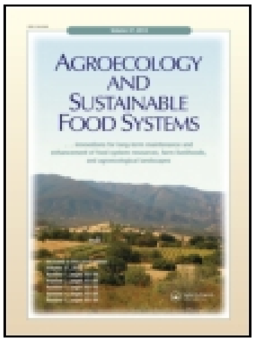

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Adapting Agriculture to Climate Change: A Global Initiative to Collect, Conserve, and Use Crop Wild Relatives

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The main objective of the"Adapting Agriculture to Climate Change" project is to collect and protect the genetic diversity of a portfolio of plants with the characteristics required for adapting the world's most important food crops to climate change. The initiative also aims to make available this diversity in a form that plant breeders can readily use to produce varieties adapted to the new climatic conditions that farmers, particularly in the developing world, are already encountering. Such adaptation is a key component of securing the world's future food production. This paper serves to inform interested researchers of this important initiative and encourage collaboration under its umbrella.

KEYWORDS crop wild relatives, food security, climate change, biodiversity conservation, plant breeding

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AGRICULTURAL PRODUCTION IS UNDER THREAT

The world's human population is predicted to reach over 9.3 billion by the year 2050 (U.S. Census Bureau 2014) and shifts in diets toward animal products, oils, and other resource intensive foodstuffs are placing ever more pressure on agricultural systems to increase production (Kastner et al. 2012). At the same time, degraded soils—as well as water, arable land, and other resource limitations—challenge production, and climate change represents an increasingly serious threat (Lobell et al. 2008). This widening mismatch between demand and supply is causing grave concern for future food security.

By 2050, much of the world will experience a growing season that will likely have higher temperatures than the hottest growing seasons of recent times and this increase in temperatures will probably be accompanied by more variable rainfall (Battisti and Naylor 2009). Crops will be impacted in various ways. For example, rice flowers show increased sterility at higher temperatures. Maize is also very sensitive to drought at the time of flowering. Wheat senescence starts earlier and is faster under warmer conditions (Lobell et al. 2012). Adding up these and other effects, models show possible yield losses of 6–10% per 1°C of warming in the average temperature of the growing season (Guarino and Lobell 2011). This means the world could see significant production losses in the future.

Taking more land under cultivation to increase food production is not an option in most parts of the world without serious impacts on wild biodiversity and the provision of ecosystem services—increasing agricultural yields in a framework of sustainable intensification is therefore an important solution (Garnett et al. 2013). Significant headway can be made by improving agricultural practices and creating more favorable policy environments—for example to avoid food wastage—but such measures can only provide a partial solution. It will be crucial to adapt agriculture to the increasingly challenging environmental conditions by breeding new crop varieties. The list of possible plant traits that could be used is long, including everything from enhanced root growth to faster grain filling.

THE ROLE OF CROP WILD RELATIVES IN FUTURE FOOD SECURITY

Domestication has led to a severe reduction in genetic diversity within most crops when compared to their wild relatives (domestication bottleneck, e.g., Olsen and Gross 2008). To meet the challenges of the future, plant breeders will need all the genetic diversity that they can get. Some of this diversity can be found in landraces and heirloom varieties that are still being cultivated by farmers around the world. However, a much wider spectrum of diversity can be found in the genomes of the wild plant species closely related to crops (so called crop wild relatives, or CWR). CWR have been successfully used in plant breeding in the past (Hajjar and Hodgkin 2007). They are of key importance to breeding efforts that aim to help adapt agriculture to climate change (Guarino and Lobell 2011). For example, a wild rice (*Oryza officinalis*) has recently been used to change the time of flowering of the rice cultivar Koshihikari (*O. sativa*) to avoid the hottest part of the day (Ishimaru et al. 2010). Figure 1 shows a set of further examples of how such CWR have been used successfully in the past and which CWR taxa are promising targets for crop improvement efforts in the future. The Adapting Agriculture to Climate Change project will help secure and make available to plant breeders the underutilized diversity in these CWR.

