

Crop Science special issue: Adapting agriculture to climate change: A walk on the wild side

Benjamin Kilian¹ | Hannes Dempewolf¹ | Luigi Guarino¹ | Peter Werner¹ |
Clarice Coyne² | Marilyn L. Warburton³

¹ Global Crop Diversity Trust, Platz der Vereinten Nationen 7, Bonn 53113, Germany

² USDA ARS Plant Germplasm Introduction and Testing Research Unit, 50 Johnson Hall, Pullman, WA 99164, USA

³ USDA ARS Crop Host Plant Resistance Research Unit, Box 9555 Mississippi State, Starkville, MS 39759, USA

Correspondence

Benjamin Kilian, Global Crop Diversity Trust, Platz der Vereinten Nationen 7, 53113, Bonn, Germany.

Email: benjamin.kilian@croptrust.org

Plant domestication and crop improvement have resulted in reduced genetic diversity in most of our cultivated crops, thus limiting their potential to adapt to future challenges (Byrne et al., 2018; Keneni, Bekele, Imtiaz, & Dagne, 2012; Tanksley & McCouch, 1997; Swarup et al., 2021). One response to mitigate the impact of climate change on agricultural systems is to develop improved varieties that are genetically tolerant or resistant to the new range of abiotic and biotic challenges. Improvement via crop breeding requires access to novel variants of genes for complex adaptive traits. Crop wild relatives (CWR) and landraces are a potentially valuable source of these alleles (Cossani & Reynolds, 2015; Seiler, QiL, & Marek, 2017). However, these materials are often difficult to work with and require genetic selection to make them agronomic and useful in a breeding program, a process commonly referred to as ‘pre-breeding’. This term was first used by Rick (1984) and refers to a wide range of activities designed to (i) identify beneficial traits in CWR and other plant genetic resources (PGR), and (ii) transfer these traits into breeding lines (Ortiz, 2002; Sharma, Upadhyaya, Varshney, & Gowda, 2013). Pre-breeding forms a bridge between the genebanks that hold and safeguard CWR and landraces, and breeders and farmers who use them.

Pre-breeding is a long, laborious process, which includes multiple crossings and trait evaluations, and is risky and costly (Dempewolf et al., 2017). Thus, pre-breeding efforts tend to

be avoided whenever possible, especially by advanced breeding programs. However, climate change is forcing breeders to seek useful traits from all available sources, no matter how challenging. Utilizing CWR in pre-breeding can access diversity for specific traits of importance that are not present in the elite crop genotypes that are generally used in breeding programs. As the pace of change of temperature, rainfall, and pest and pathogen attack increases, and extremes become normal, long-term efforts and substantial investment in pre-breeding are required to develop improved varieties that are well adapted to the various challenges ahead of us.

One unique, global initiative to facilitate the use of CWR in breeding new, improved crop varieties is the project “Adapting Agriculture to Climate Change: Collecting, Protecting and Preparing Crop Wild Relatives” (<http://www.cwrdiversity.org/>; (Dempewolf et al., 2014, 2017)). This is the first systematic global long-term investment supporting the use of CWR across multiple genebanks to generate knowledge and pre-breeding materials contributing to adaptation to climate change. The aim is to build capacities in developing countries in order to use this diversity where it is needed most. The project focussed its pre-breeding efforts on 19 crops important for food security. Of key importance has been the establishment of partnerships between CGIAR centers, advanced research organizations and national breeding programs around the world. A total of 19 pre-breeding

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partnerships are being supported in 50 countries by the project. Partners from more than 100 organizations worked together, including farmer organizations and the private sector. The pre-breeding lines and information produced are being made available via the multilateral system (MLS) of the Plant Treaty. Most projects have already deposited advanced material in genebanks for conservation and future use. Our intention in this special issue of *Crop Science* is to promote global awareness of the progress made by the pre-breeding component of the project and to highlight newly available pre-breeding materials and related information obtained from this major global initiative.

We present a series of 17 research articles on 13 crops reporting successful implementation of CWR utilization in pre-breeding. The contributions cover all activity areas in the pre-breeding continuum, and thus connect genebanks with breeding pipelines. We have also included a review article and a collaborative paper describing an advanced database that provides a common platform for storing, visualizing and sharing pre-breeding data.

