

Crop wild relatives: the road to climate change adaptation

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The world population is projected to be 9.7 billion in 2050 (Khan et al. 2020). Accordingly, to fulfil the expected rise in global food demand, the agricultural production must increase by around 60–70% by 2050. However, there are a number of factors such as reduced crop diversity, biotic and abiotic stresses along with drastic climate change that are very likely to affect crop productivity (Rajpal et al. 2023). In 21st century, the increase in the level of environmental stresses with the ongoing climate change is already predicted in global climate forecasts. Thus, the production of resilient genotypes can help to lessen the consequences of such global climate change. The genetic diversity of contemporary cultivars has, however, been reduced as a result of domestication and targeted trait selection. Hence, it is necessary to identify novel genetic resources to promote adaptability to the ongoing and expected environmental issues.

Crop wild relatives (CWRs) are crucial genetic resources with rare alleles and expanded genetic diversity that can help to improve crop adaptability to different stress conditions associated with continuously changing climate (Kahraman et al. 2017; Khan et al. 2021). Thus, it is essential to conserve as well as use these genetic resources effectively in order to generate climate-resilient crops and to guarantee global food and nutrition security. However, the heritable characteristics of CWRs have not been thoroughly explored and should be studied in detail for the efficient usage of CWRs. It is necessary to analyse their nutritional content, genetic variation, tolerance towards different environmental constraints, and productivity in the scenario of climate change (Athar et al. 2023). Thus, this special issue presents the studies highlighting the successful utilisation of CWRs for modern agricultural development. The special issue comprises eight research and five review articles that emphasise different beneficial aspects of CWRs.

Some of the CWRs survive in extreme environments and can be efficiently used to increase the adaptability of modern genotypes to such environments. Higher genetic improvements can be achieved by integrating desirable genes from wild/relative species into the gene pools of major food crops. Identification of QTLs related to micronutrients and grain yield facilitates marker-assisted breeding for the development of new varieties. Curti et al. (2022) characterised the wild ancestor of quinoa populations (*Chenopodium hircinum* Schard.) that can survive in the hottest environments to quantify the variations among sites of origin. The results revealed that late-flowering wild quinoa populations could survive in hot climate; thus, longer vegetative growth can be a beneficial trait to develop *Chenopodium* spp. with heat stress tolerance. Bharamappanavara et al. (2023) determined genomic regions related to yield traits in mapping populations obtained from backcrossing of *Oryza sativa indica* and *O. glaberrima*. The authors reported a QTL hotspot near marker RM510, and a QTL *qGY-4.1* that is associated with grain yield and can be used for increasing yield in *O. sativa* cultivars via molecular breeding. Duan et al. (2022) identified 16 QTLs related to grain zinc (Zn), manganese (Mn) and copper (Cu) contents, and 29 QTLs associated with other grain-related traits in the backcross inbred lines (BIL) developed from an interspecific backcross of Xieqingzao B and Dongxiang wild rice (*Oryza rufipogon* Griff.). Pyramiding of such QTLs can be done to simultaneously improve these traits in modern rice cultivars.

An efficient breeding plan can be established for different crops by utilising their variability in yield and related traits. Chokheli et al. (2022) estimated the genetic polymorphism of five rare species of the genus *Crambe* and established a genetic formula to identify these species. Among the five studied species, *Crambe steveniana* and *Crambe tataria* were closely related. Naik et al. (2022) identified significant variation in germplasm lines of

under-utilised pseudocereal buckwheat grown in different locations of the northwestern Himalayan region. Among all the studied traits, number of primary branches showed the highest phenotypic coefficients of variation. Similarly, [Soni and Munjal \(2023\)](#) estimated heat stress tolerance of different wheat genetic resources including wild germplasm employing the stay-green trait. Interestingly, genotypes with stay-green trait were grouped together with genotypes with high grain yield and low leaf senescence rate and several genotypes were identified as potential candidates for breeding for heat stress tolerance.

[Joshi et al. \(2023\)](#) characterised several chickpea accessions at the seedling establishment stage and revealed novel salinity-tolerant genetic resources. Identifying the tolerance level of genetic resources at seedling stage can enable the early selection of appropriate donors and recipients for breeding programs. Genetic resources can be effective source of tolerance to not just individual stresses but combined stresses as well ([Pandey et al. 2023](#)). Salinity and alkalinity often exist as combined stresses in agricultural fields all around the world. Screening of seedling growth attributes revealed significant variation in 105 *Avena* accessions grown under combined salinity and alkalinity stress. Seedling vigor index and final germination percentage were positively correlated in the studied genotypes. Genotypes IG-20-477, OS-377, IG-20-798, and IG-20-575 were suggested to be appropriate donors for developing tolerance to high saline-alkaline stress according to the measured stress tolerance index based on multiple traits ([Ahmed et al. 2023](#)).

The review articles in this issue focused on diverse aspects related to the deployment of wild genetic resources of different species. During evolution, plants developed adaptive characteristics *via* the process of natural selection. The artificial selection by humans during the domestication process expedited the process of integrating desirable traits. However, it led to loss of several adaptive and crucial traits that are required for survival in natural growth conditions. Pod shattering is one of those traits that the ancient selection process was focused on minimising ([Ogutcen et al. 2018](#)). Although the selection process has largely reduced shattering in crops, it is still a cause of large losses in several crops. [Sofi et al. \(2022\)](#) presented a review with in-depth understandings of evolutionary relevance, mechanical features, and genomic and genetic resources for pod shattering with particular reference to common bean. Wild bananas with greater resistance to different biotic and abiotic stresses have been under-explored until date. [Panwar et al. \(2022\)](#) provided the first detailed review on the deployment of banana wild relatives and their related germplasm for the improvement of biotic and abiotic stress tolerance in modern cultivars, with a specific emphasis on Fusarium wilt, Black Sigatoka, and viral diseases in cultivated bananas. Utilisation of wild genotypes for abiotic stresses such as drought and salinity has also been discussed. With untapped genetic diversity,

banana genetic resources could be utilised for fibre, forage, medicines and food.

[Naikawadi et al. \(2022\)](#) provided a comprehensive review on *Ensete* species that possess several cosmeceuticals, nutraceuticals, and bioactive compounds other than being a staple food source. The authors presented a systematic analysis of their conservation and domestication, and agronomic, medicinal and nutritional traits. In another review, [Sood et al. \(2022\)](#) highlighted the need for successful utilisation of wild oat species for the nutritional improvement of cultivated oat (*Avena sativa*). Different wild forms of oats have been reported to have higher quality, protein, β -glucan, starch, and other metabolic and nutritional components along with tolerance to several biotic and abiotic stresses. Several approaches such as conventional breeding and molecular strategies including genetic engineering, QTL mapping, genomic selection, and speed breeding have been discussed.

Wild relatives not only have the importance for the development of food crops, but also hold significant potential for the improvement of forage crops. In a review, [Indu et al. \(2022\)](#) emphasised the adaptive mechanism of wild relatives of forage crops to changing climate. Other than discussing the biotechnological strategies, authors appraised the cutting-edge breeding tools that can be used in the upcoming stress breeding programmes for establishing climate resilient forage crops.

This special issue may serve as a baseline source to assist improvement of different crops *via* involvement of CWRs and may enhance global awareness towards the existence of potential CWRs and their adaptive features under stress conditions.

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