

# Transcript abundance, biochemistry & physiology of carbon metabolism in soybean leaves grown at elevated CO<sub>2</sub> under Free-Air CO<sub>2</sub> Enrichment



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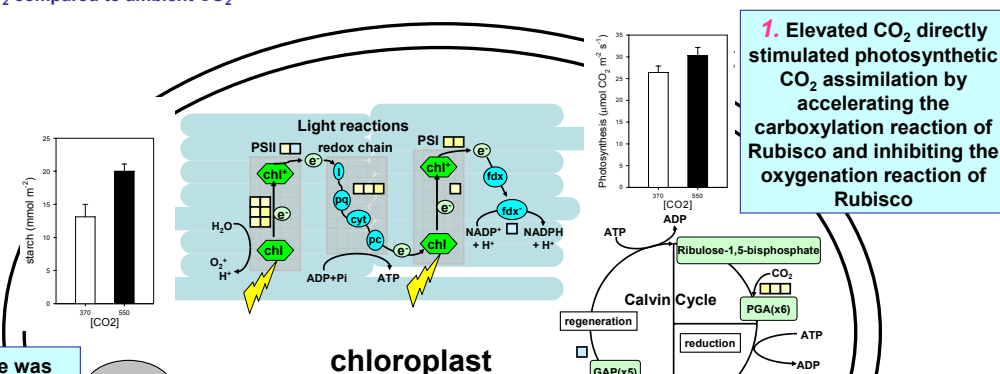
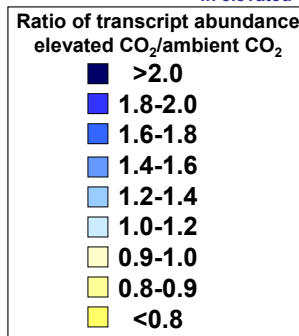
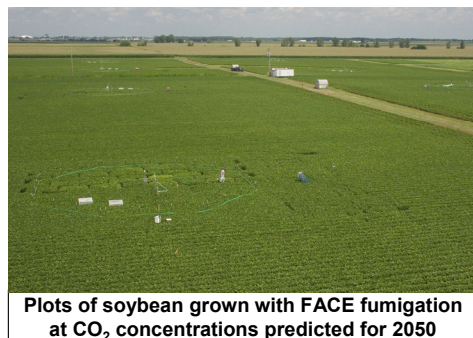
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## INTRODUCTION & AIM

- Atmospheric CO<sub>2</sub> will increase to 550 μmol mol<sup>-1</sup> by 2050
- Growth at elevated CO<sub>2</sub> is known to stimulate C<sub>3</sub> photosynthesis and growth
- But, little is known about how carbon metabolism acclimates to the increased supply of photoassimilate
- This study aimed to identify changes in transcript abundance at elevated CO<sub>2</sub> which underlie changes in carbon assimilation, utilization and respiration
- This is a first step towards identifying key regulatory steps in metabolism which control or constrain plant responsiveness to elevated CO<sub>2</sub>

## EXPERIMENTAL DESIGN

- Soybean was grown in the field, following standard agricultural practice, at the SoyFACE facility in Champaign, Illinois, USA
- 4 ambient CO<sub>2</sub> plots (380 ppm) and 4 elevated CO<sub>2</sub> plots (550 ppm), each of 20-m diameter
- Fumigation from planting until harvest using Free-air CO<sub>2</sub> Enrichment (FACE) technology
- In 2005, samples were collected at midday on 6 dates during reproductive growth including full bloom, pod growth and pod filling
- Photosynthetic gas exchange, carbohydrate pool sizes and transcript abundance of the youngest fully expanded leaf were assessed
- Transcript abundance was assessed using 48 Affymetrix soybean gene chips. Each chip was hybridized with pooled transcripts from 1 leaflet from each of 6 individuals per plot. Significant changes in transcript abundance at elevated CO<sub>2</sub> were identified as probe-sets for which the main effect of CO<sub>2</sub> was significant (p<0.05) across all days by ANOVA.
- Each box below (■) represents a unique transcript associated with an enzyme or structure. The color signifies the ratio of abundance in elevated CO<sub>2</sub> compared to ambient CO<sub>2</sub>



**5. At elevated CO<sub>2</sub> transcript abundance was greater for enzymes involved in synthesis of cell wall precursors and cellulose**

