



Introduction and Background

V-ATPases are ATP-dependent proton pumps that regulate pH of endomembrane compartments in the cell.

- Subunit H (VHA-H) is thought to be the complex activator (Flannery & Stevens, 2008)
- Encoded by a single gene *VHA-H* -> evidence of two splice isoforms
- Other subunits' isoforms shown to exhibit specificity in localization and function (Dettmer et al., 2010)
- May also occur in *VHA-H* isoforms
- V-ATPases play critical role in pollen development and drought stress tolerance (Dettmer et al., 2005, Liu et al., 2018)
- Localization of *VHA-H* provides insight into V-ATPase activity regulation

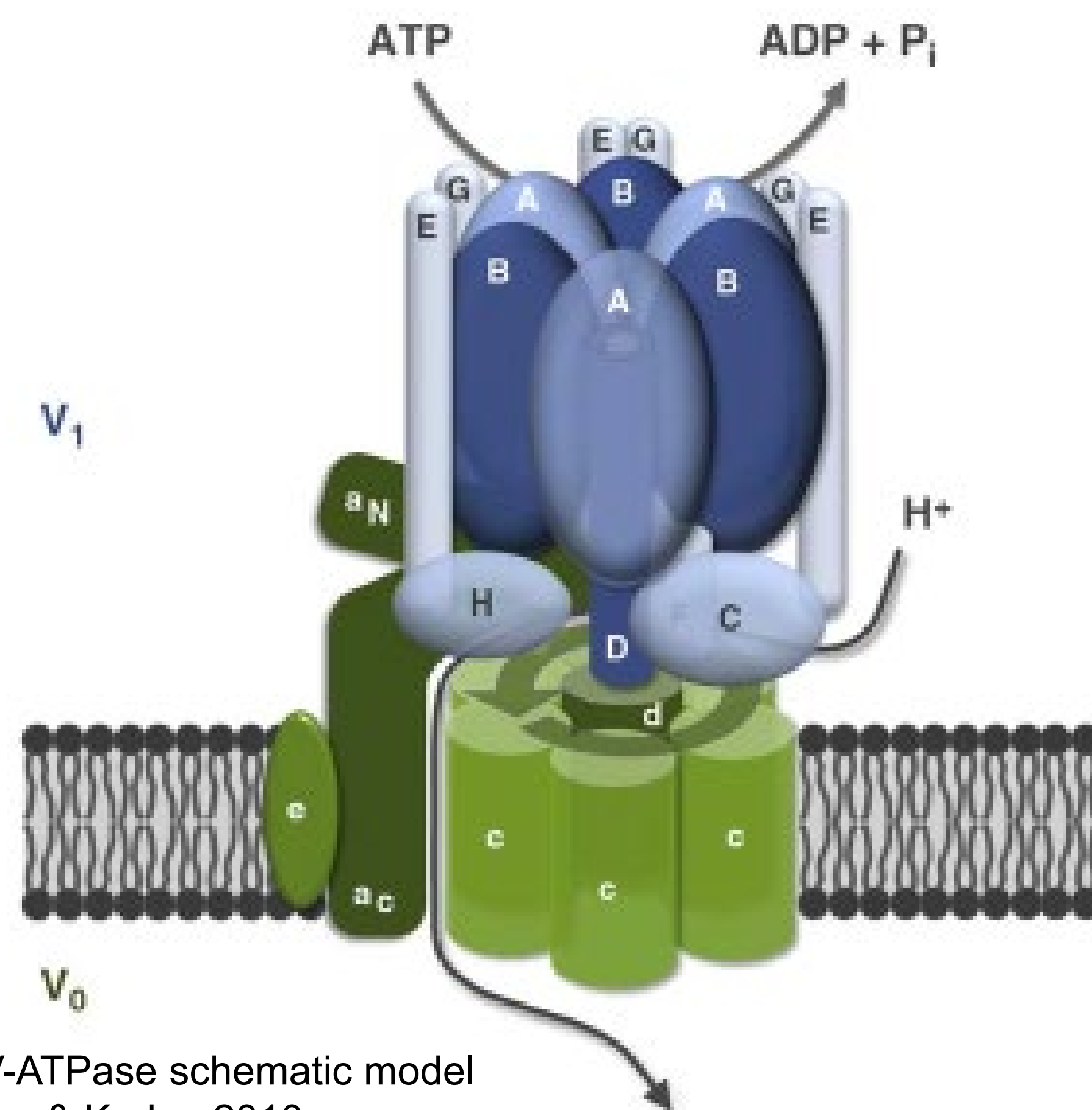


Figure 1: V-ATPase schematic model
Schumacher & Krebs, 2010

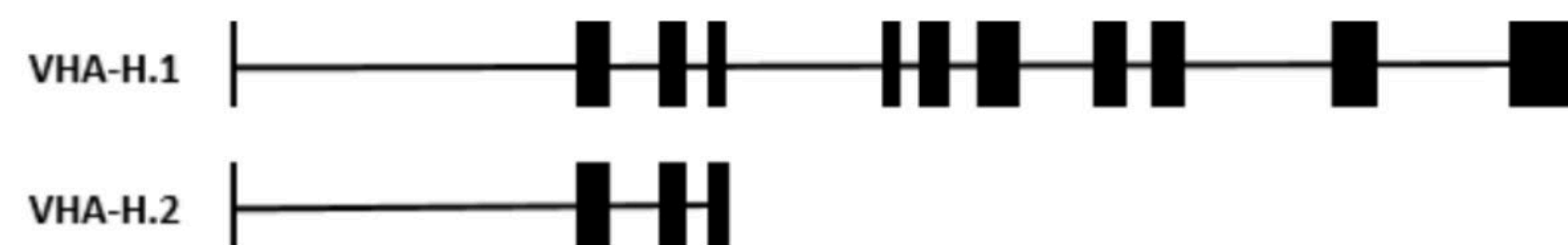


Figure 2: *VHA-H* gene schematic
Taehoon Kim

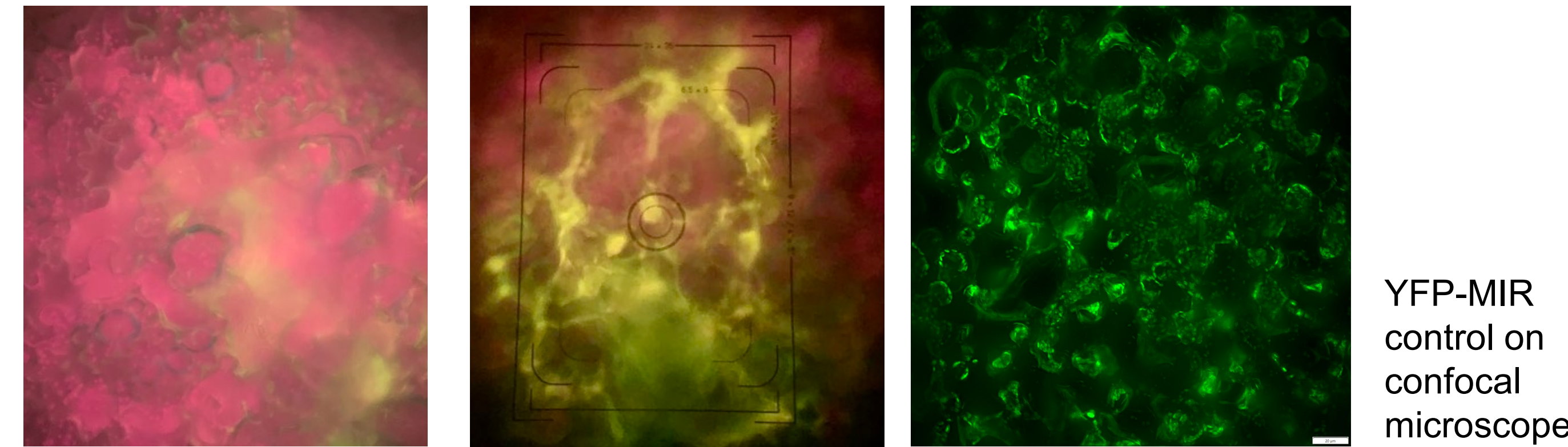
Hypothesis

It is expected that there may be differential localization between splice isoforms *VHA-H1* and *VHA-H2*.