Although adaptation to drought, cold, and salinity have all been improved in crops through the use of CWR, the most common examples of use center around host plant resistance to biotic stresses. This is important since the ranges of many plant pathogens are predicted to shift with the changing climate and, therefore, many areas of the world may experience disease pressures not previously faced (Garrett et al. 2006). Counterintuitively, CWR have also contributed to increased yields and to quality traits, despite the wild species themselves displaying poor values for those traits (Tanksley and McCouch 1997). A call for action, emerging from a recent meeting of international experts on crop wild relative genomics (December 2012 in Asilomar, CA), has highlighted the need to better explore untapped plant biodiversity, including wild relatives, housed in seed banks around the world, as our best chance of improving crops in the face of climate change (McCouch et al. 2013).

There are approximately 50,000 to 60,000 species of CWR, of which 10,000 may be considered of high potential value to food security, with 1,000 of these being very closely related to the most important food crops (Maxted and Kell 2009). Up to 75% of these species may be threatened in the wild, and climate change is projected to impose further pressures (Jarvis et al. 2008). The conservation of CWR is increasingly recognized as a high priority (Ford-Lloyd et al. 2011; Hunter et al. 2012), and the conservation of these species in their natural habitats is important for their continued evolution (Maxted and Kell 2009), although climate change may impact the effectiveness of some in situ conservation efforts (Jarvis et al. 2008).

THE PROJECT APPROACH

The Millennium Seed Bank of the Royal Botanic Gardens, Kew and the Global Crop Diversity Trust have embarked on a global, long-term effort to collect, conserve, and initiate the use of the wild relatives of crops. The 10-year project is focused on the wild relatives in the gene pools of 29 focal crops (i.e., apple, bambara groundnut, banana, barley, bean, carrot, chickpea, cowpea, eggplant, faba bean, finger millet, grasspea, lentil, oat, pea, pearl millet, pigeon pea, potato, rice, rye, sorghum, sunflower, sweet potato,

