genetic resource potential of crop wild relatives of sweetpotato [*Ipomoea batatas* (L.) Lam., *I.* series *Batatas*]. *Frontiers in Plant Science* 6: 251.

Citation

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- More information about the project, visit www.cwrdiversity.org.

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