Viewing Localization using YFP

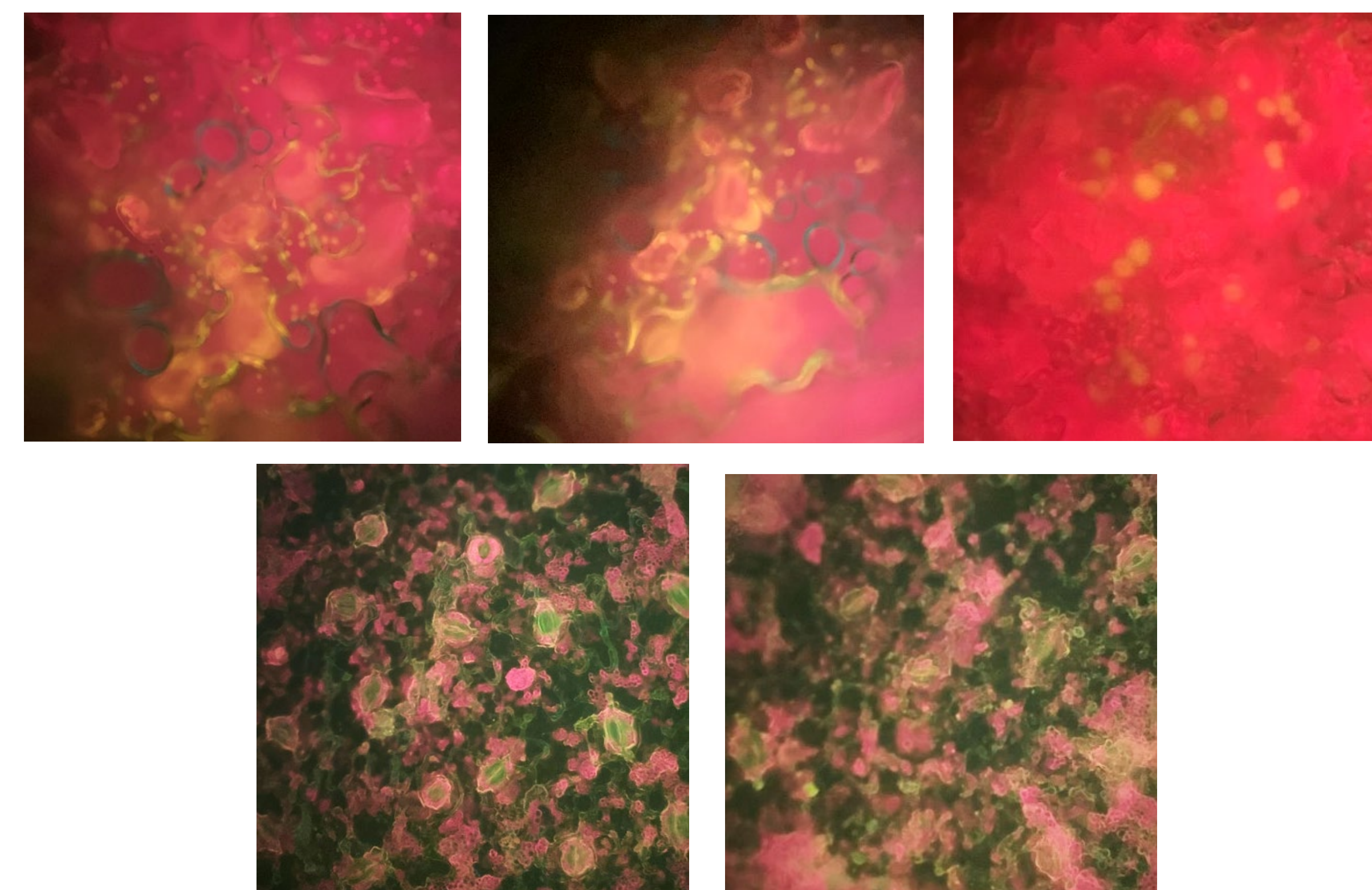
- Constructs of yellow fluorescent protein fused with H1/H2 subunit genes cloned into *Agrobacterium* Ti plasmid; transformed into tobacco leaves
- Viewing signals: fluorescent light microscope using UV light and GFP filter

