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Cover page

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Genetic resources and new breeding tools for sunflower improvement

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Sunflower is one of the major oil crops of today, however due to its wide distribution, as well as its drought tolerance it may gain even more on its significance and become the main oil crop of the future, especially in the light of global environmental changes. This imposes a great responsibility on sunflower breeders to create more productive sunflower genotypes for future environmental changes. Exploitation of the available genetic resources in combination with the use of modern molecular and breeding tools could lead to considerable improvements in sunflower, especially with regard to different stresses and better adaptation to the climate change. Utilization of sunflower wild relatives for sunflower improvement is a long-term process which requires a lot of resources and work - from collecting of wild relatives, their maintenance, their testing and mining for desirable genes to the valorization in breeding programs. Genome-wide prediction, also known as genomic selection (GS), is one of the tools that could accelerate this process, through efficient and targeted improvement of populations and identification of parents for rapid genetic gains and improved stress resistant varieties. The application of tissue culture techniques and genetic engineering for improving the existing and introducing new traits from wild relatives into cultivated sunflower did not have much success, mainly due to the difficulty of regenerating plants in a reproducible and efficient way. Development of new breeding techniques, such as genome editing, could provide new perspectives for more efficient sunflower breeding. Generally, traits related to stress resistance are complex phenotypic traits controlled by polygenes, and it is usually necessary to study more than a single gene or single class of genes to understand molecular mechanisms underlying respective tolerance. Genome editing could be very useful to evaluate and validate the strength of the predictive value of a given candidate gene by easily transferring its best alleles into a set of different genetic backgrounds representative of the diversity of the genetic material used in the selection schemes. Institute of Field and Vegetable Crops, Novi Sad, Serbia, handles the largest World collection of sunflower genetic resources, consisting of over 7,000 sunflower inbred lines developed from different genetic sources and 21 perennial and 7 annual species (447 accessions in total). The new breeding tools will be used for further exploitation of this collection for improvement of cultivated sunflower and creation of resilient varieties for the areas and traits where classical breeding reached its limits.

***Key* words:** *Helianthu annuus* L., gene pool exploitation, resilience, breeding