

Interrogating evolution to identify genes for drought-resistance in *Zea mays* L. in the face of global warming

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INTRODUCTION

Maize (*Zea mays* L.) is one of the most important food crops in the world for feeding people, as forage for cattle, and for synthesizing pharmaceutical drugs and other products. Drought affects maize at every stage of growth, and global climate warming forecasts anticipate an increase of drought frequency and intensity. Drought resistance in maize is a polygenic trait, and a number of breeding programs have been devised through the years to identify traits related with this character.

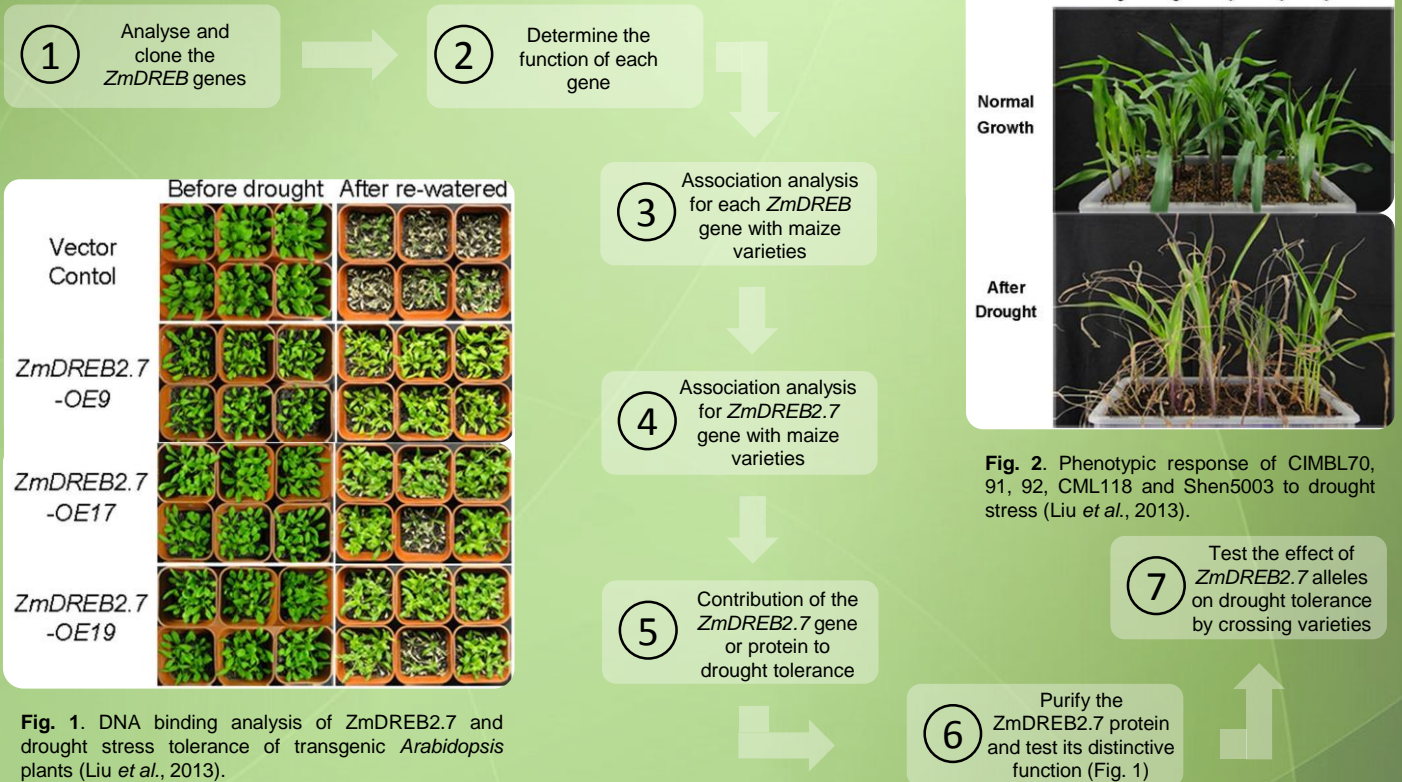
The “omics” breakthrough has provided new tools for linking the genetic changes to the phenotypic effects in specific biological contexts, such as drought.

Objectives. The main objective of this work is to introduce a new omics-based methodology which uses the evolutionary knowledge to further study and understand a certain trait (drought) as of correlating it with natural variation, consisting in analysing the natural variation of *DREB* (*Dehydration Responsible Element Binding*) genes

in maize. This approach has also commercial applications like the possibility of selecting certain traits. Therefore, it complements the present classical selection techniques.

Methodology. This article is a bibliographical review, and it has been built using databases like PubMed or Google Scholar. Searches have been done using key words such as “maize” AND “drought”. Some resources that the databases offer, such as related citations, have also been used.

APPROACH



CONCLUSIONS

Future expectations of global warming is increasing the need for understanding how drought is tolerated in plants, although the complexity of the trait is complicating to reach this objective.

The breakthrough of omic sciences and its advances are fostering the emergence of novel approaches. The one described here has been used before in *Arabidopsis* for years thanks to the broad knowledge of its genomics. Now, with the availability of genetically diverse collections comprising hundreds of maize varieties, this approach has been possible to use in this species.

Therefore, the role of basic sciences like studying, annotating and analysing the genome of organisms has an important relevance not only for the theory, but also to use it in practical applications such as breeding.

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