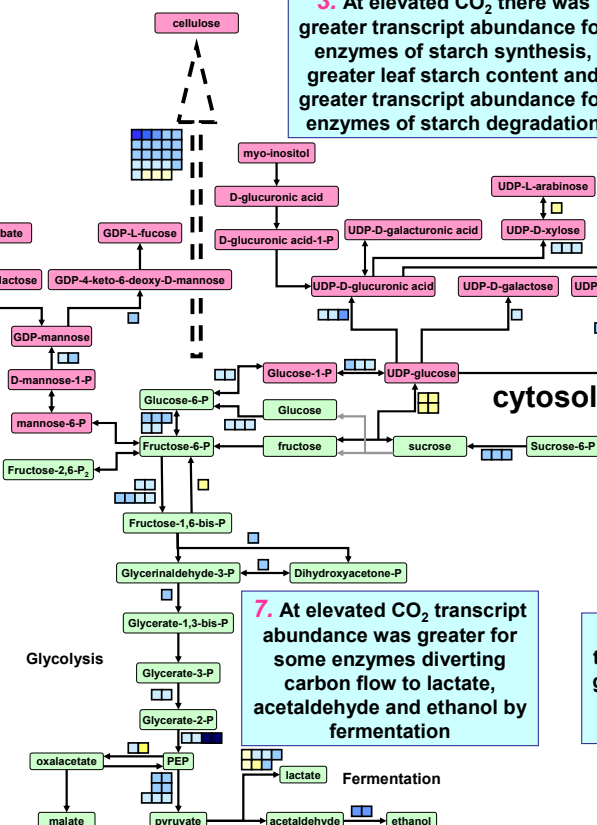
**3. At elevated CO<sub>2</sub> there was greater transcript abundance for enzymes of starch synthesis, greater leaf starch content and greater transcript abundance for enzymes of starch degradation**

**2. At elevated CO<sub>2</sub> transcript abundance was lower for RuBisCo large subunit N-methyltransferase, RuBisCo activase, chlorophyll A-B binding protein, and some components of the electron transport chain. This is consistent with previous observations of photosynthetic acclimation to elevated CO<sub>2</sub>**

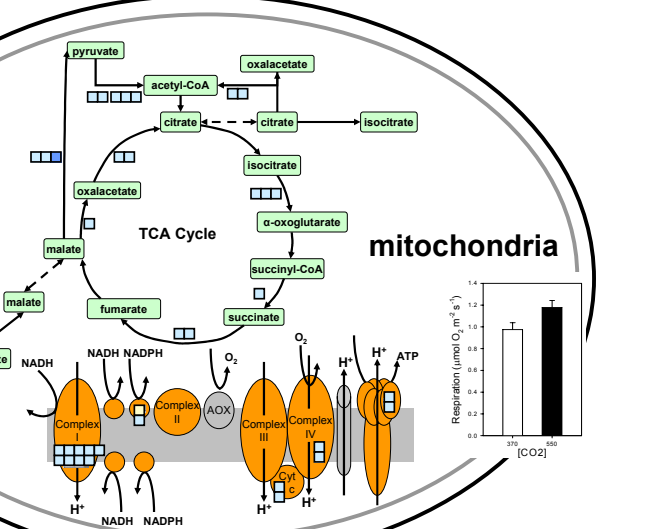
**6. At elevated CO<sub>2</sub> transcript abundance was greater for many enzymes in glycolysis. Greater carbon flux towards the TCA cycle and biosynthetic pathways may also have been favored by decreased transcript abundance for the key regulatory enzyme fructose-1,6-bisphosphatase.**

There was decreased transcript abundance for sucrose synthase at elevated CO<sub>2</sub>, with unknown effects on carbon flux between synthesis of cell wall precursors and glycolysis.

**4. At elevated CO<sub>2</sub> transcript abundance was greater for transporters exporting sugar from the chloroplast**



**8. At elevated CO<sub>2</sub> transcript abundance was greater for transporters of metabolites across the mitochondrial membrane**



**9. At elevated CO<sub>2</sub> increased abundance of transcripts in the TCA cycle and mitochondrial electron transport chain coincided with greater nighttime respiratory O<sub>2</sub> uptake. There was no change in abundance of transcripts for AOX, UCP or alternative NADH dehydrogenases. At elevated CO<sub>2</sub> there was increased abundance of transcripts for synthesis of some amino acids (aromatics, aspartate family, glutamate family, cysteine), some secondary compounds (terpenes), and lipid synthesis/degradation**

## CONCLUSION

- Acclimation of carbon metabolism to growth at elevated CO<sub>2</sub> was primarily characterized by increases in transcript abundance for components of respiratory metabolism
- These changes were on average greater and more numerous than decreases in transcript abundance for components of the photosynthetic machinery, which have been the focus of most prior studies.
- The increased abundance of transcripts related to: (1) carbon storage, (2) biosynthetic pathways such as cell wall synthesis, and (3) energy production corresponded with enhanced photosynthetic CO<sub>2</sub> fixation, starch accumulation and respiratory O<sub>2</sub> uptake at elevated CO<sub>2</sub>
- The next step towards identifying key regulatory processes is assaying the activity of enzymes which control flux in C and N metabolism and displayed altered transcript abundance under elevated CO<sub>2</sub> (e.g. FBPase, PFP, PFK)

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