

META-ANALYSIS AS A TOOL TO IMPROVE THE KNOWLEDGE OF THE MOLECULAR RESPONSE MODEL TO ABIOTIC STRESS OF FAGUS SYLVATICA L.

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Plants trigger several molecular and physiological responses to cope abiotic stresses (as drought, salt, heat and cold) which have a negative effect on plant growth and development. A meta-analysis was performed in order to provide a quantitative summary of the data from several studies and fill the knowledge gap about this topic especially in forest trees. This study evaluates if candidate genes for abiotic stresses in *Fagus sylvatica* L. are also candidate genes for herbaceous plants with the purpose to better define the molecular response model of *F. sylvatica*. Firstly, we carried out a systematic review regarding the activity of 24 candidate genes selected for *F. sylvatica* under abiotic stress. Subsequently, after choosing the inclusion criteria, 73 out of 509 reports, 12 candidate genes were included in this analysis. We performed an exploratory meta-analysis based on the random-effect model and the combined effect-size approach (Cohen's d). The results were presented through forest and funnel plots, that have shown high heterogeneity between primary studies. According to data collected inherent the regulation of these genes in response to various stresses, we can say that the candidate genes observed for *F. sylvatica* may also be considered as candidate genes in other plant species. These results allowed us to set up models of plants response to abiotic stresses implementing the stress models in forest species. The information collected will serve to fill the knowledge gaps regarding the pathways of response to abiotic stresses and the application of study methods based on meta-analysis. The study approach used could be extended to observe larger database and different species. This work is

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