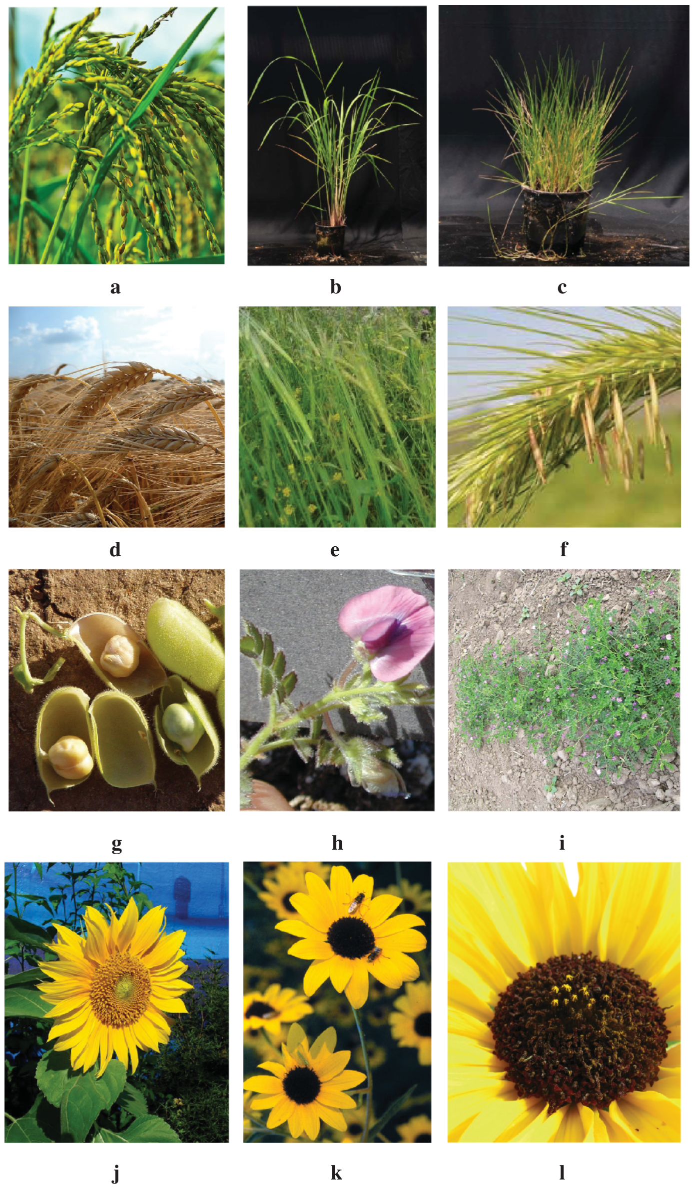

FIGURE 1 Use of CWR: a) rice (*Oryza sativa*); b) *Oryza longistaminata*—drought tolerance (Brar 2005); c) *Oryza coarctata*—tolerance to salinity (Jena pers. comm., October 15, 2013); d) barley (*Hordeum vulgare*); e) *Hordeum spontaneum*—drought tolerance (Ceccarelli pers. comm., as cited in Hajjar and Hodgkin 2007); f) *Hordeum bulbosum*—disease resistance, drought, salt, and frost tolerance (Pickering et al. 2006); g) chickpea (*Cicer arietinum*); h) *Cicer reticulatum*—drought and heat tolerance (Yadav pers. comm., as cited in Hajjar and Hodgkin 2007); i) *Cicer echinospermum*—drought and heat tolerance (Canci and Toker 2009); j) sunflower (*Helianthus annuus*); k) *Helianthus paradoxus*—tolerance to salinity (Miller and Seiler 2003); l) *Helianthus argophyllus*—tolerance to drought (Rieseberg and Baute pers. comm., February 15, 2012). Panels a, d, g, j are examples of the past and possible future use of CWR for crop improvement in the context of climate change. Panels b, e, h, k show examples of how wild relatives have been used in the past. Panels c, f, i, l display examples of wild relatives that harbor traits of interest for future use.

vetch and wheat) of major importance to food security, all of which are included in Annex 1 of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA; Food and Agriculture Organization of the United Nations [FAO] 2009). In close collaboration with national agricultural research and natural resources programs in developing countries and programs of the International Agricultural Research Centers of the CGIAR and other crop expert institutions, the project will:

1. identify those CWR that are missing from existing gene bank collections, are most likely to contain diversity of value to adapting agriculture to climate change, and are most endangered;
2. collect them from the wild and conserve them in gene banks for conservation;
3. evaluate these and other CWR materials already in collections for useful traits and prepare them for use in crop improvement; and
4. make the resulting products and information widely available.

1) Identify Those CWR That Are Missing from Existing Collections, Are Most Likely to Contain Diversity of Value to Adapting Agriculture to Climate Change, and Are Most Endangered

No global assessment yet exists of the state of conservation of CWR of potential use in adapting crops to climate change. A very limited number of crop gene pools (e.g., *Phaseolus, Vigna*) have been the focus of a thorough analysis of gaps in ex situ conservation of CWR (Maxted et al. 2004; Ramírez-Villegas et al. 2010). Such analyses have typically lacked assessment of vulnerability in situ and the prioritization of those species most likely to be of use in crop improvement. Furthermore, until recently, the technologies were insufficiently developed to permit comprehensive compiling, analyzing, and visualizing of the multilayer datasets necessary. Consequently, for most crop gene pools, there are no global strategies and country-level guides for comprehensive collecting to safeguard ex situ those CWR.

The collation of CWR taxa for over 173 crop gene pools into a checklist has been the first step undertaken by the project, through collaboration with the University of Birmingham, UK (Vincent et al. 2013). The project partners have used this checklist to focus compilation of eco-geographic data from major herbaria, gene banks, online datasets and taxonomic experts. The project database contains more than 5.4 million records, over 15,000 of which are newly digitized by the project from herbarium specimens. This dataset forms the basis for the gap analysis, a collaborative initiative lead by the International Center for Tropical Agriculture (CIAT), which is now identifying gaps in ex situ collections for all of the world's major crop gene pools, including the subset of 29 focal gene pools of the project, the results of which have recently been reported online (Crop Wild Relatives and Climate Change 2013).

