Investigating genetic loci that encode plant-derived paleoclimate proxies

 $\label{eq:main_algo} \begin{array}{l} Amanda \ L.D. \ Bender^{1*}, \ Melanie \ Suess^{1}, \\ Daniel \ H. \ Chitwood^{2} \ and \ Alexander \ S. \ Bradley^{1} \end{array}$

 ¹Dept. of Earth & Planetary Sciences, Washington University in St. Louis, MO 63130, USA (*bender@levee.wustl.edu)
²Donald Danforth Plant Science Center, St. Louis MO 63132

Long chain (> C_{25}) *n*-alkanes in sediments predominantly derive from terrestrial plant leaf waxes. Hydrogen isotope ratios (δD) of leaf wax hydrocarbons correlate with δD_{H20} of precipitation and are commonly used as paleoclimate proxies. However, biological variability in the isotopic fractionations between water and plant materials also affects the *n*-alkane δD values. Correct interpretation of this paleoclimate proxy requires that we resolve genetic and environmental effects.

Genetic variability underlying differences in leaf wax structure and isotopic composition can be quantitatively determined through the use of model organisms. Interfertile *Solanum* (tomato) species provide an ideal model species complex for this approach. We used a set of 76 precisely defined hybrids (*introgression lines* [ILs]) in which small genomic regions from the wild tomato relative *Solanum penellii* have been introduced into the genome of the domestic tomato, *S. lycopersicum*. By characterizing quantitative traits of these ILs (leaf wax structure and isotopic composition), we can resolve the degree to which each trait is regulated by genetic versus environmental factors.

We present data from two growth experiments conducted with all 76 ILs. In this study, we quantify leaf wax traits, including δD , $\delta^{13}C$, and structural metrics including the methylation index (a variable that describes the ratio of *iso*and *anteiso*- to *n*-alkanes). Among ILs, δD values vary by up to 35% and 60% for C31 and C33 *n*-alkanes, respectively. Many ILs have methylation indices that are discernably different from the parent *Solanum* (p < 0.001). This suggests that methylation is a highly polygenic trait. This pattern is similar to the genetics that control leaf shape [1], another trait commonly used as a paleoclimate proxy. Based on our preliminary analysis, we propose candidate genes that control aspects of plant physiology that affect these quantitative traits.

Our results have important implications for uncovering the degree to which we can expect environmental versus genetic factors to modulate variability in *n*-alkane δD values. These findings can inform the interpretation of the proxy signal recovered from the geological record.

[1] Chitwood et al. (2013). The Plant Cell 25, 2465-2481.