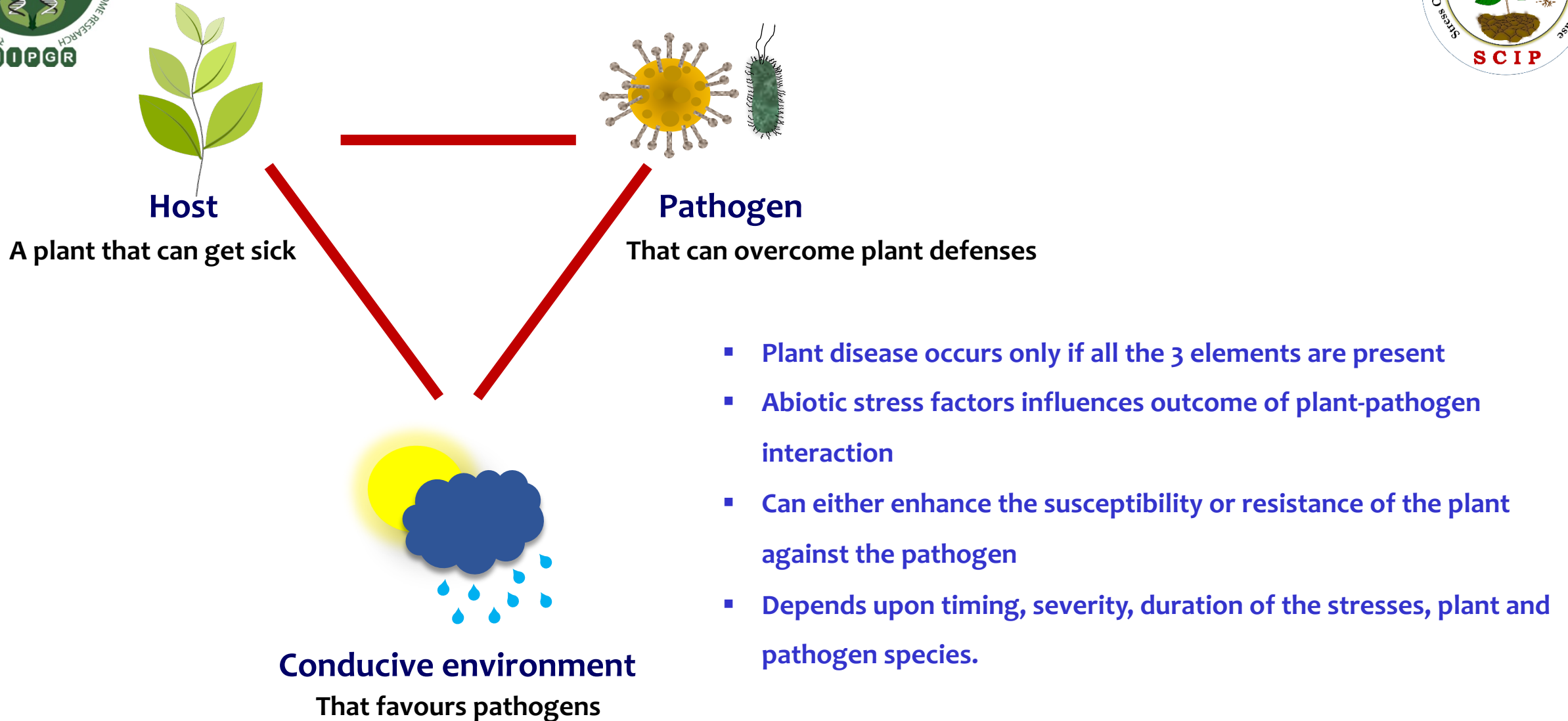


# Impact of drought stress on pathogen induced defense response

Presented by  
**Aanchal Choudhary**  
PhD scholar

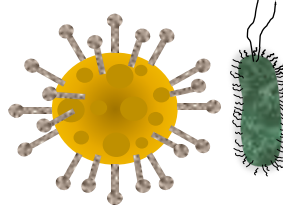
**National Institute of Plant Genome Research, Aruna Asaf Ali Marg,  
New Delhi- 110067, India**

# Plants in the field are often exposed to a multitude of simultaneously occurring stress in nature

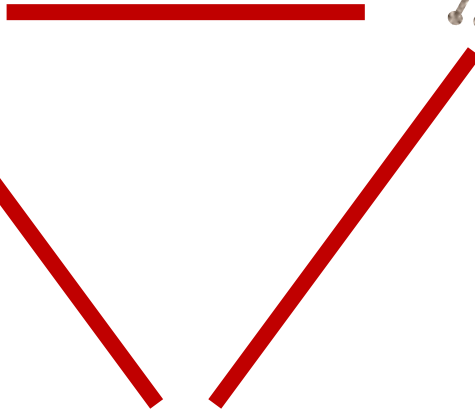




*Arabidopsis thaliana*



*Pseudomonas syringae*



Drought

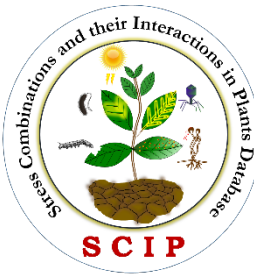
Majority of the combined stress studies are with **host bacteria**

Limitations:

- Host bacteria either evades or overcomes the defense machinery of the plant, eventually resulting in plant death.
- Long term drought experiments cannot be undertaken.
- Difficult to differentiate the effector-mediated changes from the plant mediated changes under combined stress



Depending upon the nature of plant–pathogen interactions, plants have two main defense mechanisms, **host resistance** and **nonhost resistance**.



