

Adapting agriculture to climate change: The role of crop wild relatives

Summary Statement from a Bellagio Meeting 6-10 September 2010



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Introduction

This Statement summarizes the results of the third in a series of consultations between agricultural scientists (in particular those interested in the conservation and use of crop diversity in plant improvement) and climate scientists on how to adapt agriculture to climate change. The first meeting, also held at Bellagio (3-7 September 2007), looked at the *Conservation and Use of Global Crop Genetic Resources in the Face of Climate Change*. It identified three major challenges facing the adaptation process: collecting crop diversity before it disappears, using it to breed better adapted crops, and informing key players of the increased need for the conservation and effective use of crop genetic resources in the face of climate change.

The second meeting, held at Stanford University on 16-18 June 2009, looked more specifically at breeding, and in particular at *Climate Extremes and Crop Adaptation*. Among other things, it recommended that efforts to develop heat tolerant cultivars of the major cereals be intensified, and that greater investments be made in genotyping and phenotyping the variation already held in genebanks, and in collecting remaining diversity.

This third meeting in the series, and second at Bellagio, focused on a specific area of intersection between the ground covered by the previous consultations: the role of plants that are closely related to crops but are not themselves cultivated (crop wild relatives, or CWRs for short) in breeding cultivars better adapted to future climates. We structured the discussion into three sections, and summarize the results in the same way below. We also note that the tight focus of this short meeting on CWR is not meant to indicate that other strategies for adaptation are less worthwhile. For example, changes in agronomic practices, such as the adoption of conservation agriculture, may well be an effective adaptation strategy, and one that complements crop genetic improvement. It was also often noted that the use of CWRs is but one of many tools in the breeder's toolbox.

Why should crop wild relatives be used in crop breeding?

We started by considering the evidence that CWRs are in fact useful tools in the struggle to adapt agriculture to climate change. It is appropriate to first outline the scale of the challenge. Growing season temperatures by the middle of the 21st century will bear little resemblance to what most regions experienced in 1900-2000. By 2070-2100, the coolest growing season for a given location may well be warmer than anything witnessed prior to 2000 at that location. The frequency of 4-6 month droughts will increase 2- or 3-fold. It will truly be a different world, and one that for agriculture will be much more demanding, especially in the tropics. 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 up with warming. When you add up these effects, and others, crop physiological and other models show possible yield losses of 6-10% per 1°C of warming in the average temperature of the growing season. This means we could be seeing significant impacts on production by 2030, let alone 2070. The list of possible traits that could be used to counteract these changes is long and occasionally contradictory, including everything from enhanced root growth to faster grain filling. However, given the relentlessly increasing human population, the goal in adapting to climate change must be not just to improve crop performance under stress, but also to maintain and even increase yields in good conditions.

This will prove a difficult balancing act. What reasons are there to think that CWRs could help us pull it off? First is the fact that by and large they contain more genetic diversity than their cultivated cousins, due to the domestication bottleneck that crops have been subjected to. Figures vary, but rice and wheat retain probably only about 30-40% of the genetic diversity of their wild relatives, soybean 50%, and maize probably closer to 75% (Figure 1).