YFP Control

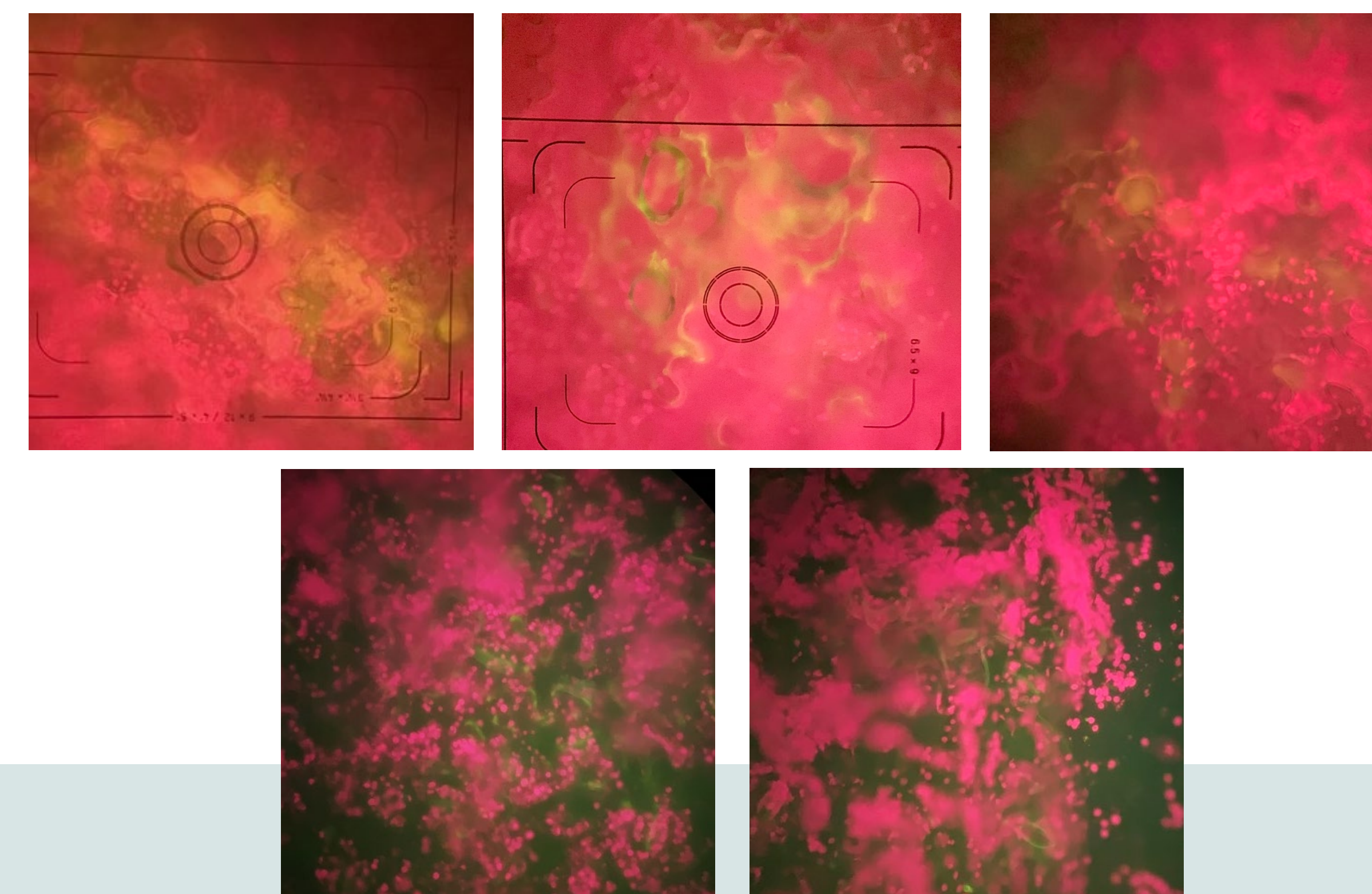


YFP-MIR control on confocal microscope

YFP-H1



YFP-H2



Transient Transformation in *N. benthamiana*



Tobacco leaves syringe-infiltrated with *Agrobacterium* constructs

YFP signals observed from 2-7 days post-inoculation using whole leaf tissue and epidermal peels

Results and Next Steps

- YFP-H1 signals exhibit localization in vesicles and cell membranes, possibly guard cell membranes and cytosol
- YFP-H2 signals exhibit localization in cell membranes and cytosol, possibly guard cell inner membranes
- Differences in localization of splice variants suggests that there may be difference in functions between *VHA-H1* and *VHA-H2*
- Resembles differential localization and function found in *VHA-E* isoforms

Next Steps:

- Further validation of signal localization data using laser scanning confocal microscopy
- Stable transformation of *O. sativa vha-h* CRISPR mutants via *Agrobacterium* and tissue culture organogenesis for functional analysis

References

1. Dettmer, J., Liu, T., & Schumacher, K. (2010). Functional analysis of *Arabidopsis* V-ATPase subunit VHA-E isoforms. *European Journal of Cell Biology*, 89, 152-156.
2. Dettmer, J., Schubert, D., Calvo-Weimar, O., Stierhof, Y., Schmidt, R., & Schumacher, K. (2005). Essential role of the V-ATPase in male gametophyte development. *The Plant Journal*, 41, 117-124.
3. Flannery, A. R., & Stevens, T. H. (2008). Functional characterization of the N-terminal domain of subunit H (Vma13p) of the yeast vacuolar ATPase. *The Journal of Biological Chemistry*, 283(43), 29099-29108.
4. Liu, N., Ni, Z., Zhang, H., Chen, Q., Gao, W., Cai, Y., Li, M., Sun, G., & Qu, Y. (2018). The gene encoding subunit A of the vacuolar H⁺-ATPase from cotton plays an important role in conferring tolerance to water deficit. *Frontiers in Plant Science*, 9(758). doi: 10.3389/fpls.2018.00758
5. Schumacher, K., & Krebs, M. (2010). The V-ATPase: Small cargo, large effects. *Current Opinion in Plant Biology*, 13, 724-730.