### Host resistance

- controlled by single R genes
- less durable
- mostly cultivar- or accession-specific

### Non-host resistance

- multi-gene trait governing multiple layers of defense barriers
- durable and robust resistance
- broad-spectrum resistance mechanism
- allows the plants to defend themselves from a diverse array of potential pathogens
- **Preformed barriers** such as cell wall, cuticle, phytoanticipins
- **Induced defense responses** such as lignin accumulation, production of antimicrobials like phytoalexins, HR response, induction of PR proteins

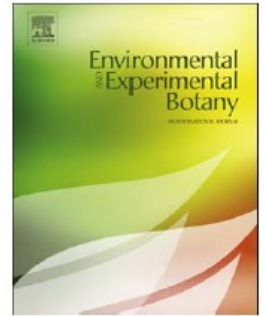
**No studies have yet examined how drought may potentially influence NHR**



Contents lists available at ScienceDirect

## Environmental and Experimental Botany

journal homepage: [www.elsevier.com/locate/envexpbot](http://www.elsevier.com/locate/envexpbot)



### Transcriptomic changes under combined drought and nonhost bacteria reveal novel and robust defenses in *Arabidopsis thaliana*



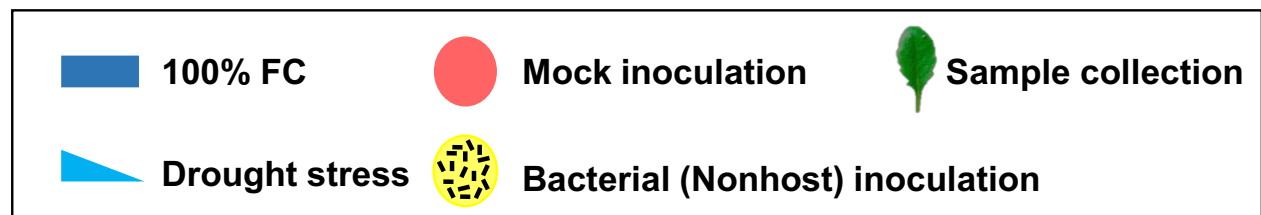
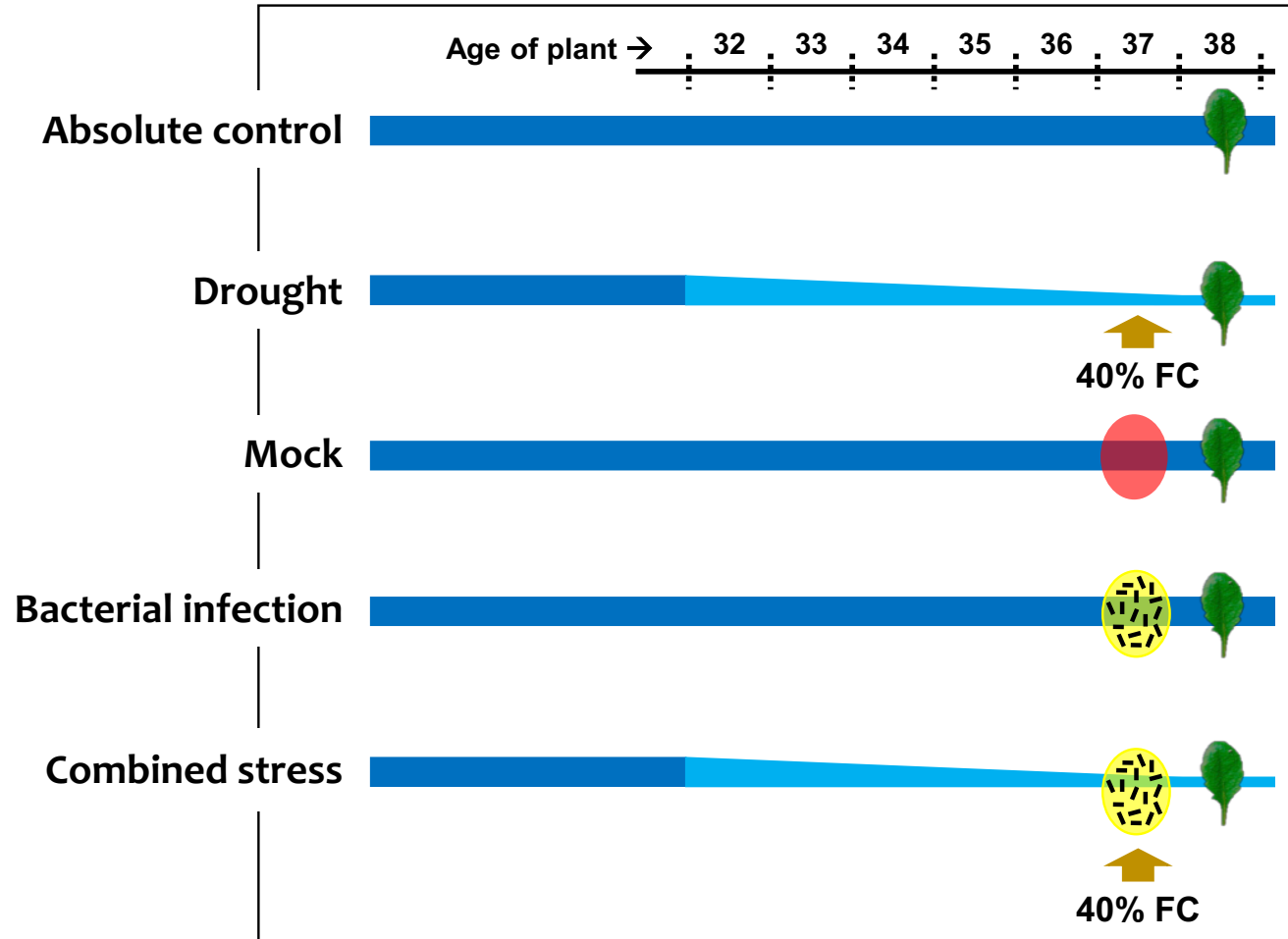
Aanchal Choudhary<sup>a,1</sup>, Aarti Gupta<sup>a,1</sup>, Venkategowda Ramegowda<sup>b,2</sup>, Muthappa Senthil-Kumar<sup>a,\*</sup>

<sup>a</sup> National Institute of Plant Genome Research (NIPGR), Aruna Asaf Ali Marg, New Delhi 110 067, India