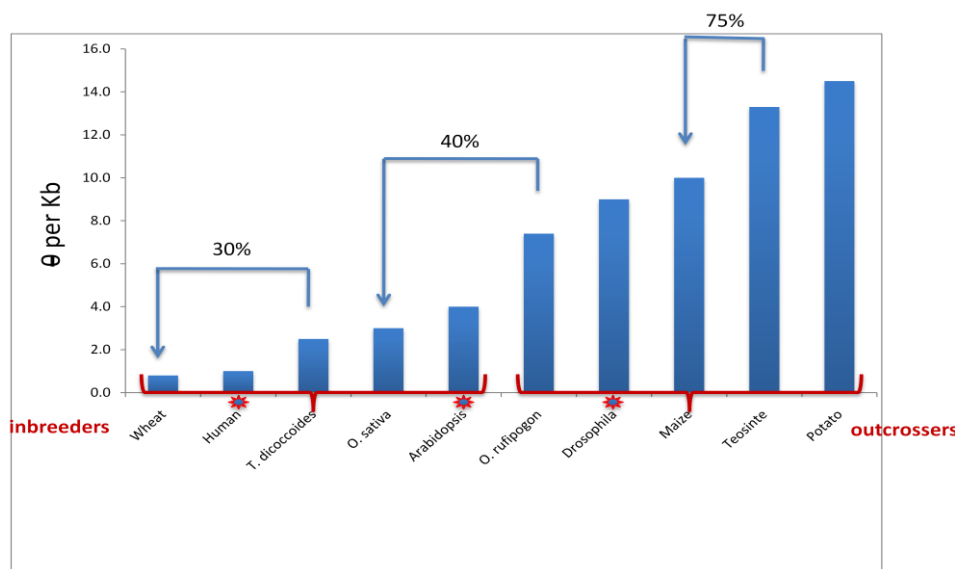


Figure 1. Genetic diversity in various cultivated crops and wild relatives. Arrows indicate the proportion of wild diversity retained in maize, wheat, and rice cultivated genepool.

Secondly, we know that many CWRs grow in conditions of climate and soil that would be considered marginal for the crop, or even outside its normal range. We also know that many show marked morphological and physiological differences from the crop, such as perenniality, fleshy roots and distinct phenology. Some of these are likely to be of relevance for climate change adaptation.

Finally, we have the considerable evidence provided by past efforts to use CWRs in plant breeding. For example, a CWR has recently been used to change the time of flowering of rice to avoid the hottest part of the day (Ishimaru et al. 2010). Although adaptation to drought, cold and salinity have all been improved in crops through the use of CWRs, as well as nutritional quality, the most common examples of use in fact centre around host plant resistance to biotic stresses. A recent literature review carried out by a member of our group for FAO showed that 39% of papers on the use of CWRs involve breeding for host plant resistance to pathogens and pests (Maxted & Kell in press). Another, somewhat different example of the successful use of CWRs is the work to re-synthesize bread wheat by going back to its ancestors and re-running the process of domestication, in a sort of evolutionary do-over. We also heard of a similar, not as widely known, effort with groundnut (peanut).

There have been attempts made to quantify in economic terms the contribution of CWRs to global agriculture, but these are not particularly consistent, which is something that we think ought to be rectified. It is in fact an irony of CWR conservation and use – one of five we encountered in our discussions – that we know they are important, but have not been able to quantify this. However, it is clear that their contribution to breeding improved cultivars is substantial in a number of crops. Overall, CWRs have played a more important role in past plant breeding efforts than many realized. Table 1 lists some examples for rice, as presented by one of the participants. Hybrid rice was made possible by an accession of a wild relative

from Hainan Island, China which was male sterile. A single accession of wild rice (*O. nivara*) is also the source of grassy stunt resistance in many modern cultivars.

Table 1. Rice varieties released through hybridization with wild species.

| Trait | Wild species | Varieties released | Country |
|---|--------------------------|---|---|
| Grassy Stunt Virus resistance | <i>O. nivara</i> | Many rice cultivars | Rice growing countries in Asia |
| Brown Planthopper resistance | <i>O. officinalis</i> | MTL98,MTL103 MTL 105, MTL114 | Vietnam |
| Acid sulfate tolerance | <i>O. rufipogon</i> | AS996 | Vietnam |
| Tungro resistance | <i>O. rufipogon</i> | Matatag 9 | Philippines |
| Bacterial Blight resistance | <i>O. longistaminata</i> | NSICRc112 | Philippines |
| Blast resistance | <i>O. rufipogon</i> | Dhanrasi | India |

Beyond rice, roughly 40% of wheat cultivars released by CIMMYT each year have a re-synthesized wheat parent, according to CIMMYT pedigree data presented by a participant. Similarly, one of the more successful potato cultivars in China (CIP-24) includes in its extensive pedigree going back decades genetic material from Mexican wild relatives collected in the 1930s. In cassava, CWRs have provided host plant resistance to various pathogens and pests, including bacterial blight, and Cassava Mosaic Disease virus, as well as post-harvest physiological deterioration.

