Online Proceedings

Session 1I

McNair Session - Exploring Science from Cells to Exoplanets

Session Moderator: Janneke Hille Ris Lambers, Biology
MGH 254
12:30 PM to 2:15 PM
* Note: Titles in order of presentation.

Effect of Daily Temperature Changes in *FLOWERING LOCUS T* Expression Profiles in Nature
Dianne Laboy, Junior, Pre-Sciences
Levinson Emerging Scholar, McNair Scholar
Mentor: Takato Imaizumi, Biology
Mentor: Akane Kubota, biology

Climate change is forecasted to have an impact in agricultural productivity. To ensure security of crop yields, we must develop a better understanding of flowering mechanisms in plants. Research on flowering mechanism has been performed mostly under simplified lab growing conditions. However, in the natural environment, plants experience dynamic changes in abiotic factors like temperature throughout the day. To better understand how flowering is regulated under natural conditions, we focused on the expression profiles of *FLOWERING LOCUS T* (*FT*), which correlates with the flowering time in plants. *FT* expression is known to peak in the evening under long day lab conditions (16 hours of light, 8 hours of darkness, 22^{o}C constant). However, under natural long day conditions (Summer Solstice in Seattle, 16 hours of light, 8 hours of darkness, average highest temperature 21^{o}C) we have observed an additional morning peak. We have been able to recreate the observed expression of *FT* in the lab by modulating temperature oscillation and light quality of long day lab conditions. In this project, we first asked if the observed *FT* pattern is widely conserved in different wild type accessions in *Arabidopsis thaliana*. We grew different accessions under re-created lab growth conditions and analyzed *FT* expression using quantitative PCR. So far we have seen similar *FT* expression patterns among some accessions, suggesting that morning peak of *FT* is conserved among these lines. Second, we studied which timing of the day temperature acts as a cue to affect morning *FT* expression. We grew plants under various temperature conditions and compared results to the observed *FT* expression in nature. The results from this project will contribute to the development of new modified lab growth conditions that represent natural conditions and give a better understanding of the mechanism that controls *FT* regulation in nature.

Poster Session 2

Commons East, Easel 84
1:00 PM to 2:30 PM

Regulatory Mechanism of *FLOWERING LOCUS T* Mediated by *PHYTOCHROME A* under Natural Conditions
Jessica Imel, Senior, Biochemistry, Biology (Physiology)
Mentor: Takato Imaizumi, Biology
Mentor: Akane Kubota, biology

Plants respond to abiotic factors in natural settings in order to regulate physical responses at the most appropriate timing. The timing of flowering affects seed and/or fruit production in many agriculturally relevant plants, so understanding its mechanism is essential for addressing agricultural needs as climate changes. To address this aim, we have used *Arabidopsis thaliana* as a model plant to understand the molecular mechanism of seasonal flowering. It has been shown that the expression of *FLOWERING LOCUS T* (*FT*), which encodes florigen, peaks in the evening under long-day lab conditions (16 hours light, 8 hours dark, 22C) and promotes flowering in a day-length specific manner. However, our lab found that *FT* also peaks in the morning under outside long-day conditions over the summer solstice in Seattle (16 hours light, 8 hours dark, highest average temperature 21C). This double-peak of *FT* can be re-created by changing the light quality and temperature settings of long-day lab conditions. In addition, we found that a mutant of *PHYTOCHROME A* (*PHYA*), which encodes a red/far-red light photoreceptor in plants, lacks *FT* expression in a morning-specific manner, suggesting that *PHYA* is involved in regulating morning expression of *FT*. In order to understand the molecular mechanism of *PHYA*-mediated *FT* regulation, we are in the process of identifying transcription factors and other molecules that work with PHYA to induce *FT* expression. We have successfully cloned various transcription factors that are reported to act in the flowering regulatory pathway and are in the process of testing protein-protein interaction against PHYA by

yeast-two-hybrid methods. Identifying the components that act in the *PHYA-FT* pathway will allow us to further understand how light affects flowering regulation.