<sup>b</sup> Department of Crop Physiology, University of Agricultural Sciences, Bangalore, 560 065, India

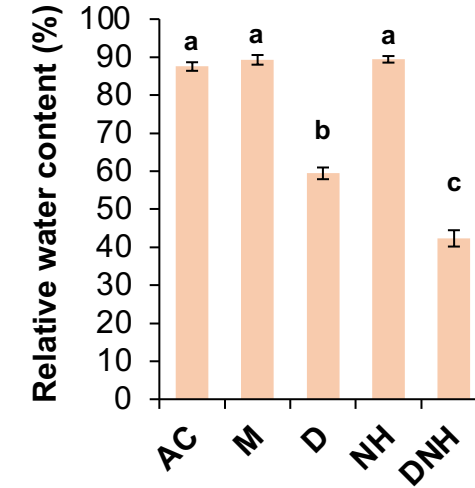
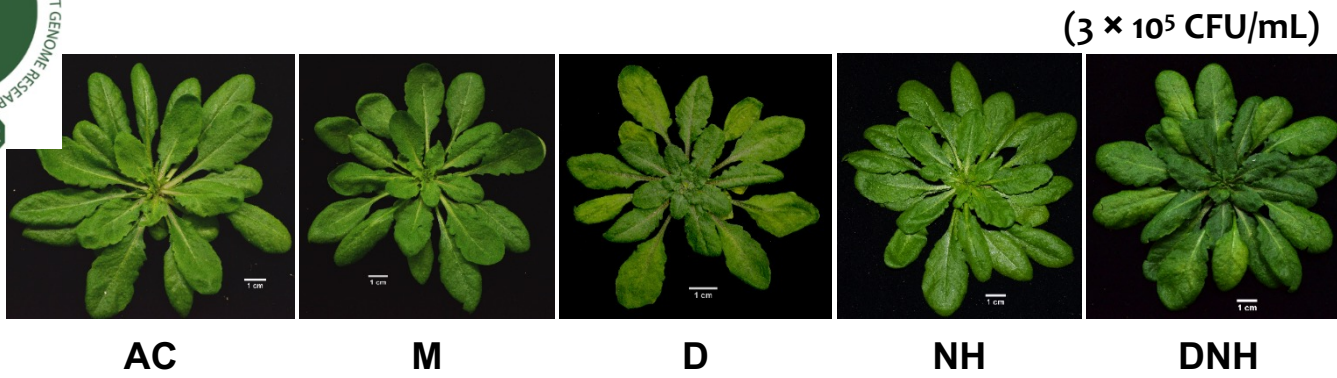
Nonhost bacterial pathogen, *Pseudomonas syringae* pv. *tabaci*

# Stress treatments

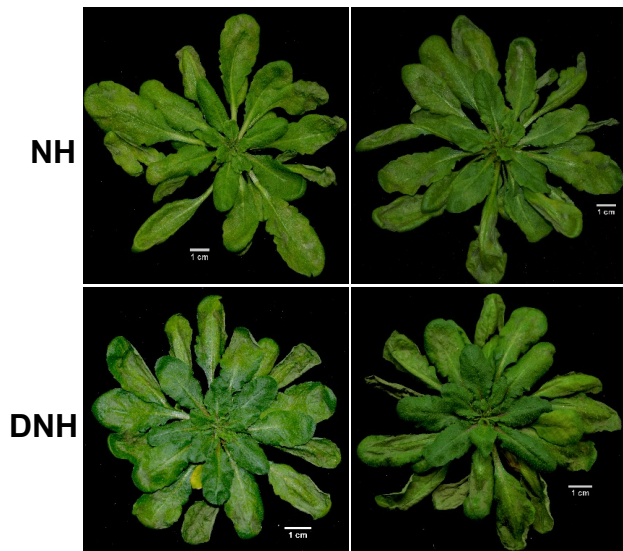




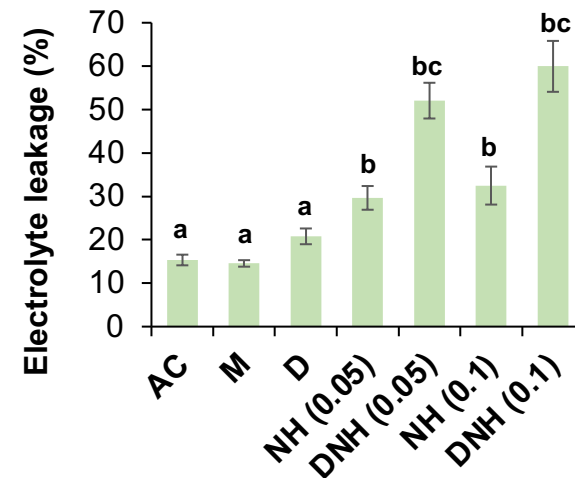
# Morpho-physiological response of *A. thaliana* under combined stress



- Programmed cell death is a well-established hallmark of NHR
- Plant triggers a rapid and localized cell death at the site of infection, the **Hypersensitive response** to restrict the pathogen spread