Throughout the meeting we were very careful to be explicit about possible counter-arguments. In this case, we weighed these strong arguments for use of CWRs against the potential downsides, which in fact are numerous. CWRs are often difficult to cross with the crop, and useful traits always come with a lot of “useless” genetic baggage, so-called linkage drag. That can make CWR use in breeding programmes a long-term proposition, necessitating a lengthy process of pre-breeding in which the relevant traits are gradually transferred to an elite background. Increasingly, this is being done with the help of molecular markers that tag the appropriate, useful bits of the genome and allow them to be tracked efficiently among the progenies of inter-specific crosses.

Another line of argument against CWRs relates not so much to the difficulty of their use, but rather to doubts about their utility for traits other than the ones controlled by few genes. For example, most successes have been in simpler traits like host plant resistance to pests rather than highly complex ones like adaptation to drought-prone environments. However, this may simply reflect the focus of past efforts or the fact that more complex traits are harder, though not impossible, to transfer with existing approaches. In spite of these concerns, it became quite clear in the discussion that professional plant breeders are not generally averse to the use of CWRs. It is just that most of them cannot invest in it, given their need to deliver improved varieties in a short period of time. This presents a second great irony: CWRs are acknowledged as useful in plant breeding, but incentive structures are not adequate at the moment to support their systematic use. We will return later to the question of if not the breeder, then who?

It is worth noting, though, that while re-synthesizing wheat took a long time, breeding progress (in all kinds of directions) is faster now that they are available, much faster than what can be achieved with landraces. Crosses of re-synthesized wheats with modern cultivars have produced new cultivars that are much better adapted to harsh environments. Much progress can therefore be made by going through a process of undirected diversification first. Public sector plant breeders are in a particularly good position to explore and exploit the diversity around the crop in this way, to ready it for surprises that await us.

We then moved on to discussing how we can prioritize CWR species, and specific populations, for conservation and use in breeding.

What crop wild relatives should be prioritized for conservation and use, and where?

If you look at the 80+ crops in the FAOSTA database, and count up all their closest related wild species (i.e. those which are easiest to cross with the crop), you come up with a list of about 1,100 species. Although large, this number does not represent an unmanageable number of species to conserve. Unfortunately, the vast majority of these are represented in genebanks by <10 seed samples, and many not at all. In addition, an ecological niche modelling study (Jarvis et al. 2008) of the wild relatives of three crops suggests that many of these species are threatened in the field by climate change, with levels of threat differing significantly among crops, in many cases substantially above the 20% or so baseline level recently estimated for plants in general (<http://www.kew.org/news/one-fifth-of-plants-under-threat-of-extinction.htm>). This is the third great irony: CWRs are potentially very useful in adapting to climate change, but are in turn threatened by it. However, the threat from landuse change and invasive species may in fact be even stronger in some cases.

We saw during the meeting the results of spatial analysis to identify taxonomic, geographic and environmental gaps in *ex situ* collections, as proxies for genetic gaps. Such methods hold great promise as a way to efficiently prioritize taxa and populations for collecting and use. They have already been applied to about a dozen crops, which allowed the identification of areas where the wild relatives of multiple crops should be collected, adding to the efficiency and significantly reducing the cost of any global initiative. More crops need to be analyzed in this way, which will mean a major effort of data gathering, digitization and geo-referencing. It was, however, also noted that the results of such an exercise may well be different if it was carried out based on individual country priorities for conservation and use, rather than from a global perspective. Also, a truly comprehensive approach to CWR conservation would include an *in situ* dimension. That means the protection of the habitats in which they occur, though given the likely effects of climate change, not necessarily in conventional protected areas as currently envisaged and configured. Interestingly, we heard evidence from a recently-completed project that *in situ* conservation can in fact increase use by plant breeders, by stimulating their interest and piquing their curiosity. While *ex situ* conservation may be absolutely necessary for effective and sustainable use of genetic resources of CWRs, it is not sufficient for ensuring the survival of the full range of genetic diversity they contain.

There was broad, and broadly predictable, agreement on the importance of targeting conservation activities on gaps in collections and threatened taxa and areas. The discussion on the advisability of focusing on potential stress “hotspots” proved less predictable, and more contentious. A common assumption is that we are most likely to find drought adaptation, say, in areas undergoing constant drought stress. This has in fact proved to be so in various studies. Others stressed the need to focus on (dissimilar) geographic areas expected

to harbour most genetic diversity. Such areas will potentially have a more diverse genetic basis, with multiple strategies for dealing with stress, whereas the extreme areas may have narrowed the genepool to a single strategy which may not be useful for crops, especially when considering the need to maintain yield potential in good conditions. Adaptation does not necessarily mean high yield. Optimal sampling strategies for the provision of useful genes in CWRs seems to be an area which is ripe for research.