In the wide range of pre-breeding activities considered, the starting point is to fill diversity gaps in genebank collections by acquiring new germplasm with unique priority traits. In *"Filling the gaps in gene banks: Collecting, characterizing and phenotyping wild banana relatives of Papua New Guinea,"* Eyland et al. (2021) deliver a proof of the principle that wild banana diversity is not yet fully represented in *ex situ* genebanks and that wild *Musa acuminata* ssp. *banksii* populations (the ancestor of most edible bananas) contain individuals with beneficial traits, useful for drought tolerance breeding programs.

The next step in the pre-breeding process is to characterize and evaluate CWR populations and CWR-derived lines. A set of papers focuses on improving **drought, heat or salinity stress-related traits** and includes Humphries et al. (2021), *"Characterization and pre-breeding of diverse alfalfa wild relatives originating from drought-stressed environments,"* who report that newly developed alfalfa hybrids between *Medicago sativa* x *M. arborea* and *M. sativa* x *M. truncatula* from the tertiary genepool offer new diversity useful to improve growth habit, seed size, fall dormancy and forage yield. Simon et al. (2021), in *"Wild carrot diversity for new sources of abiotic stress tolerance to strengthen vegetable breeding in Bangladesh and Pakistan,"* describe new sources of heat and drought tolerance in two wild *Daucus* species (also see the podcast about their paper: <https://fieldlabearth.libsyn.com/carrot-stress-tolerance-and-wild-relative-breeding-with-dr-simon-philipp>). Aberkane et al. (2021), in *"Evaluation of durum wheat lines derived from interspecific crosses under drought and heat stress,"* conclude that gene introgression from wild diploid and wild tetraploid wheat-derived materials pays off and can increase wheat resilience. Drought tolerant genotypes with high values of relative chlorophyll

content and more green leaves at maturity have been identified by Ochieng et al. (2021), in *"Novel sources of drought tolerance from landraces and wild sorghum relatives"*. Kouassi et al. (2021), used an original approach to estimate drought tolerance scores for vegetative growth and yield related traits in *"Genetic parameters of drought tolerance for agromorphological traits in eggplant, wild relatives, and interspecific hybrids."* Finally, Nhanala and Yencho (2021), in *"Assessment of the potential of wild Ipomoea spp. for the improvement of drought tolerance in cultivated sweetpotato (Ipomoea batatas) (L.) Lam,"* conclude that cultivated and wild sweetpotatoes respond differently to drought.

A second set of papers in this pre-breeding category aims at improving **biotic stress-related traits** and includes Rehman et al. (2021), *"Traits discovery in Hordeum vulgare subsp. spontaneum accessions and in lines derived from interspecific crosses with wild Hordeum species for enhancing barley breeding efforts,"* who show that high levels of resistance to the net form of net blotch, scald, leaf rust and powdery mildew were identified in CWR-derived barley lines, including some that were resistant to all four diseases. In *"Novel sources of resistance to blast disease in finger millet,"* Dida et al. (2021) show that wild finger millet was generally more resistant to the blast disease caused by *Magnaporthe grisea* compared to cultivated finger millet. In *"Wild Lathyrus species as a great source of resistance for introgression into cultivated grass pea (Lathyrus sativus L.) against broomrape weeds (Orobancha crenata Forsk. and Orobancha foetida Poir.),"* Abdallah et al. (2021) identify complete resistance against both weeds in wild *L. articulatus*.

