

Introduction

- Crops will face drought periods
- A virus helps the plant survive drought.
- WRKY Transcription factors activated.

Solanum Lycopersicum aka Tomatoes

- Diverse genus of important cash crops
- Model system with a short maturing process and small genome



Members of Solanaceae family. Picture from pdb.emo

TMV and STMV

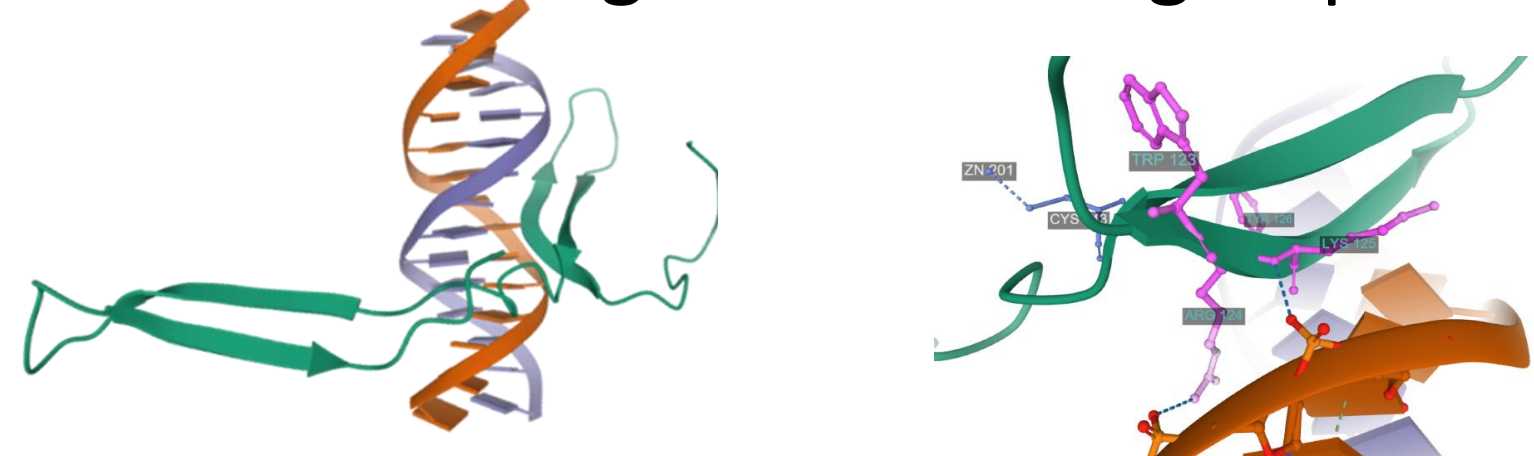
- Mild strain used to observe effects
- Triggers plant's immune system
- Does not mutate plant genome (non-GMO)
- Widespread in many plants



Tomato leaf with mosaic pattern phenotype associated with TMV. Picture from the Schroeder lab.

What is a WRKY Transcription Factor

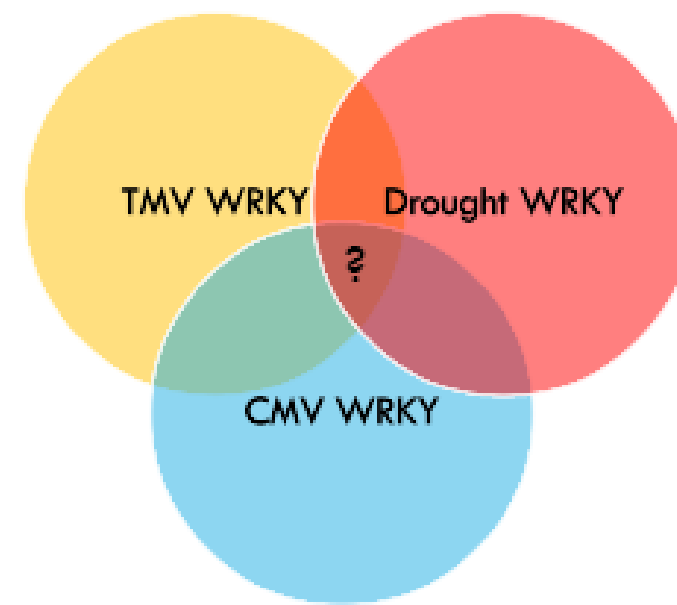
- Transcription factors regulate the activation of gene expression
- WRKY's are specific to plants
- WRKY stands for the amino acids tryptophan (W), arginine (R), lysine (K), tyrosine (Y)
- WRKY turns on genes in response to drought and viruses
- WRKY's are organized into 3 groups