$(5 \times 10^6 \text{ CFU/mL})$      $(2 \times 10^7 \text{ CFU/mL})$

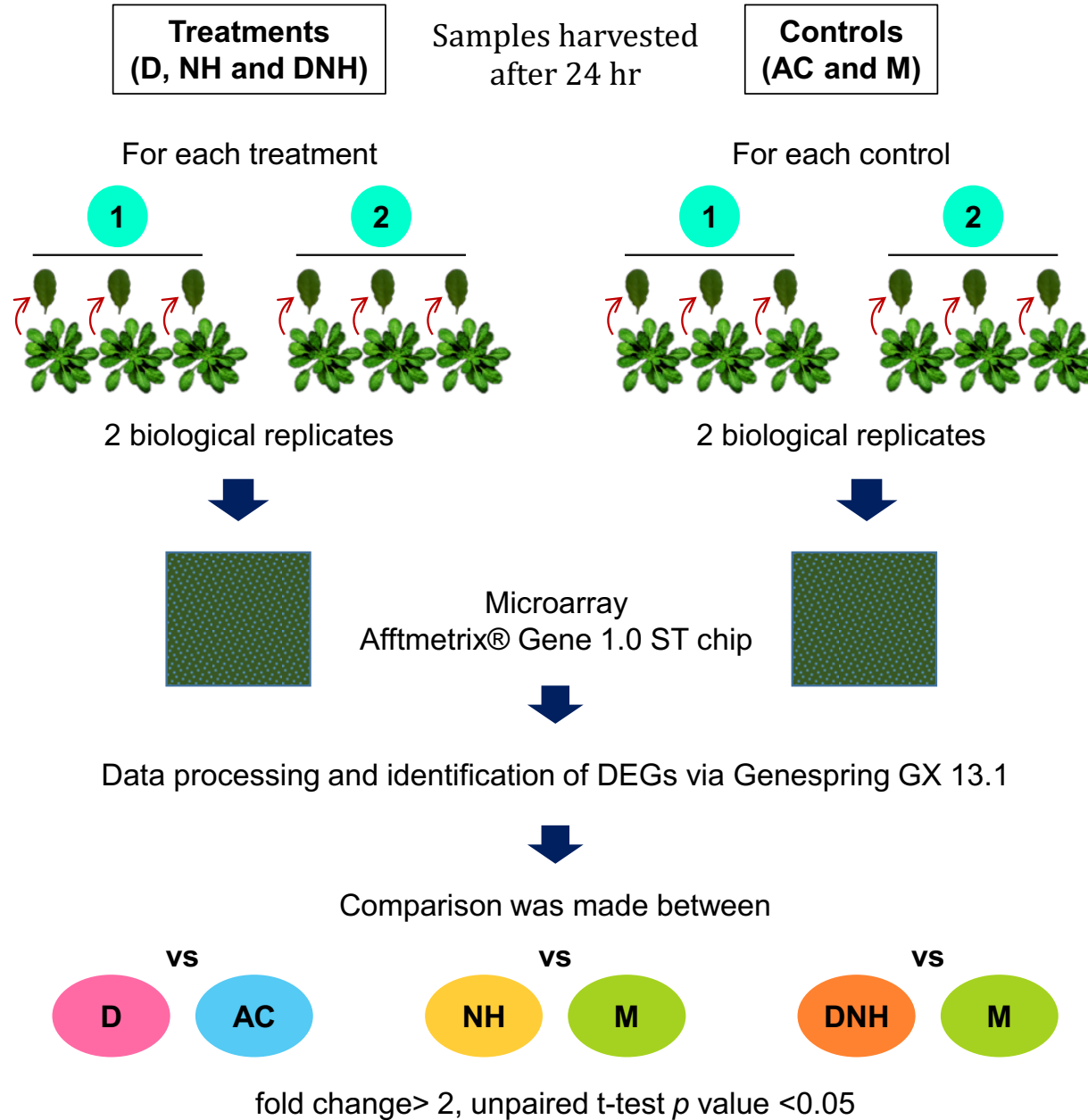


An early and comparatively more robust HR in combined stress plants

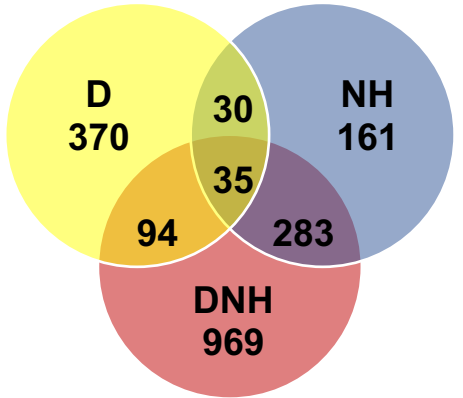
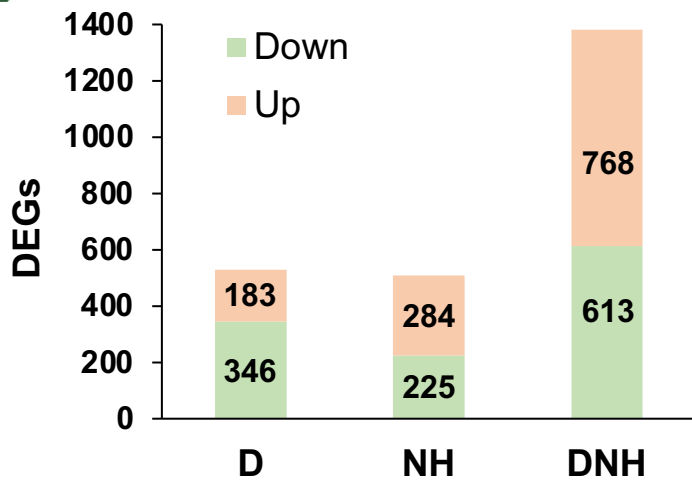


To explain the molecular basis of the robust defense response observed under combined stress,  
**whole-genome transcriptomic analysis** was carried out

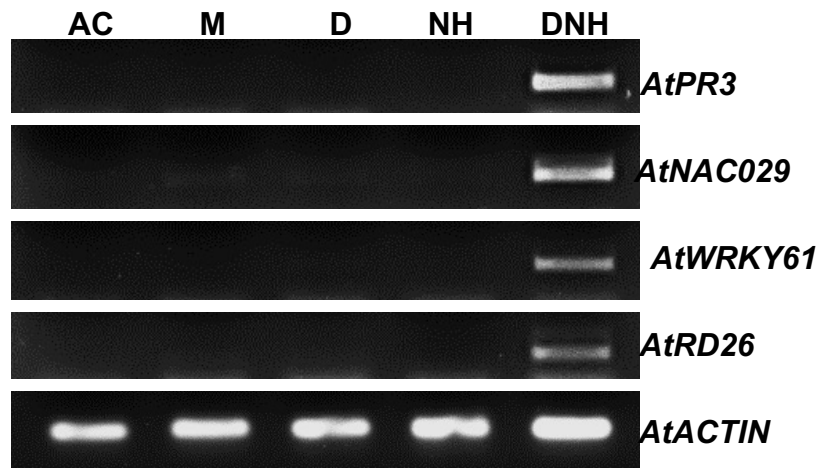




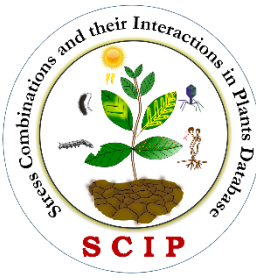
# Transcriptomic profile of *A. thaliana* subjected to drought, nonhost pathogen and their combination



