

*Dear Faculty, Postdocs, Students, and Friends:*

**You are cordially invited to a seminar presented by**



**Dr. Kathleen Greenham**

*Dept. of Plant and Microbial Biology  
University of Minnesota*

**Title:**

**“Integrating time into transcriptional networks for  
pattern discovery”**

**DATE: Friday, February 26, 2021**

**TIME: 12:00 pm PST**

**ZOOM MEETING ID: 935 2068 0213**

**PASSCODE: 334093**

***Host: Dawn Nagel***

**Abstract:** The genus Brassica contains crops with leaf, flower and root vegetables for consumption, oil production, and fodder. *B. rapa* captures much of this diversity in one species with Chinese cabbage, pak choi, oilseed, turnip, and leafy vegetable varieties. This variation provides a rich source of genetic and physiological diversity to be explored. As with many crops, *B. rapa* is polyploid, diverging from *Arabidopsis thaliana* roughly 24 million years ago (MYA) and undergoing genome triplication followed by extensive gene fractionation. As a consequence, the genome architecture has diverged from *Arabidopsis* leaving open many questions as to how the expansion of the *B. rapa* genome has influenced physiological processes. We are interested in how the circadian clock coordinates plant responses to environmental stressors. Our goal is to decipher this temporal regulation and manipulate the timing of certain processes to generate higher performing crops. Incorporating time into our experimental design provides us with the resolution to associate diel transcriptional patterns with metabolic and physiological outputs. In this talk, I will share evidence for genome wide expansion and divergence of the circadian network in *B. rapa* followed by new results looking at intraspecific variation in temporal networks and how they may relate to differences in physiological and metabolic responses to stress.