A molecular approach to understanding plant response to global climate change in a Californian grassland ecosystem

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Global warming affects the climate in multiple ways from increased temperature to altered rainfall pattern. Understanding the effect of these climatic changes on different ecosystems is paramount. We are currently investigating the coordinated responses to climate change of soil microorganisms and plants from a Californian grassland ecosystem through a multidisciplinary project. Our aim is to link the different responses, scaling from gene expression to ecosystem function. Here we discuss some aspects of the plants response at the molecular level.

Our experimental setup reproduced a Californian annual grassland ecosystem in climate-controlled greenhouses. A total of 152 mesocosms were filled with three horizons of natural soil packed to specific bulk density and instrumented to follow precisely the plant growth conditions. Seeds, collected from the grassland, were dispersed on the mesocosms to generate monocultures of *Avena barbata* (the dominant species in many California grasslands), or mixed communities including five additional grasses and two forbs. Leaf and root samples were collected at the peak of the growing season from *A. barbata* plants grown under low, ambient and high precipitation treatments and in two different soil types.

The availability of genomic sequences for *A. barbata* was limited and only a few cDNA have been cloned and sequenced previously. We used genomic data from other grass species to design PCR primers in order to amplify specific sequences in our focal species. Using the PCR cloning approach we have sequenced target genes and subsequently studied their expression using real-time RT-PCR. The target genes were selected for their key role in both nitrogen and carbon metabolism. Preliminary data suggests that, at the time of sample collection, plants grown under low precipitation treatments were subjected to mild water stress. Under these conditions, ribulose-1,5-bisphosphate carboxylase/oxygenase (*Rubisco*) gene expression was shown to decline by 40%. The expression of nitrate reductase (*Nia*) and chloroplastic glutamine synthetase (*GS2*) was maintained suggesting that nitrate was still available to the plants for uptake. The decline in ADP-glucose pyrophosphorylase (*AGPS*) expression may indicate that less carbon was available for storage in the form of starch. At high precipitation, the levels of *Nia* and *Rubisco* mRNAs decreased while those of *GS2* and *AGPS* were maintained. Under these conditions, the soil pools of nitrate and ammonium were lower compared to the ambient conditions, which could explain the pattern of expression seen for *Nia* and *Rubisco*. Furthermore, the up-regulation of the cytosolic GS isoform may indicate a greater need for nitrogen remobilisation in the leaf, which is consistent with a lower nitrogen supply. These results will be integrated with ongoing studies of leaf metabolite levels, plant physiology and ecosystem function to understand the potential significance of genomic responses to climate change.