An Approach to Analyzing Changes in Gene Expression of Non-model Plant Species Grown Under Elevated CO₂ and Soil N Levels

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METHODS

**Tissue Collection** → **RNA Isolation** → **Quantify RNA**

**Analyze Data** → **RT-qPCR**

**Identify Target Genes**

**METHODS CONTINUED**

**Identify Target Genes**

We plan to measure expression of several critical gene products involved in photosynthesis such as nitrate reductase and nitrate transporters. Exact genomic sequences from wheat will be used as reference sequences. Genes involved in these pathways will provide insight into the mechanisms underlying acclimation to elevated CO₂ (Fig. 1).

**RT-qPCR**

Once specific genes have been selected for further observation, the RNA from these genes will be amplified into cDNA using **RT-qPCR**. RT-qPCR is a commonly used technique for measuring the relative abundance of specific sequences to determine relative gene expression (Fig. 4). Fluorescent tags are used to measure amplification of sequences in real time.

**Quantification of Gene Expression**

Non-specific fluorescent dyes interchelate double-stranded DNA during the PCR cycles, resulting in fluorescence. The amount of mRNA in the sample is directly correlated to the number of cycles required before fluorescence is detected (Fig. 5). Once the relative abundance of mRNA is quantified for each leaf sample, the data will be compared between the various treatments.

**IMPLICATIONS**

Our findings will help explain the molecular mechanisms behind physiological responses to future atmospheric CO₂ levels. This will contribute to more accurate modeling of future responses of vegetation to climate change. This information may also inform genetically modified crop species more equipped to grow under future climate conditions.

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**REFERENCES**