

BOOK OF ABSTRACTS

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Stronger together: genetics and ecophysiology of drought stress in *Fagus sylvatica*

T3.2 Can adaptive genomic drive sustainable forest management under climate change?

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Abstract: European beech (*Fagus sylvatica* L.) has a large distribution area across the European continent. At its southern edge, this species is confronted with different climatic conditions than in Central or Northern Europe: average annual temperature is higher; precipitation is lower. To investigate possible different drought stress tolerances of beech provenances, a provenance trial ("climate forest") was established in the Grunewald Forest in Berlin/Germany, where individual trial members (a group of trees) can be irrigated, while other trial members are affected by the (naturally occurring) drought conditions in summer. A drought stress experiment was initiated in the summer of 2022 with one provenance each from Germany, France, Italy, and Spain. In a unique interdisciplinary approach, ecophysiological, biochemical and genetic analyses were performed following different stress intensities. The data will be used to unravel possible different drought stress tolerances of individual European beech provenances.

Genetic regulation of drought stress will be investigated by transcriptome analysis. For this purpose, mRNA was isolated from leaf samples of selected trial members and a sequencing approach was conducted. Based on the deciphered mRNA sequences, the activity of the different genes will be determined. Biochemical measurements will be performed for the levels of the drought stress markers proline, malondialdehyde and peroxide, among others. Together with physiological data such as photosynthetic activity, stomatal conductance, and water potential, the analytical triad should provide a comprehensive picture of the drought stress response of the trees in this trial.

We expect answers to the questions: what is the overall response of European beech under drought stress? Do the selected provenances differ in their drought stress response? Which genes are switched on or off, and how fast or how strongly is gene activity regulated? Is the provenance-dependent differential stress tolerance related to differential gene regulation? The findings from this collaborative research may be helpful to develop genetic, biochemical and/or ecophysiological markers which can be used to select suitable drought-tolerant provenances.