cousin
Crop Cousins, promise for the future

Practice Abstract **n. 15**

# How genomics can help to unlock wild genetic potential for crop improvement

## A roadmap from wild genomic sequences to improved varieties

### *Introduction*

*Modern crops have undergone a domestication bottleneck, limiting the genetic diversity available for breeding. Crop wild relatives (CWRs) are a valuable reservoir of genetic variation. Genome sequencing enables the generation of maps that guide the identification of genetic variants that can be targeted for introgression from the wild into the domesticated background.*

## Objectives

Over centuries of farming, modern crops have become highly productive, but they have also lost many of the resilient, valuable traits found in their wild ancestors. Beneficial traits like deeper roots or resistance to infections are encoded in the plant DNA but remain largely unexplored in CWRs. Today, we can use whole-genome sequencing to characterize the genetic makeup of CWRs and bring those traits back. By scanning the entire genetic code of these wild species, we aim to identify the exact genes or genetic rearrangements responsible for these rugged traits. We will design genetic markers targeting these regions that will drastically speed up the introgression of wild beneficial traits into our high-yielding crops.

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## Results

Through the COUSIN project we have generated high quality genomic maps for twelve CWR related to wheat, barley, pea, lettuce and cabbage. This resource allowed us to characterize the genetic differences between CRWs and crops and identify CWR genes that regulate beneficial traits. For example, a genome-wide association analysis in the wheat CWR *Aegilops biuncialis* has uncovered regions associated with resistance to yellow rust and powdery mildew. In addition, the wheat CWR genomic map generated by COUSIN has greatly facilitated the screening of *Aegilops* introgressions in the wheat background. The barley CWR genomic map is being used to identify wild genes responsible for better performance in organic farming, using the progeny of a cross between a wild barley and an elite cultivar.

## Recommendations

The high quality CWR genomic resources generated will facilitate the work of pre-breeders, as they will be able to study wild species to develop markers and accurately introgress beneficial genes in modern varieties through marker-assisted introgression. This reduction in complexity will make this approach attractive to companies that have, until now, relied solely on traditional breeding.

The characterization of CWR genomes allows the identification of novel genes associated with beneficial traits and pinpoint the underlying causal mutations. This represents a strong opportunity to accelerate breeding in the context of the future approval of New Genomic Techniques (NGTs) in Europe.

## Further reading

- Aamir W. Khan, Vanika Garg, Manish Roorkiwal, Agnieszka A. Golicz, David Edwards, Rajeev K. Varshney. Super-Pangenome by Integrating the Wild Side of a Species for Accelerated Crop Improvement. Trends in Plant Science, Volume 25, Issue 2, 148-158. https://doi.org/10.1016/j.tplants.2019.10.012.

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