Left: Cartoon representation model of Rice WRKY (green) binding at DNA major groove (Red orange). Right: Main amino acids (magenta) binding to DNA. Zinc ligand (light blue) included. From Protein Data Bank 6IR8 (Cheng 2019)

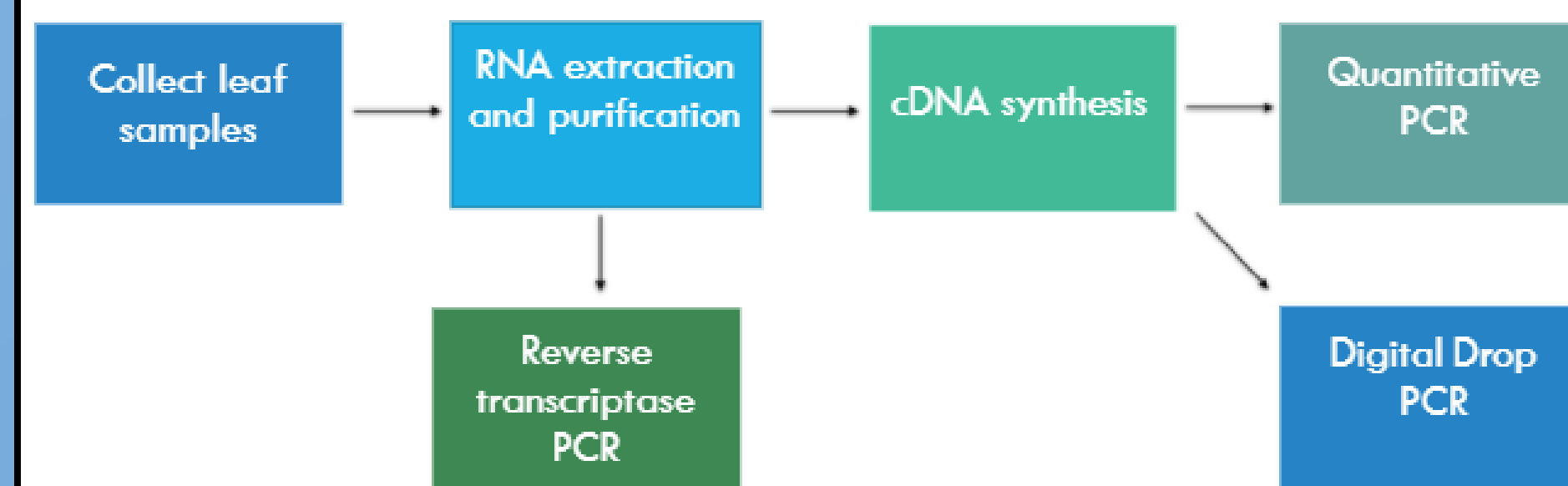
Hypothesis:

The WRKY genes expressed in both TMV and CMV infections will also be expressed in drought conditions



Methods

Flow of Experiment:



