

2021

Protein Prenylation in the moss *Physcomitrium patens*

Zayna Qaissi

University of Louisville, zayna.qaissi@louisville.edu

Anam F. Ahmed

University of Louisville, anam.ahmed@louisville.edu

Mark P. Running

University of Louisville, mark.running@louisville.edu

Katherine Vo. Brown

University of Louisville, katherine.brown@louisville.edu

Follow this and additional works at: <https://ir.library.louisville.edu/tce>



Part of the [Plant Biology Commons](#)

Recommended Citation

Qaissi, Zayna; Ahmed, Anam F.; Running, Mark P.; and Brown, Katherine Vo. (2021) "Protein Prenylation in the moss *Physcomitrium patens*," *The Cardinal Edge*: Vol. 1 , Article 4.

DOI: [10.18297/tce/vol1/iss1/4](https://doi.org/10.18297/tce/vol1/iss1/4)

Available at: <https://ir.library.louisville.edu/tce/vol1/iss1/4>

This Research Abstract is brought to you for free and open access by ThinkIR: The University of Louisville's Institutional Repository. It has been accepted for inclusion in The Cardinal Edge by an authorized editor of ThinkIR: The University of Louisville's Institutional Repository. For more information, please contact thinkir@louisville.edu.

Protein Prenylation in the Moss *Physcomitrium patens*

Zayna Qaissi^{1,2}, Anam Ahmed^{1,2}, Katherine Brown¹, Mark Running^{1,3}

¹ The University of Louisville, Louisville, KY, USA

² Co-presenters

³ Faculty Mentor

ABSTRACT

Protein prenylation is the addition of a 15 or 20 carbon lipid to a cysteine near carboxyl terminus of target proteins. Prenylation increases hydrophobicity, which facilitates membrane associations and protein-protein interaction. Protein prenylation is generally conserved among eukaryotes, and mutations in genes that carry out prenylation are lethal in animals and yeast. In plants prenylation mutations are not always lethal, but they do affect development, disease resistance, biofuel production, and drought response, among other processes of agricultural interest. To understand the evolutionary and developmental implications of plant protein prenylation, we used the sequenced, annotated, and translated genome of the moss *Physcomitrium patens* to search for proteins that meet minimal criteria for prenylation; specifically the presence of a sequence that includes cysteine and one of six specific amino acids at the C terminus. We then analyzed these proteins with an online prenylation prediction program to assess their likelihood of being prenylated based on additional sequence motifs. Although the number of prenylated proteins has not been confirmed, we estimate that there are 300. We then determined potential biological function of putative target proteins by using BLAST sequence similarity searches to identify related genes with known function. We plan to use these data to select prenylated proteins with functions of interest for *in vivo* studies using genetic and molecular tools to investigate their roles in plant development and environmental response.

REFERENCES

<http://www.jbc.org/cgi/doi/10.1074/jbc.M115.673491>