Combining the first two sessions, we identified certain characteristics of CWRs and their populations that are likely to be most important for crop improvement for climate change adaptation:

- CWRs that are found in areas of high or variable stress.
- CWRs that are as dissimilar from the crop as possible in adaptation.
- CWRs that are relatively easy to cross with the crop.
- CWRs of crops that are self-pollinating species or inbreeders.
- CWRs of crops that underwent a severe genetic bottleneck on domestication.
- CWRs of crops that have a well-explored landrace diversity, and where progress appears limited by a lack of additional diversity.

There is perhaps a fourth irony here. The wild relatives which are most different from the crop are perhaps the most likely to have novel variation, and therefore to be the most useful; however, they are also likely to be the ones which are most difficult to use, because of crossing barriers.

Although perhaps a minor point, we also discussed the possibility of developing some CWRs into totally new crops.

However, successful use requires a considerable investment in pre-breeding (or crop germplasm enhancement). This is an investment that is arguably not being made at present to a sufficient extent due to market failure, that is the inability to recoup investment costs and generate profit within a reasonable timeframe. This was also a main theme of the previous Bellagio meeting. The importance of pre-breeding as a public good is undeniable, but who will fund and carry it out? We therefore next discussed possible changes in the way genebank curators and plant breeders do business and interact with each other that would improve the effectiveness of CWR use, including through pre-breeding. This led us to a discussion of a question that was posed earlier: if not the plant breeder, who?

How can we use crop wild relatives most effectively?

Here we come face to face with the fifth of the great ironies of CWR conservation and use, which is that what you see is not necessarily what you get. CWRs may well have alleles for useful traits, but these are often hidden by the effects of other genes, and can only be discovered by evaluating the progenies of crosses. We heard about a number of strategies for uncovering the useful traits, from rice, cassava and groundnut in particular, but other crops as well. Although advanced biotechnologies such as embryo-rescue and molecular markers predictably feature in the toolkit of the breeder who uses CWRs regularly, it was perhaps more surprising to hear about the continued importance of fields such as basic taxonomy (i.e. the study of the classification of organisms) and cytology (i.e. the study of the physical characteristics of chromosomes).

A multitude of products have successfully been developed by pre-breeding programmes and handed over to breeders for further development: simple interspecific hybrids, introgression lines, near-isogenic lines, pyramided lines, recombinant inbred lines and chromosome segment substitution lines. “Handed over” is perhaps the key phrase here, and somewhat misleading. In some crops, there is already in place an integrated pipeline, or “plant breeding consortium,” linking genebanks, trait specialists, germplasm enhancers and breeders, and molecular biologists. We saw this in rice during the meeting in great detail, and heard about it in wheat too. But we also saw an example in groundnut in Brazil where a genebank curator led a major taxonomic, cytological and molecular research programme over 20 years, involving many postgraduate students, to arrive at the position where pre-breeding products were of some interest to the national breeding programme.

Given this, it is worthwhile asking whether increased interest in CWR conservation and use will drive a transformational process in genebanks and their relationship with users, and in particular germplasm enhancers and breeders (if indeed such a distinction is worthwhile) and molecular biologists. This is a transformational process that some would argue is much needed, and long overdue. While in some cases it may well be a viable option for genebank professions to actively engage in germplasm enhancement themselves, blurring the always anyway contentious dividing lines between conservation and use, in other cases it will be more of a question of ensuring that a consortium involving different plant breeding and advanced genetics institutions is in place and functioning effectively to address clearly defined problems. In either case, a measure of culture change will be necessary on all sides. And this will need to be supported by capacity building, including in perhaps somewhat unfashionable disciplines, such as cytogenetics. A mentoring approach was mentioned as a possible option for delivering this improved capacity efficiently. There needs to be a larger pool of people able and willing to integrate genetic resources conservation, crop breeding and advanced plant genetics.