2) Collect Novel and Threatened Diversity of CWR From the Wild and Provide Them to Gene Banks for Conservation; Share Them with Breeding Programs Accessible to Researchers and Other Users Worldwide

International efforts in collecting plant genetic resources in general have been in decline in recent decades. Wild species are widely thought to be under-represented in ex situ collections at 2–18% of total holdings. There are also very large gaps in species coverage (FAO 2010). Coordinated by the Millennium Seed Bank, the project will support country partners in collecting CWR gene pools from their native habitats worldwide. In total, it is envisaged that between 2013 and 2017, national partners will collect over 6,000 CWR accessions. The Millennium Seed Bank will produce detailed collecting guides and provide other capacity building to national partners. Together with the seeds and pressed plant specimens, vital field data, such as precise information on the collecting location and a description of the plants from which the seeds are collected, will be gathered. Seed will be held by the country of origin, the Millennium Seed Bank, the appropriate CGIAR international collection and at the Svalbard Global Seed Vault. Seeds for long-term conservation will be dried and stored at low temperature following international gene bank standards. Germination protocols will be established for species new to long-term conservation. Seeds will be available for evaluation and crop improvement efforts under the terms and conditions of the ITPGRFA.

3) Evaluate the Newly Collected CWR and Other CWR Already in Collections for Useful Traits; and Prepare Them for Use in Crop Improvement

Germplasm lines incorporating novel, useful diversity from CWR will be developed and made available to breeders and farmers worldwide for enhancing crop adaptation to climate change. In the past, CWR have been used in breeding efforts for a variety of traits. However, for most of these crops, many CWR taxa have never been used in improvement. Furthermore, few (if any) of the varieties that have resulted from crosses that included CWR have ever been systematically evaluated for their performance in a set of different conditions that simulate likely future climate change scenarios. No major advances have ever been made with regards to the use of CWR for improving several other crops, such as alfalfa, apple, bambara groundnut, carrots, eggplant, faba bean, cowpea, finger millet, grasspea, pigeon pea, rye, sorghum and sweet potato—all of which are priority crop gene pools for this project. The use of CWR for the development of materials that are of interest to breeders is commonly referred to as "pre-breeding." The project will engage with different national and international partners to support such pre-breeding work in several of the 29 focal crops, using some of the newly collected accessions but also CWR accessions and existing pre-bred lines that are already available in gene banks but have not been previously used. The outcomes of the meeting on crop wild relative genomics, as reported by McCouch et al (2013), includes a roadmap for more efficient use of CWR diversity and is an important point of reference for pre-breeding activities under this project. In an effort to demonstrate the utility of these newly developed materials to the community of breeders, the project will also support efforts to evaluate them under field conditions.

4) Make the Resulting Information Widely Available So That Researchers, Collection Holders, Breeders, and Other Users of Plant Genetic Resources Have Access to Information and Information Systems for Improved Conservation and Use of CWR

Currently, information systems providing access to data on the identity, location, and usefulness of germplasm, including CWR, held ex situ, are limited in their coverage. Agricultural research for adaptation to climate change is thus constrained by lack of information regarding existing germplasm collections (FAO 2010). A gene bank data management system (GRIN–Global) and an online information portal on ex situ collections (GENESYS) have been developed by previous projects by the Global Crop Diversity Trust. However, an investment for widespread deployment and adoption by national programs is still needed. This will be made available through this project in order to incorporate more gene banks, a broader range of data and the results of evaluation of the products of the project.

EXPECTED RESULTS

We believe that this project will contribute significantly and globally to biodiversity conservation, agricultural development, and food security, ultimately, benefitting food producers and consumers worldwide. The outputs will include:

- online global checklist of CWR;
- list of priority species for collecting worldwide;
- maps displaying the results of the gap analyses;
- seed collections in long term storage;
- germination protocols;
- pre-bred material and evaluation data.

The project has developed a resource website, which aims to serve as the platform from which all outputs of the project will be made publicly available (Crop Wild Relatives and Climate Change 2013).

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