	D	NH	DNH	No. of genes
Tailored responses	↑	↑	↑	4
	↓	↓	↓	6
	↓	↑	↑	17
	↑	↓	↓	8
Shared genes				



- Transcriptome of plants under combined stress is significantly different from that under single stresses
- Several transcripts specifically respond to the stress combination

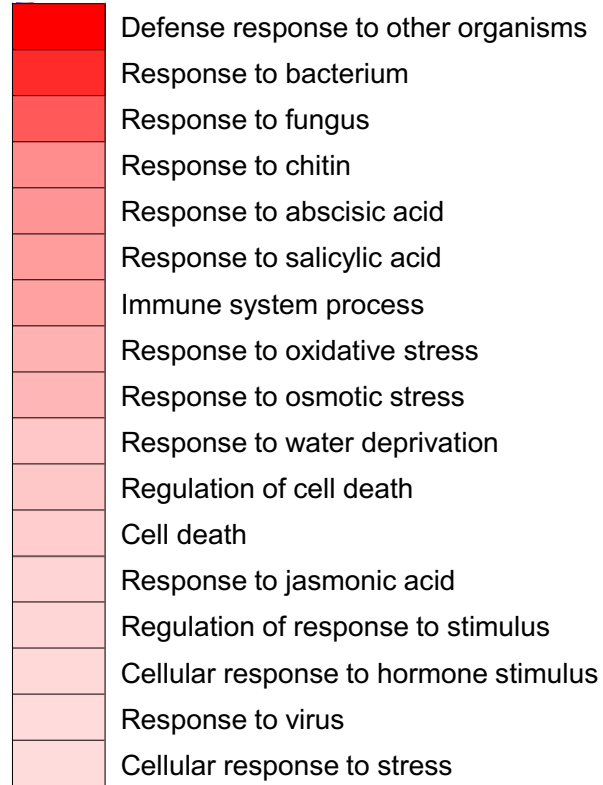


The development of HR involves a cascade of signalling events and is preceded by the **induction of defense-related genes** and **production of ROS** resulting in an **oxidative burst**

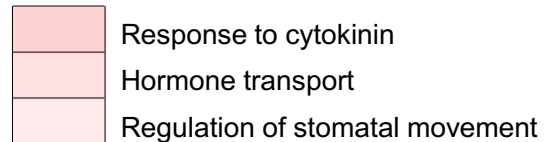
## Biological process enrichment

### DNH-specific genes

#### Upregulated



#### Downregulated



0 29

### DNH

GENE ID	Gene name
AT2G19190	FRK1
AT4G23810	WRKY53
AT3G12500	PR3
AT1G62300	WRKY6
AT1G74710	ICS1
AT5G26920	CBP60G
AT2G38470	WRKY33
AT2G14610	PR1
AT3G56400	WRKY70
AT1G02450	NIMIN1
AT5G22570	WRKY38
AT5G05190	EDR4
AT3G48090	EDS1
AT1G02930	GST1
AT4G39030	EDS5
AT1G75040	PR5
AT3G04720	PR4
AT4G01250	WRKY22
AT2G15480	UGT73B5
AT3G20600	NDR1
AT3G26090	RGS1
AT3G10340	PAL4
AT3G52430	PAD4
AT2G43000	NAC042
AT4G33430	BAK1

-6 9

## Defense-related genes

Processes associated with **response to defense**, **oxidative stress** and **cell death** were highly enriched under combined stress

## ROS

AT4G02380	LEA5
AT5G24110	WRKY30
AT1G61120	GES
AT5G01600	FER1
AT3G49120	PRXCB
AT2G33380	PXG3
AT5G20230	BCB
AT4G26070	MEK1
AT5G58940	CRCK1
AT1G45145	TRX5
AT5G59820	ZAT12
AT5G03630	MDAR2
AT2G40000	HSPRO2
AT5G39610	ANAC092
AT4G18880	HSFA4A
AT1G02930	GSTF6
AT3G45640	MPK3
AT4G12720	NUDT7
AT4G21850	MSRB9
AT5G46350	WRKY8
AT5G19875	Unknown protein
AT5G50350	Unknown protein
AT5G05410	DREB2A
AT3G02840	Unknown protein
AT5G49570	PNG1
AT4G21840	MSRB8
AT4G34710	ADC2
AT1G70520	CRK2
AT1G19020	Unknown protein
AT3G22200	GABA-T
AT3G62030	CYP20-3
AT4G09010	APX4
AT3G11630	BAS1
AT5G56550	OXS3
AT3G26060	PRXQ
AT3G47450	NOA1
AT2G19310	HSP20-like
AT5G51720	NEET
AT1G77490	TAPX
AT5G43750	PNSB5
AT5G13930	CHS

## HR

AT3G52400	SYP122
AT3G13672	SINA2
AT5G13320	PBS3
AT1G08450	CRT3
AT1G29690	CAD1
AT2G13790	BKK1
AT3G48090	EDS1
AT4G34180	CYCLASE1
AT5G48380	BIR1
AT4G12720	NUDT7
AT3G44880	ACD1
AT1G73260	KTI1
AT1G28380	NSL1
AT4G25110	MC2
AT1G73500	MKK9
AT3G11820	SYP121
AT1G14780	MACPF domain protein
AT1G19250	FMO1
AT5G47120	BI1
AT5G66850	MAPKKK5
AT5G12080	MSL10
AT5G48030	GFA2
AT2G31170	SYCOARATH
AT4G37930	SHM1

