

Impact of UV-B Radiation on Corn (*Zea mays* L.)

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Description: Plants capture solar energy through photosynthesis and are the major contributors of fixed energy into biological processes. Conversion of “old” fixed carbon generated by vascular plants constitutes much of our current oil and gas reserves. Flowering plants now dominate the earth, and most species use C₃ (standard) photosynthetic reactions as found in lower plants and conifers. Corn is among a handful of flowering plants that utilize a more efficient photosynthetic process termed C₄ photosynthesis, which makes it a candidate for energy farming such as alcohol production. Furthermore, corn is the most important US crop in terms of acreage, value in the export market, and diversity of uses.

Solar energy contains UV-C (220 – 280 nm), UV-B (280-320 nm) and UV-A (320-400 nm), but UV-C is completely absorbed by the atmosphere and most UV-B is absorbed by ozone. Consequently as terrestrial plants absorb light energy for photosynthesis, they are inevitably exposed to some highly energetic UV-B and to UV-A. Plants have evolved avoidance mechanisms such as sunscreen pigments and diverse repair processes to cope with UV exposure, because this radiation causes direct damage to proteins, DNA, lipids and RNA in cells. Human activities have decimated the ozone layer, particularly in Polar Regions, resulting in periodic higher fluence UV-B radiation that exceeds normal repair capacities. Furthermore UV-B and UV-A elicit physiological and developmental changes in corn and other plants that result in increased shielding.

Using DNA microarrays we are defining the changes in gene expression that accompany responses to UV-B. We have studied gene expression from environments lacking UV-B, normal solar fluence, and supplementary UV-B in both field and greenhouse conditions. In our initial experiments (Casati & Walbot 2003) we compared the responses of plants with high levels of the effective sunscreen anthocyanin pigment, to plants with low or no anthocyanin. This analysis and dose-response studies permitted identification of gene expression changes to low, medium, and high fluence UV-B. We discovered that organs that receive no direct radiation nonetheless show gene expression changes within one hour, indicating that there is a systemic and coordinated response to UV-B treatments (Casati and Walbot 2004).

An aspect of our analysis of anthocyanin, a class of flavonoid pigment, was using a combination of genetics and molecular analysis to determine how the pigment is transferred from the site of synthesis in the plant cytoplasm to the acidic vacuole. The pigment is more effective in the vacuolar environment. We were the first to provide proof of the type of pump used to transfer anthocyanin across the tonoplast membrane into the vacuole (Goodman *et al.* 2004).

We recently defined the plant ribosome – the site of new protein synthesis – as a major site of RNA damage. Because ribosome cannot be repaired, the entire molecular machine must be synthesized de novo; although protein synthesis is impaired during UV-B exposure, messenger RNAs for the proteins to build new ribosomes are selectively translated into protein. We are interested in defining the regulatory steps that permit this adaptive response.

Current studies utilize a suite of Mexican and South American corn lines grown about 2000 meters near the equator; this high altitude maize lines receive a much higher fluence of UV-B than standard U.S. lines. Using the high altitude corn we are defining adaptations (genetic changes) and acclimations (physiological responses) that could be useful in breeding more UV-resistant maize.

To verify results from microarray hybridization we use real-time RT-PCR to measure precisely the levels of messenger RNA for the most interesting candidate genes. We have also conduct two-dimensional gel electrophoresis to identify which proteins are altered in abundance or migration (most likely the result of post-translational modifications) after UV-B exposure; protein identification is conducted by mass spectrometry.

Status: This work is continuing under a USDA grant funded through September 2006. Current efforts are directed at protein identification and the definition of novel pathways of damage repair and signal transduction that UV-B damage has occurred in the leaves.

Publications:

Goodman, C. D., P. Casati, and V. Walbot, “A multidrug-resistance associated protein involved in anthocyanin transport In *Zea mays*.” In press for the Plant Cell, 2004.

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Casati, P. and V. Walbot, “Gene expression profiling in response to ultraviolet radiation in *Zea mays* genotypes with varying amounts of flavonoids,” Plant Physiology 132: 1739-1754, 2003.

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