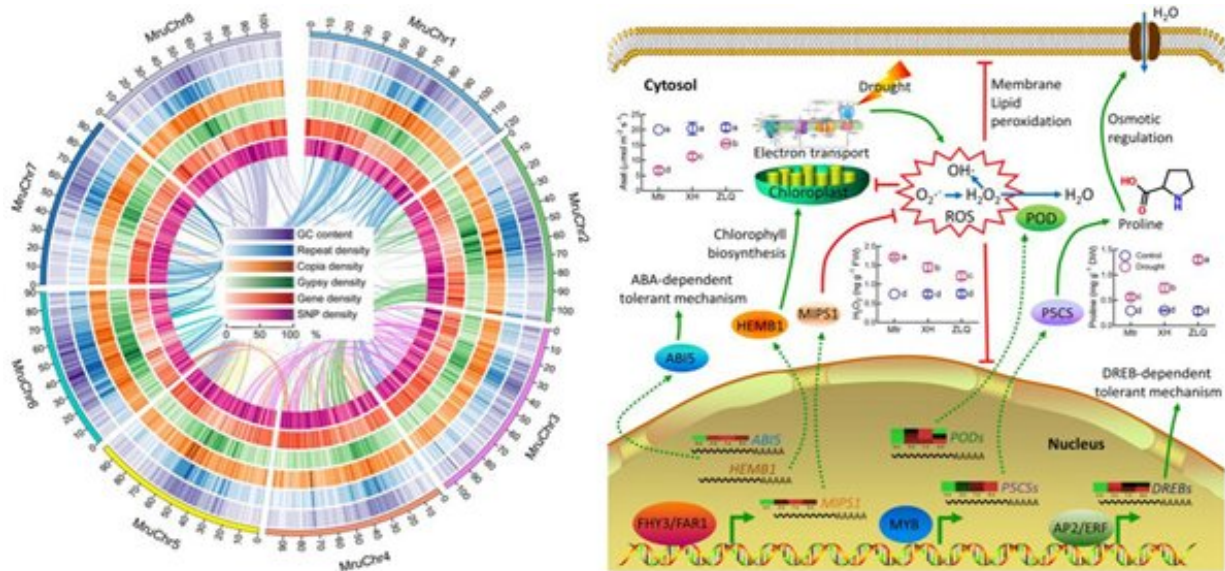


Genome of wild legume provides insights into tolerance to environmental stress

May 14 2021, by Li Yuan



Distribution of genomic features within the *M. ruthenica* genome and proposed mechanisms behind tolerance of *M. ruthenica* to drought stress . Credit: WANG Tianzuo

Medicago ruthenica, a wild and perennial legume forage widely distributed in semi-arid grasslands, is distinguished by its outstanding tolerance to environmental stress. It is a close relative of commonly cultivated forage of alfalfa (*Medicago sativa*).

The high tolerance of *M. ruthenica* to [environmental stress](#) makes this

species a valuable genetic resource for understanding and improving traits associated with tolerance to harsh environments.

Scientists from the Institute of Botany of the Chinese Academy of Sciences (IBCAS) and their collaborators sequenced and assembled genome of *M. ruthenica*. They elucidated mechanisms underlying the tolerance of *M. ruthenica* to environmental stress by [comparative genomics](#) and transcriptomic analyses.

This study was published in the journal *BMC Biology* on May 6.

The researchers discovered that expanded FHY3/FAR1 family was involved in tolerance of *M. ruthenica* to drought stress. They found that many genes involved in tolerance to [abiotic stress](#) were retained in *M. ruthenica* compared to other cultivated *Medicago* species.

They identified hundreds of candidate genes associated with drought tolerance by analyzing variations in [single nucleotide polymorphism](#) using accessions of *M. ruthenica* with varying tolerance to drought.

Transcriptomic data revealed the involvements of genes related to [transcriptional regulation](#), stress response and metabolic regulation in tolerance of *M. ruthenica*.

"The high quality genome assembly and identification of drought-related genes in the wild species of *M. ruthenica* provide a valuable resource for genomic studies on perennial legume forages," said Prof. ZHANG Wenhao, corresponding author of the study.

More information: Tianzuo Wang et al. The genome of a wild *Medicago* species provides insights into the tolerant mechanisms of legume forage to environmental stress, *BMC Biology* (2021). [DOI: 10.1186/s12915-021-01033-0](https://doi.org/10.1186/s12915-021-01033-0)

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