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Effects of high levels of CO2 on gene expression in two different genotypes of *Fagus sylvatica*

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Background

The scenario of a changing environment, widely termed as global change is mainly caused by human activities. Oil and carbon combustion, the use of chlorofluorocarbons, and deforestation are one of the main factors responsible for increasing CO_2 concentration and for an increase of air temperature. In addition global changes will affect precipitation patterns, nitrogen concentration in the atmosphere and enhanced UV-B radiation. Forest trees constitute a relevant economic and ecological resource that is under severe pressure by such environmental changes.

However, the response of forest trees and in particular of the important forest tree species *Fagus sylvatica* to elevated CO_2 levels on a gene expression basis is unknown so far. The principal aim of this study is the investigation of two different genotypes of *Fagus sylvatica* upon increased CO_2 by microarray and gene expression analyses.

Materials and methods

Shoots of *F. sylvatica* (Germany) and *F. sylvatica* "purpurea tree" (Germany) were grafted on *F. sylvatica* rootstocks. Plants were kept for 10 days under controlled conditions in climate chambers using the same temperature and light parameters, whereas the CO_2 concentration was approx. 380-400 ppm (ambient) in the control chamber and 1000 ppm (high) in the CO_2 chamber. Five leaves were taken from arbitrary chosen plants in control and high CO_2 chamber at 2 different time points (T2=2 days and T10=10 days) with 3 biological replicatesper each genotype per each sampling time point. The leaves were immediately frozen in liquid nitrogen and stored at -80°C. Extraction of total RNA was according to Kiefer *et al*[1] and microarray analyses were carried out as described by Olbrich *et al*[2]. Real Time PCR (RT-PCR) [3,4] analyses were carried out for selected genes to evaluate changes in gene expression.

Results

The microarray resulted in differentially expressed gene at T2 and T10 in each beech genotype analyzed. In particular, genes involved in photosynthesis and chloroplast biogenesis were up regulated at T2. A similar trend was been for genes involved in sugar metabolism. This indicates that, at high CO_2 concentration, the activity of the photosynthesis machinery will be accelerated and, therefore, also the one of the glycolysis pathway which brings to an accumulation of carbon. After 10 days of high CO_2 level, few of these genes were down regulated but most of them are expressed at normal level. This effect has previously been described in most of the studies on pot-grown other C3 plants under elevated CO_2 which have indicated photosynthetic acclimation [5]. This response was particularly evident for the *F. sylvatica*"-purpurea tree" showing a different behaviour to the second beech genotype.

RT-PCR for genes involved in photosynthesis, chloroplast biogenesis and sugar metabolism are in progress for both genotypes.

Conclusions

A lot of studies have reported contradictory responses of higher C3 plants to elevated levels of CO_2. This observation has also been made in the two German beech genotypes analyzed in this work confirming high expression variability between different genotypes of the same plant

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species. Therefore, considering the importance to preserve the forest ecosystems under global climate change, further investigations are necessary to understand the regulatory events associated with the adaptive acclimation responses of trees.

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References
1. Kiefer E, Heller W, Ernst D: **A simple and efficient protocol for isolation of functional RNA from plant tissues rich in secondary metabolites.** *Plant Molecular Biology Reporter* 2000, **18**:33-39.
2. Olbrich M, Gerstner E, Welzl G, Winkler JB, Ernst D: **Transcript responses in leaves of ozone-treated beech saplings seasons at an outdoor free air model fumigation site over two growing seasons.** *Plant and Soil* 2009, **323**:61-74.
3. Pfaffl MW: **A new mathematical model for relative quantification in real-time RT–PCR.** *Nucleic Acids Res* 2001, **29(9)**:e45.
4. Pfaffl MW, Horgan GW, Dempfle L: **Relative expression software tool (REST©) for group-wise comparison and statistical analysis of relative expression results in real-time PCR.** *Nucleic Acids Res* 2002, 30(9):e36.
5. Reddy AR, Rasineni GK, Raghavendra AS: **The impact of global elevated CO^2 concentration on photosynthesis and plant productivity.** *Current Science* 2010, **99**:46-57.

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