Three papers describe **a combination of multiple traits**. The usefulness of deploying CWR in durum wheat breeding for several abiotic and biotic traits was assessed by El Haddad et al. (2021), in *"Crop wild relatives in durum wheat breeding: Drift or thrift?"*, who conclude that CWR-derived lines are a good source of resistance against *Septoria* leaf blotch. Additionally, under both drought and heat stress conditions, CWR-derived lines revealed a clear superiority for grain yield and yield component traits over the best check varieties. In two papers on pearl millet, the world's hardest warm-season cereal crop, Sharma et al. (2021a) show that CWR can improve multiple traits even further. Promising introgression lines (ILs) derived from wild pearl millet with improved resistance against five highly virulent blast pathotypes, and also high dry fodder yield and seed set under heat stress conditions, are described by Sharma et al. (2021a), in *"Utilization of wild Pennisetum species for improving biotic and abiotic stress tolerance in pearl millet (Pennisetum glaucum L.)."* In an excellent overview entitled *"Harnessing wild relatives of pearl millet for germplasm enhancement: challenges and opportunities,"* Sharma et al. (2021b) reviewed the availability, importance, and strategies for utilization of CWR for crop improvement, from a breeder's perspective. They proposed a

stage-gate process for the efficient management of pre-breeding programs using CWR.

Developing nutrient-rich crop cultivars is an important strategy to combat malnutrition due to protein and mineral deficiencies. Sharma et al. (2021c), in "Characterization of cultivated and annual wild *Cicer* species for seed protein and mineral contents, and identification of promising accessions for chickpea (*Cicer arietinum* L.) improvement," identify individuals from different wild *Cicer* species that can increase concentrations of protein, Ca, Cu, Fe, Mg, Mn, and Zn in the seeds. These resources will facilitate the biofortification of chickpea.

The transfer of beneficial alleles and traits from CWR to breeding lines, and ultimately to new cultivars, is the next step in the pre-breeding process. The development of new germplasm resources with novel allelic diversity in a useful background also aids in the identification of genes that contribute to important adaptive traits. Mace et al. (2021), in "A global resource for exploring and exploiting genetic variation in sorghum crop wild relatives," describe the development of a backcross-nested association mapping (BCNAM) population for sorghum using 9 CWR accessions and two recurrent parents. The BCNAM population of 1,224 lines was genotyped using DArT markers and genome-wide association scans (GWAS) confirmed this resource as a source of new alleles for breeding for future climates. **Induced mutations** and chromosomal changes can provide breeders with additional tools in the development of new cultivars that are better suited to future climate scenarios. Innes, Denton, Dundas, Peck, and Humphries (2021), demonstrated this in "The effect of ploidy number on vigor, productivity and potential adaptation to climate change in annual *Medicago* species." This paper reported wild or induced tetraploid *Medicago* lines with the potential to increase early biomass, vigor and leaf size.

A key step in pre-breeding is ensuring that the new material appeals to users. In order to incorporate farmers' preferences, on-farm participatory evaluation studies are highly recommended. We took two such studies on board for this special issue of *Crop Science*: Tin et al. (2021a), in "Phenotypic response of farmer-selected CWR-derived rice lines to salt stress in the Mekong Delta," describe the development of CWR-derived rice lines and their evaluation in the Mekong Delta. Subsequently, 50 stable BC₃F₅ lines were selected by farmers and screened in hydroponics to assess their phenotypic response to salt stress. In the second study by Tin et al. (2021b), in "Participatory selection of CWR-derived salt-tolerant rice lines adapted to the coastal zone of the Mekong Delta," show that four lines derived from wild *Oryza rufipogon* and *O. nivara* are well adapted, with high grain yield (> 6.5 tons/ha), early maturity, and short plant height. In order to **provide pre-breeding data relevant to different stakeholders,** Raubach et al. (2021) present a rel-

evant and truly collaborative effort to manage, visualize and share data from pre-breeding projects in their paper "From bits to bites: Advancement of the Germinate platform to support prebreeding informatics for crop wild relatives." The authors describe the status of 12 Germinate databases that are currently publicly accessible.

Our intention in creating this special issue of *Crop Science* is to promote global awareness of the newly available CWR-derived pre-breeding materials and related data sets, in order to support the adaptation of agriculture to climate change. When we reflect on these 19 articles, we conclude that impressive progress has been made by this project in the introgression of beneficial traits from CWR for several crops. Promising CWR-derived lines have been identified and presented here that fully justify the expense and effort. Continuation and further support for this work is needed to achieve practical outcomes, and move the work done so far out of pre-breeding, to breeding, to new varieties contributing to livelihoods and nutrition in farmers' fields.

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