



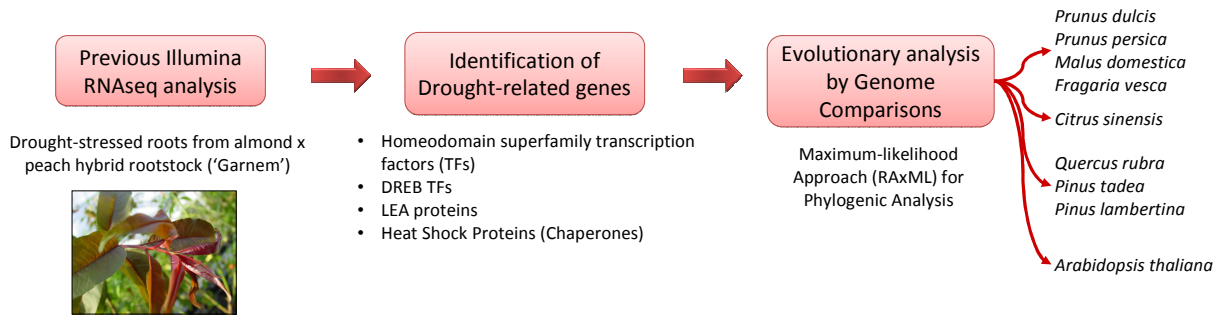
Diversity and molecular evolution of different drought-responsive genes in almond and several woody plants

B. Bielsa¹, M.J. Rubio-Cabetas¹, R.S. Dodd² and A. Fernandez i Marti^{1,2}

(1) Hortofruticulture Department. Agrifood Research and Technology Centre of Aragón (CITA), Zaragoza, Spain

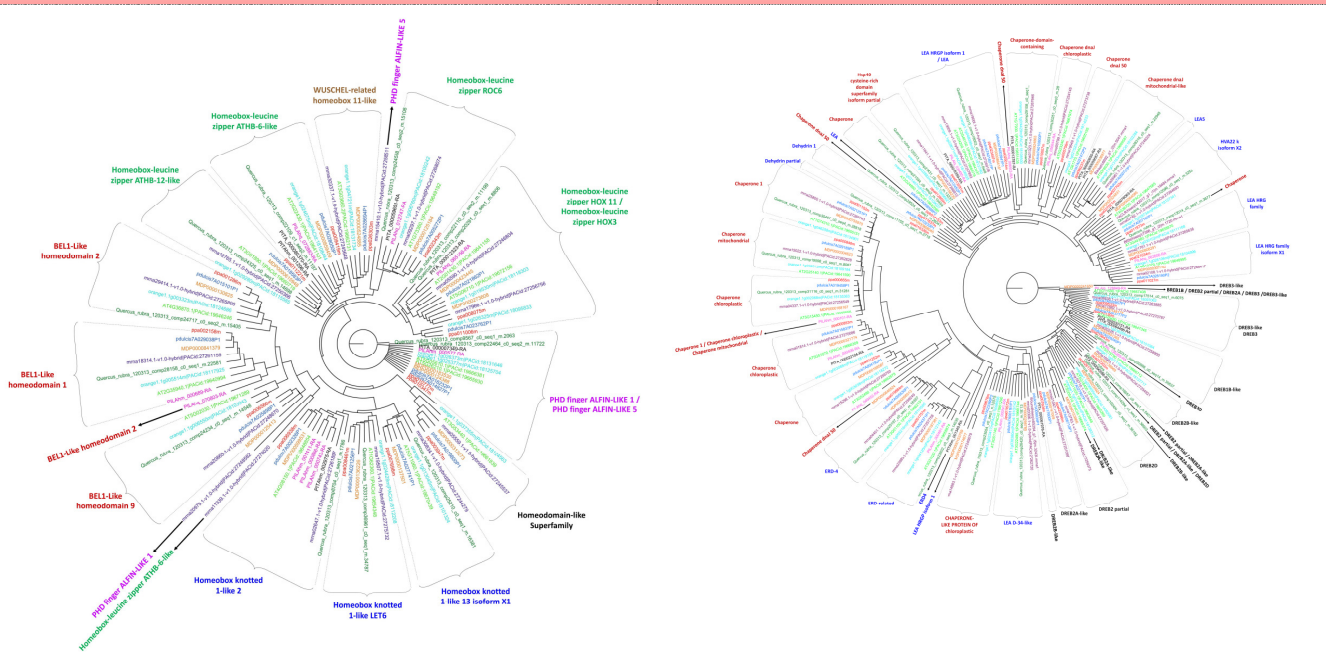
(2) Department of Environmental Science, Policy and Management, University of California, Berkeley, CA 94720, USA

Increasing drought stress, accentuated by climate change, will become one of the most negative factors to impact agriculture and will necessitate us to select drought tolerant rootstocks that are better adapted to future environmental conditions. Currently, our knowledge about the response to drought at the molecular level in woody plants is limited. The goal of our approach was to study the evolution of a number of drought-related gene families identified in a previous root transcriptomic analysis by Illumina among different woody plant species.



HOMEODOMAIN SUPERFAMILY TFs

DREB TFs – LEA Proteins - HSPs



- It is well known that the genes studied in this work play a crucial role in drought tolerance response. Homeodomain TFs regulate root development during drought. And DREB TFs trigger the activation of drought-responsive genes as well as the LEA proteins and HSPs, which are involved in osmoprotectant functions under drought stress, conferring drought tolerance.
- The resultant phylogenetic trees exhibited a very clear pattern of evolution. There has been expansion of specific gene families. Most of the gene families fell into distinct clades, indicating that these natural groups were well defined and presented high sequence identity among members. The results may indicate that these genes share a common ancestor for different plant genomes and that rates of expansion may be related to ancestral expansion rather than species-specific events.
- Thus, based on the distribution of the clades, we suggest that gene function diversification for the drought tolerance response happened prior to family extension. Further approaches are being undertaken in order to characterize the evolutionary pathway of drought stress genes in these plant species.