Plant Growth Conditions

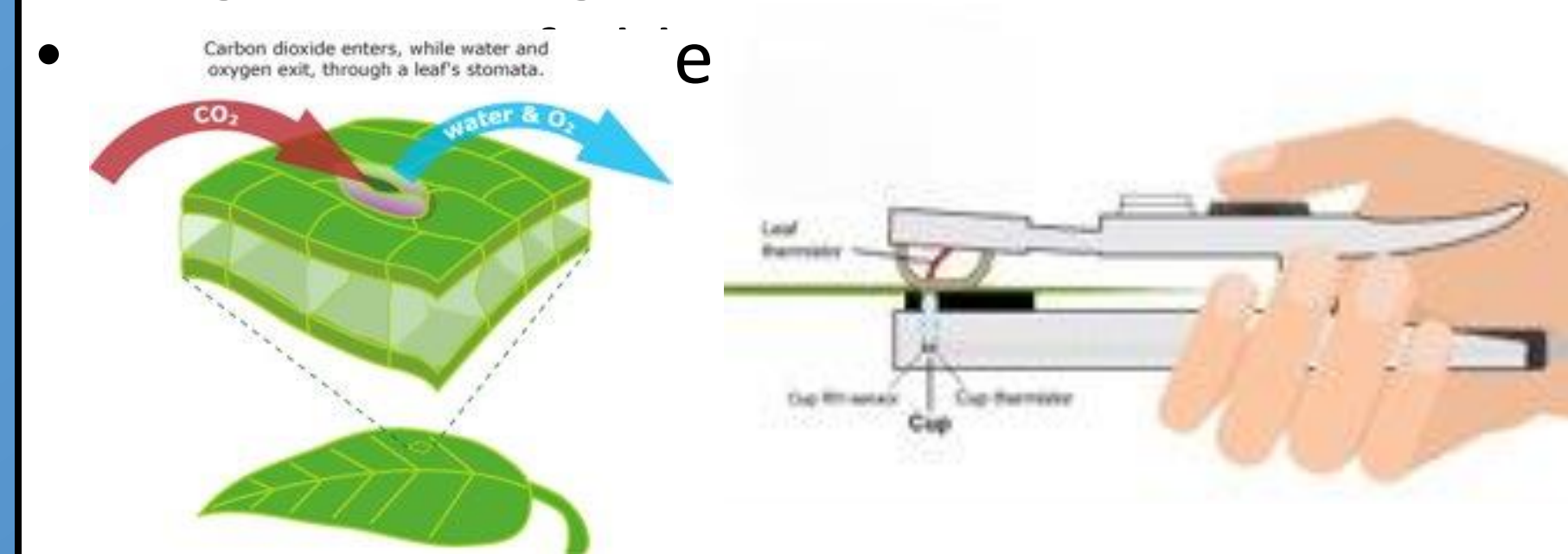
- TMV or STMV infection
- Uninfected leaves as control
- Wet or drought conditions



Left: TMV infected *Solanum lycopersicum*
Right: STMV infected *Solanum lycopersicum*
Picture from Schroeder lab.

Stomatal Conductance

- Stomatas are openings found on the underside of leaves which let CO₂ in while water and O₂ leave
- A porometer measures the time sensitive rate of gas exchange of the stomata

