

# GDCB SEMINAR

4:10-5 p.m.

Tuesday, Feb. 2, 2021

## “Orphan genes in *Arabidopsis thaliana*, *Zea mays* and *Homo sapiens*”

**Abstract:** All species possess genes whose proteins have no detectable sequence homology to proteins of any gene in any other organism. These “orphan” genes are difficult to predict and impossible to characterize functionally by sequence homology to known genes. For such genes, new approaches are needed. I will describe methods we have developed to better predict orphan genes, and the results these approaches have yielded in *Arabidopsis thaliana*, *Zea mays* and *Homo sapiens*. We have identified novel candidate orphan genes in each of the two plant species, as well as some novel candidate orphan genes that are unique to particular *Arabidopsis* and maize lines. With the emergence of SARS-CoV-2, we have switched some of our focus to address this challenge. The COVID-19 pandemic has affected African American populations disproportionately in regards to morbidity and mortality. A multitude of factors likely account for this discrepancy. RNA-Seq data provides a molecular phenotype of these factors. In African Americans as compared to European Americans, the levels of expression of novel orphan genes and genes implicated in COVID-19 vary across thousands of samples of existing RNA-Seq data from normal and diseased conditions.



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**Join meeting:**

<https://iastate.webex.com/iastate/j.php?MTID=mb238d165439455f48123c9a3d116aef8>

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