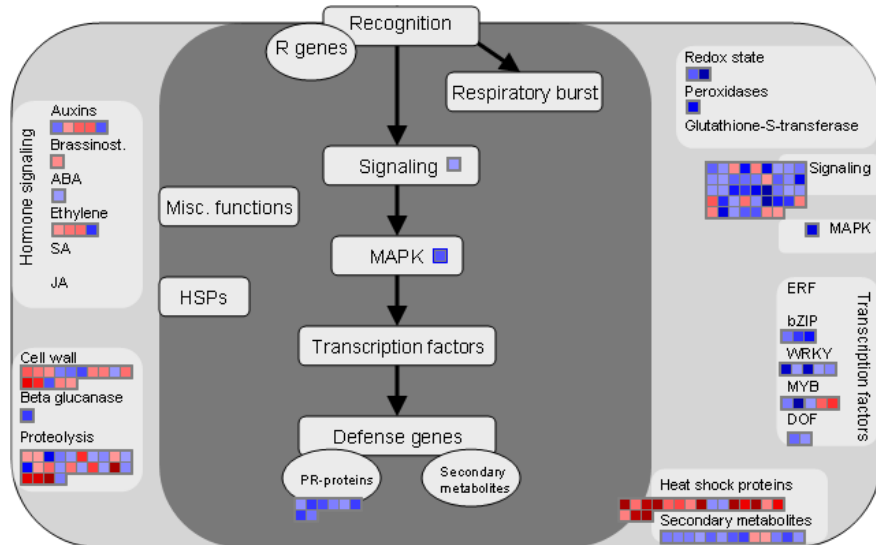
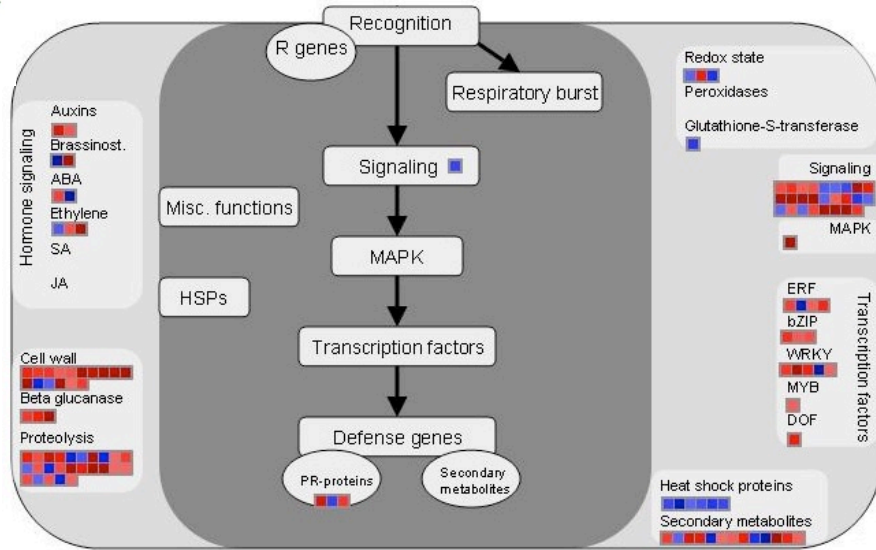
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## DNH-specific genes

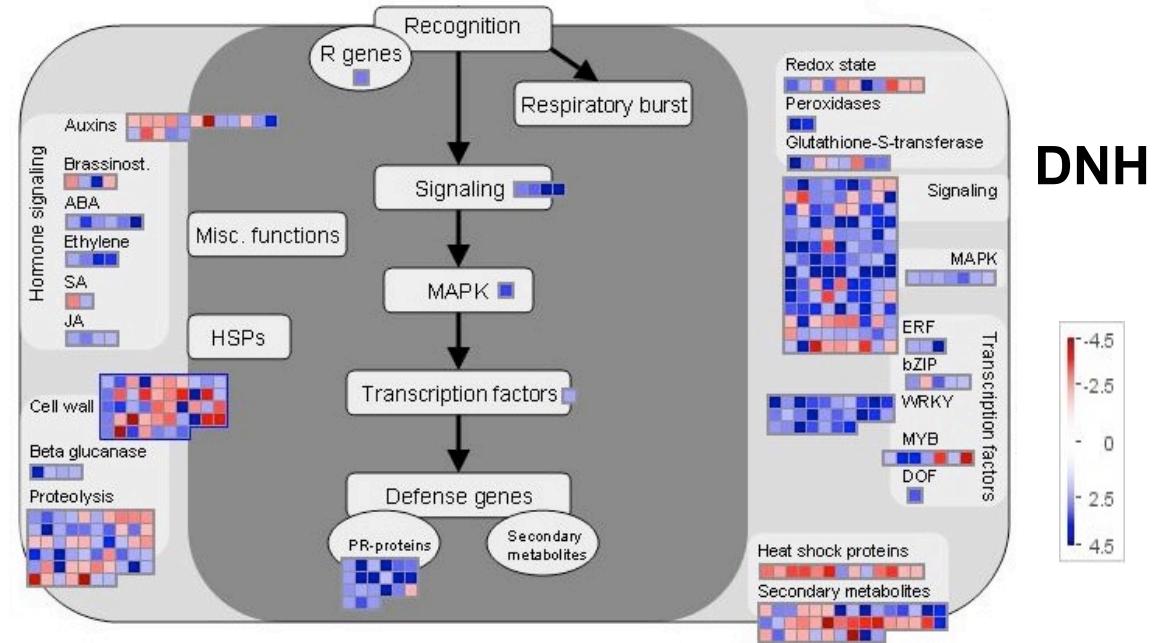
‘ROS and HR mediated cell death’ related genes

- Upregulation of several ROS-producing, scavenging and other oxidative stress-responsive genes
- Upregulation of genes involved in regulating both drought and bacterial responses
- Upregulation of genes involved in the production of phytoalexins, lignin and polyamines that play a protective role under stress conditions