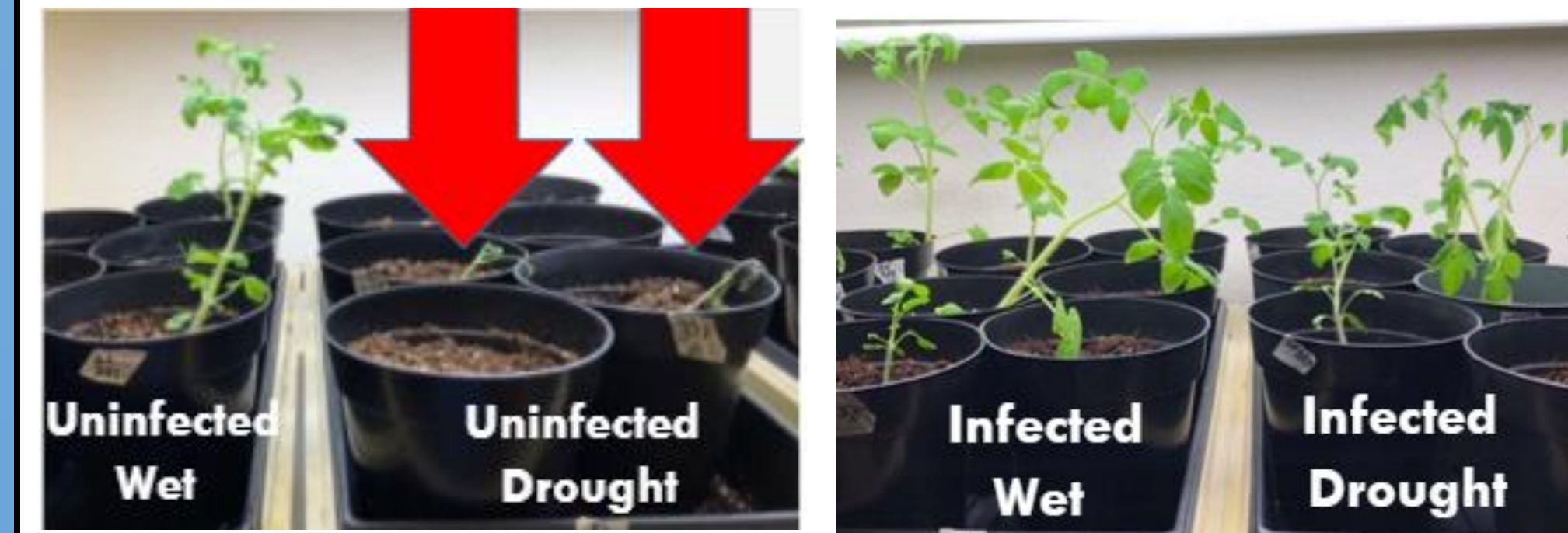


Pictures from <https://delta-t.co.uk/product/ap4/>
https://evolution.berkeley.edu/evolibrary/search/imagedetail.php?id=369&topic_id=&keywords

