In the context of climate change, water availability will be the main limiting factor affecting biomass production, in particular in intensively managed forest tree plantations. The complexity of drought stress response calls for integrative approaches combining physiological, anatomical and molecular investigations at different scales ranging from particular cells to the whole plant. Such a strategy was developed for two eucalyptus clones used in industrial plantations in the Congo Republic and known for their different water-use efficiency. These two genetic units were submitted to two watering modes in open field conditions and followed during 18 months. We will describe and compare the molecular plasticity of these two genotypes at the transcriptomic (qPCR on candidate genes and profiling without a priori based on 454 sequencing) and proteomic (2DE combined with tandem MS) levels. We will interpret the results based on the analysis of reaction norms at the phenotypic level. By doing so, this study intend to identify genes of adaptive significance to environmental constraints.