Conclusions

We concluded that a strong case can be made for the use of CWR diversity in climate change adaptation. This will involve not only the search for specific traits, for example specific adaptations to abiotic stresses using spatial analysis approaches, and their incorporation into the cultivar development pipeline, but also what might be termed the genetic widening of that pipeline. It is indeed possible that CWRs will in the end prove most important in climate change adaptation (and indeed other breeding breakthroughs) because of their contribution to broadening the genetic base of the crop through the influx of new, wider diversity. Often, this diversity is difficult to identify in the CWR phenotypes themselves, and is only revealed after screening their progeny, in conjunction with genotyping. We expect that overall broadening of diversity will have more of an impact on crops which are inbreeders, have a narrow genetic base relative to their wild relatives, whose cultivated diversity has already been thoroughly investigated, and which are approaching or are already at a yield plateau.

Priority should be given to conserving CWRs that are relatively easy to cross with the crop on the basis of the genepool and taxon group concepts, while recognizing that we do not always know which these are, and that the most divergent species may be the most interesting. Preference also seems due to species and populations that are most imminently threatened (for example on the basis of IUCN Red List categories), in particular by land use changes and, to a lesser extent, by climate change. Overall, even though climate change provides a strong rationale for conservation and use of CWRs, it should not greatly influence sampling strategies, which should aim to recover as much diversity missing from existing collections as

possible. By definition, it is this diversity that breeders will not have seen before, and will probably be most interested in.

Finally, the descendants of progenies of crosses of CWR accessions with modern crop cultivars will in many ways be more valuable than the raw CWR accessions themselves, because they are more readily usable by breeders, especially if accompanied with genetic characterization data. Evaluation should focus on these progenies, at least initially, and be accompanied with fine-scale molecular characterization. Collaboration in a problem-driven plant breeding consortium will be necessary to develop easily usable products. New institutional arrangements will be needed to allow sustained pre-breeding efforts, but so also will be capacity building, or indeed re-building.

CWRs are already being successfully used for climate change adaptation in various crops. But the process needs to be scaled up and extended to other crops, and made more efficient and effective. There needs to be a systematic and comprehensive review of current *ex situ* and *in situ* status to inform the identification of global gaps in conservation, and more detailed modelling of the likely impact of climate change on CWR diversity. Crucially, publicly funded plant breeding programmes that focus on long-term crop improvement (and which therefore often include a strong element of pre-breeding) must continue to receive support, and they must be encouraged to explore crop wild relatives. The best way to do that is to collaborate closely with the genebanks that ultimately provide the raw materials for such programmes. This could help ensure that we reap the maximum benefits from the biological diversity we are able to safeguard. It would be a tragedy if we did not.

Some key summary points and recommendations

1. Crop wild relatives (CWRs) have been important in crop improvement, with instructive examples from many crops, although no reliable estimates of the total economic value of their contribution are available.
2. CWRs will be more useful for some crops than others, depending on factors such as the extent of the domestication bottleneck, the degree of genetic diversity in landraces, their ease of crossing with the cultigen, and the prevalence of inbreeding.
3. It is difficult to predict the specific traits for which CWRs will be most useful in climate change adaptation. However, their use helps to broaden the genetic basis that underpins all crop advancement, including for traits needed to improve crop resilience in the face of climate change.
4. CWRs in many areas are threatened with extinction, primarily from landuse change, but, increasingly, also because of climate change itself. Further, gap analysis has shown that current conservation efforts (both *ex situ* and *in situ*) do not adequately cover genetic and species diversity. Collecting at least a few accessions for the roughly 1,100 close relatives of the 80 or so major crops is a feasible goal for the next decade.
5. There is a lot of hidden diversity in CWRs, and the traits of interest are not always found in the most extreme environments, nor are they always immediately visible in the CWRs themselves. For these reasons, it is important to collect CWRs from areas of high diversity, as well as from extreme environments and in areas with more variability in stresses.
6. The use of CWRs relies on successful pre-breeding: crossing CWRs with advanced cultivars to form products, which, with their associated genetic data, are more easily used by breeders. Incentives for pre-breeding are low at present and need to be greatly

improved, in particular in the public plant breeding sector, if the full value of CWRs is to be realized.

7. The appropriate people and institutions to carry out pre-breeding likely differ from crop to crop. In some cases, genebanks may be well placed to do some of this work. In all cases they should be closely involved in the process.

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