# Basal defenses of the plant are strengthened under combined stress

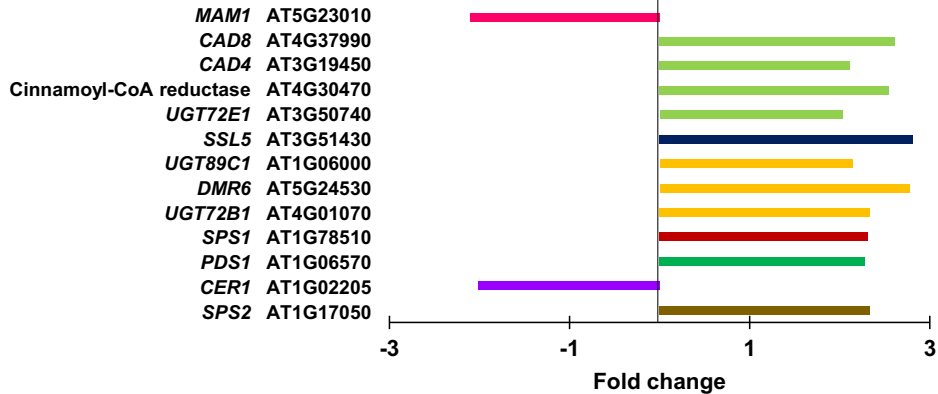
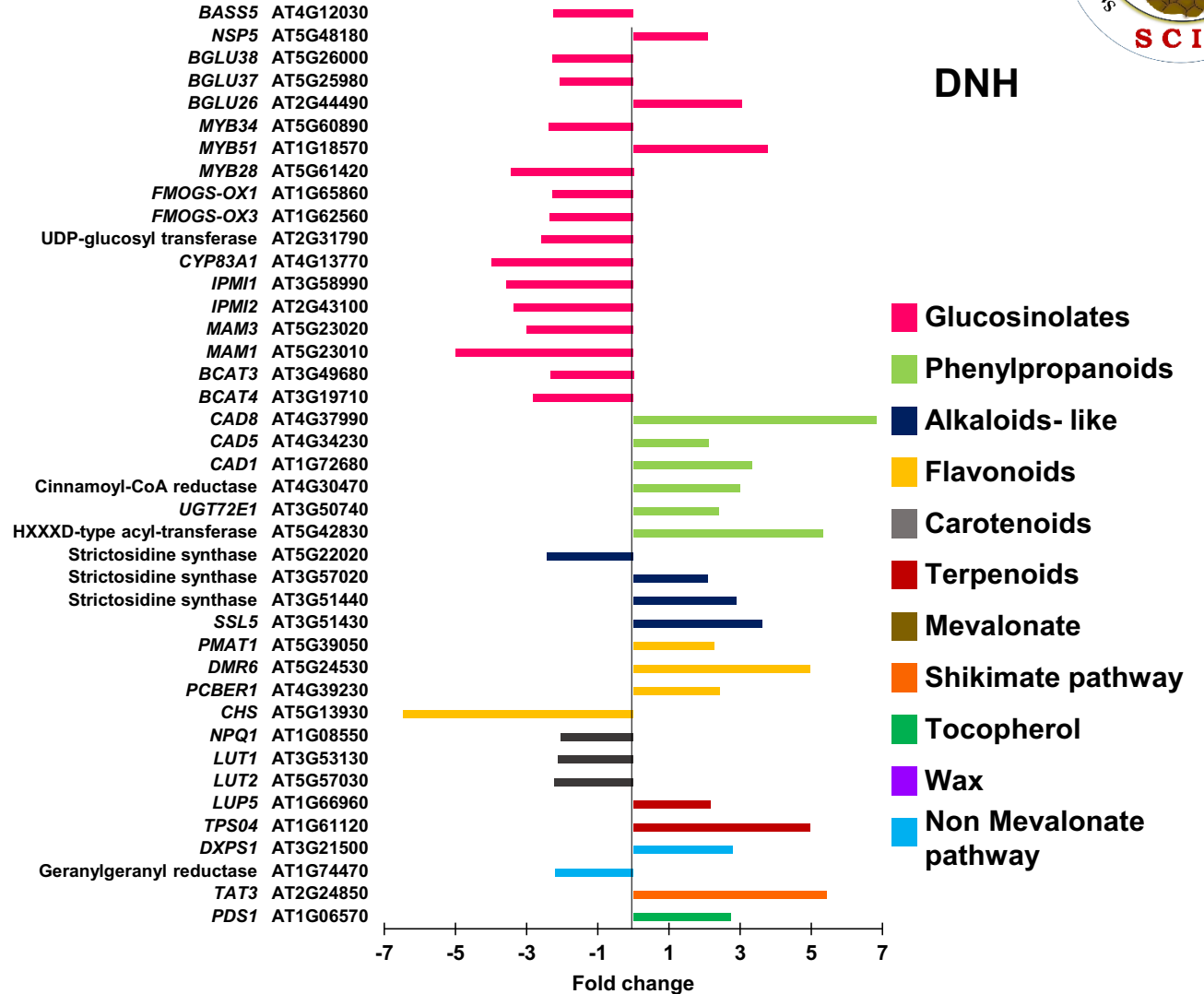
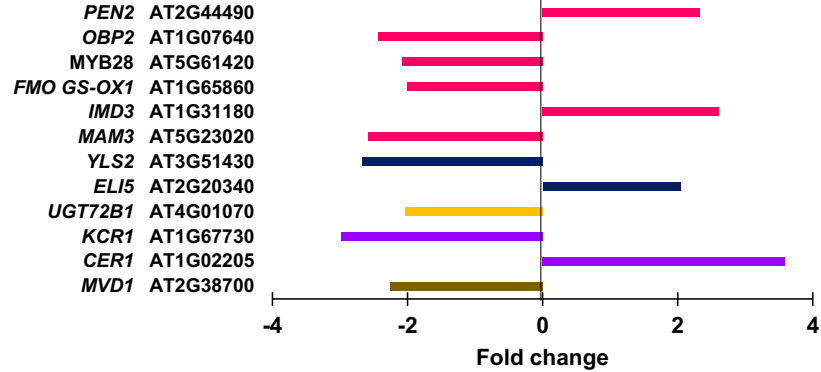


