

# 2022 HHMI Gilliam Seminars

All Seminars 12-1PM PST



Dr. Clara Williams (She/Her)

**Identifying Demethylase Transcriptional Regulators**

Mon. 4<sup>th</sup> of April 2022 HCK132

**Standing on the top of Trees**

Tues. 5<sup>th</sup> of April 2022 LSB 201



Prof. Beronda Montgomery (She/Her)

**Seeing The Light: Plant Color Vision and Developmental Acclimation**

Tues. 19<sup>th</sup> of April 2022 LSB 201

**Lessons from Plants on Human Thriving**

Wed. 20<sup>th</sup> of April 2022 HCK132



Dr. Jonelle Basso (She/Her)

**Assessment of viral influence on plant root colonization by plant growth promoting rhizobacteria**

Mon. 9<sup>th</sup> of May 2022 HCK132

**The intersectionality of mentorship and resilience within the academic landscape**

Tues. 10<sup>th</sup> of May 2022 LSB 201



Prof. Terri Long (She/Her)

**Iron at the intersection of development and multi-stress resilience**

Mon. 16<sup>th</sup> of May 2022 HCK132

**Black in Plant Biology – A Perspective**

Tues. 17<sup>th</sup> of May 2022 LSB 201

More information at:  
[tinyurl.com/HHMIgilliam](https://tinyurl.com/HHMIgilliam)

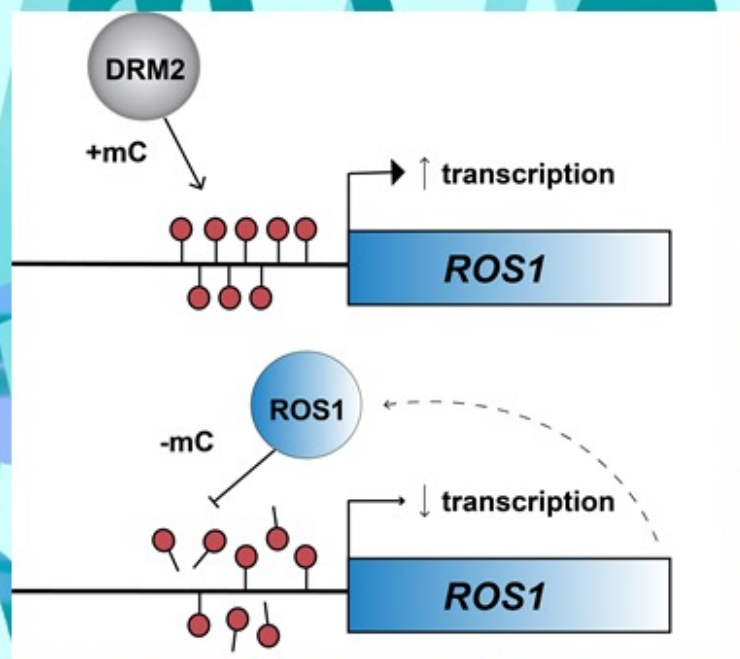
## 2022 HHMI Gilliam Seminars

Dr. Clara Williams (She/Her)

Postdoc, University of California, Berkeley

### Identifying Demethylase Transcriptional Regulators

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Methylation of cytosine is an epigenetic change that can alter the accessibility and expression of a gene without changing the DNA sequence, thus enabling plants to dynamically change the context in which the DNA is read. Methylation levels are monitored by demethylases, which act as glycosylases and remove methylated cytosines. The gene encoding ROS1, a demethylase, acts as an epigenetic rheostat—DNA methylation levels at the ROS1 transcriptional start site dictate ROS1 expression levels. This generates a feedback loop where the cell may use ROS1 to sense and maintain stable methylation levels. Yet, it is unknown how methylation status at the ROS1 promoter influences binding of transcriptional regulators. The “rheostat” promoter region of ROS1 contains evolutionary conserved E2F cis-regulatory elements. The E2Fs are a well studied transcription factor family that regulates the cell cycle and may play a key role in regulating methylation during cellular division. To identify transcriptional regulation of demethylation genes we are utilizing an in vivo DNA binding assay to determine where in the genome all six E2F transcription factor family proteins bind. I also aim to determine how methylation affects binding of specific E2F proteins by developing methods to assay the methylation-sensitivity of transcription factors in vivo. Ultimately, my research will uncover precise mechanisms and regulatory networks that link dynamic epigenetic mechanisms to cell cycle control.

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The most beneficial advancements in my career came through conversations and discussions I had with my mentors. It has been found that parental occupation can influence a minority student's likelihood to pursue a degree in a STEM field. Neither of my parents attended a four year university and could not give me any guidance as I began my college career. However, I was able to find guidance through my mentors. This is not a unique experience as minority parents are less likely to hold a PhD or other higher degrees. Given that in the current atmosphere you have a four times greater chance of earning a PhD if your parents have one, there needs to be some effort to compensate for the advantages some of us are not born into. My mentors acted as trees enabling me to gain a greater perspective on what I was capable of. Now, as I begin to plant my own roots, I hope that I can do for others what my mentors were able to do for me and uplift students above the canopy to see the opportunities out there for them.

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