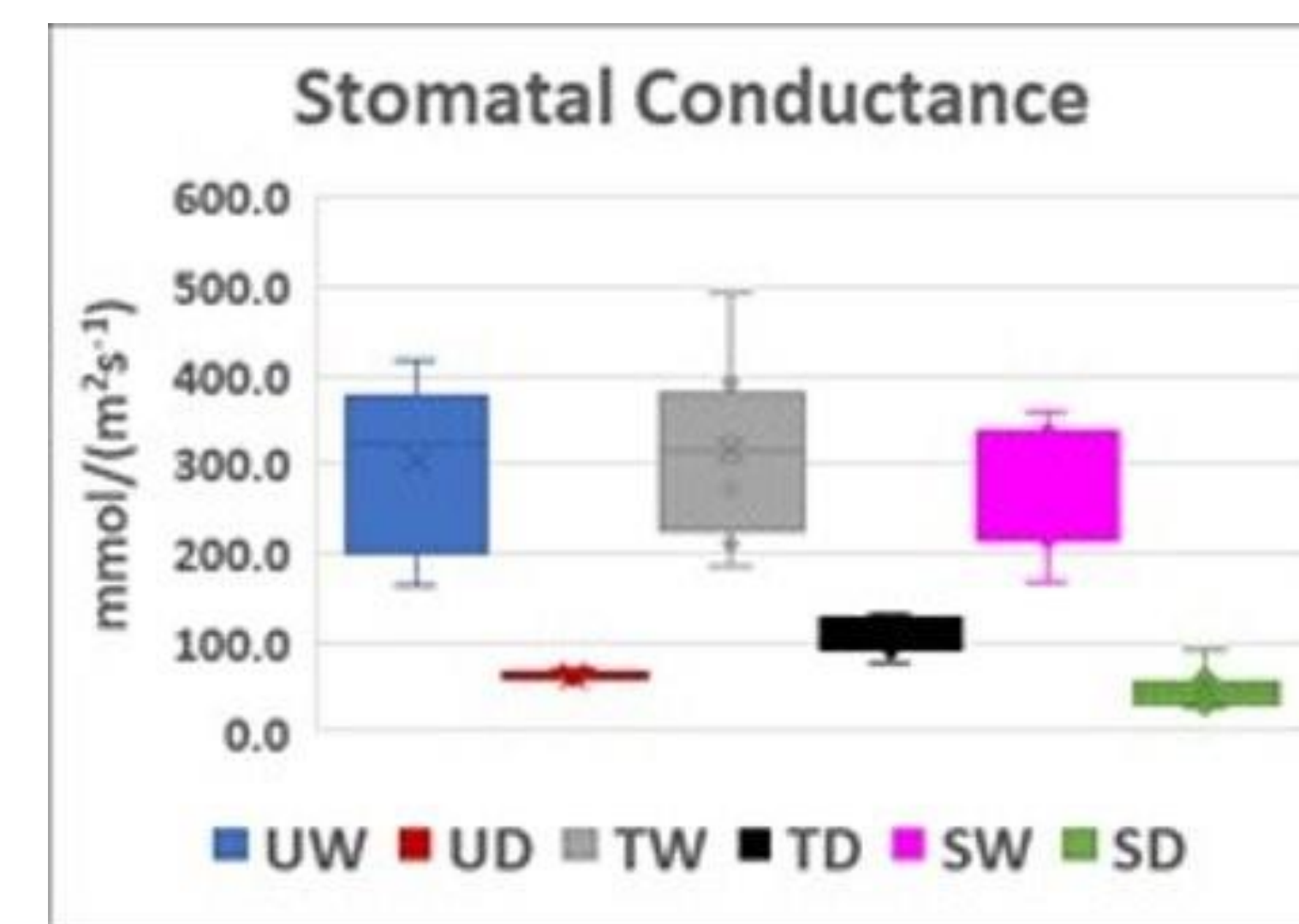
Results

Primary Phenomenon:

- STMV infected *Solanum lycopersicum* lasted longer in drought conditions (right) than wild type (left)



Stomatal conductance:



Uninfected wet (UW) and drought (UD) are used as control.

TMV infected wet (TW) and drought (TD) showed a smaller difference than STMV infected wet (SW) and drought (SD).

Picture from the Schroeder lab.

Bioinformatic Results:

AtWRKY	Gene #	Gene function	Probable SolWRKY (protein)	Gene #
18	AT4G31800.1	resistance to pathogens, co expressed with WRKY 40 and 60	1	Solyc07g047960
			2	Solyc07g066220
			40	Solyc06g068460
			46	Solyc08g067340.2
22	AT4G01250.1	immune regulator	22	Solyc01g095100
27	AT5G52830.1	defense response to bacteria	none	
33	AT2G38470.1	pathogen resistance and salt stress, targets its own genetic	26	Solyc03g082810
			31	Solyc06g066370
40	AT1G80840.1	pathogen resistant	1	Solyc07g047960
			2	Solyc07g066220
			40	Solyc06g068460
60	AT2G25000.1	pathogen resistant, forms complex with WRKY40	1	Solyc07g047960
			2	Solyc07g066220
			40	Solyc06g068460

Bioinformatics:

- Tair and Sol genomic data banks used
- BLASTp utilized

Left: Arabidopsis thaliana WRKY genes involved in immune response tomato homologs comparison by BLASTp (Birkenbihl 2017)

Big picture for Oklahomans

- Could a beneficial virus stimulate natural drought survival in crops to help farmers?
- Studying TMV in tomatoes is a safe way to study how a virus interacts with its host. So, this basic science is important for all viruses, even COVID-19.

Conclusion

Primary Phenomenon:

- The virus infected plants fared better than the uninfected plants.
- Activated WRKY genes may have a role in coordinating this survival response.

Stomatal conductance:

- There is a significant difference in the drought stomatal conductance range of the infected plants (TD and SD) compared to the wild type drought (WD).
- The stomata being more open could explain why infected plants survived longer in drought as the plant continued low rates of gas exchanges to continue normal functions.

Bioinformatic

- The data shows how WRKY's across species can have one, many, or no matches. This hints that some WRKY's work as a group

Acknowledgements

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Citations:

Cheng, X.; Zhao, Y.; Jiang, Q.; Yang, J.; Zhao, W.; Taylor, I. A.; Peng, Y. L.; Wang, D.; Liu, J., Structural basis of dimerization and dual W-box DNA recognition by rice WRKY domain. *Nucleic Acids Res* 2019. Bai, Y.; Sunarti, S.; Kissoudis, C.; Visser, R. G. F.; van Der Linden, C. G., The Role of Tomato Genes in Plant Responses to Combined Abiotic and Biotic Stresses. *Frontiers in plant science* 2018, 9, 801. Huang, S.; Gao, Y.; Liu, J.; Peng, X.; Niu, X.; Fei, Z.; Cao, S.; Liu, Y., Genome-wide analysis of WRKY transcription factors in *Solanum lycopersicum*. *Molecular Genetics and Genomics* 2012, 287 (6), 495-513. Birkenbihl, R. P.; Liu, S.; Somssich, I. E., Transcriptional events defining plant immune responses. *Current Opinion in Plant Biology* 2017, 38, 1-9.