## Stress pathways



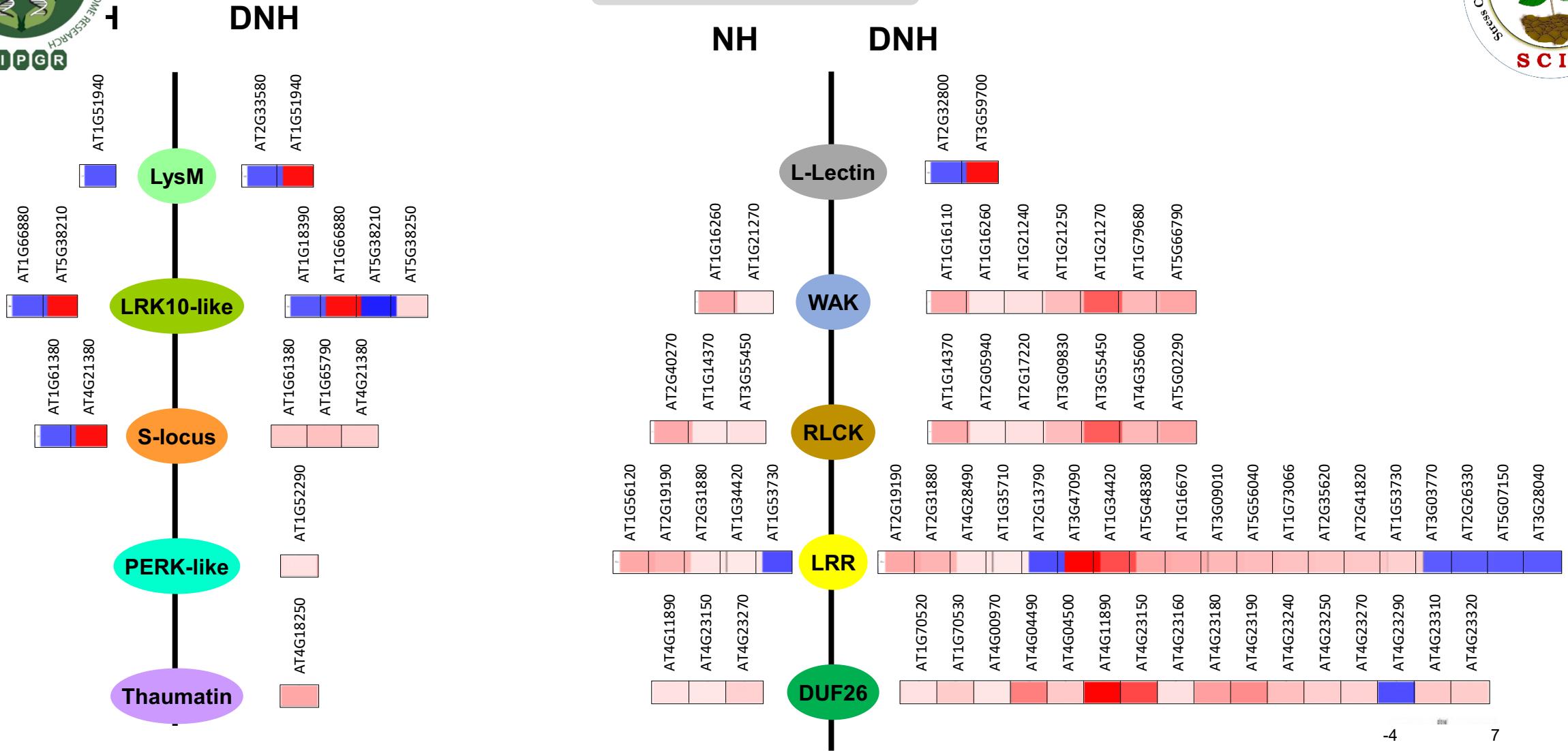


## Secondary metabolites



Substantial increase in the diversity and number of secondary metabolites under combined stress

## Receptor-like kinases

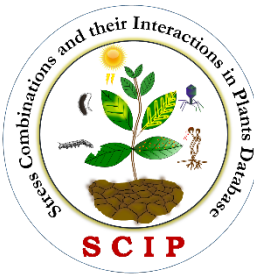


Substantial increase in the diversity and number of RLKs under combined stress



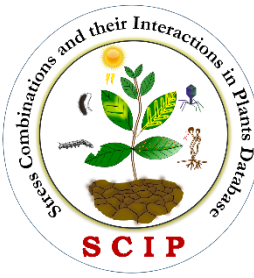
## FINDINGS

- Simultaneous exposure to drought and non host bacteria resulted in early activation of a stronger hypersensitive response
- Whole-genome transcriptome profiling revealed a massive transcriptional reprogramming involving several transcripts specifically responding to the stress combination
- Significant increase in number and expression level of genes related to ROS- and HR-related genes, basal defense signaling, secondary metabolism, and receptor-like kinases under combined stress.



## CONCLUSION

- ❑ Parallel activation of multiple defense pathways imparted robustness to the overall plant immunity under combined stress.
- ❑ The majority of the genes under combined stress were responsive to both drought and nonhost bacteria indicative of the plant's adaption for efficient utilization of limited resources under multiple stresses.
- ❑ The response of the plant under combined stress is distinct from the response to single stress and thus, necessitates undertaking actual combined stress studies.



## REFERENCES

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Gupta, A., Sarkar, A.K., Senthil-Kumar, M., 2016a. Global transcriptional analysis reveals unique and shared responses in *Arabidopsis thaliana* exposed to combined drought and pathogen stress. *Front. Plant Sci.* 7, 686. <http://dx.doi.org/10.3389/fpls.2016.00686>.

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**Thanks you**