

RNAseq expression analysis of potato tubers differing in resistance to soft rot caused by bacteria *Dickeya solani*

Renata Lebecka, Katarzyna Szajko, Anna Grupa-Urbańska, Dorota Sołtys-Kalina

Department of Potato Genetics and Parental Lines

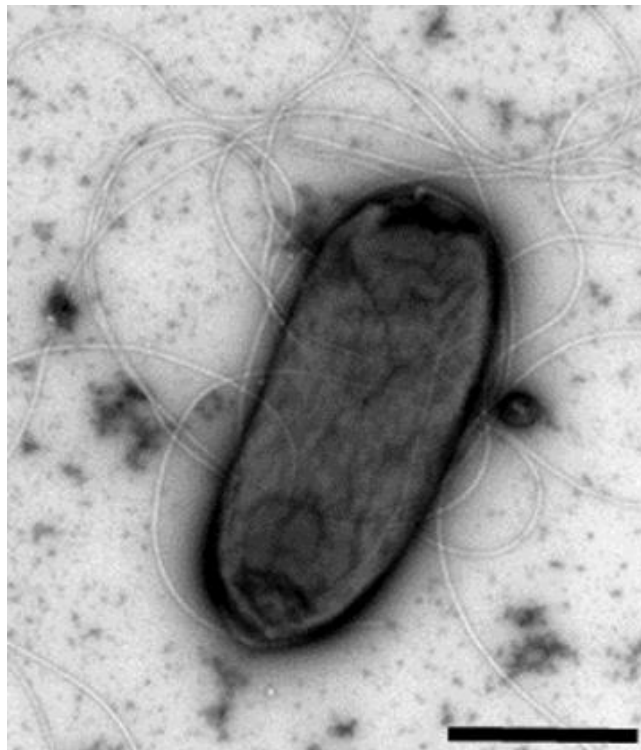
EAPR 2024, 7-12.07, Oslo, Norway



Project financed by Ministry of Agriculture and Rural Development, 2021-2027

Introduction

Dickeya solani



Lisicka et al. 2018.
Front. Plant Sci. 9:374

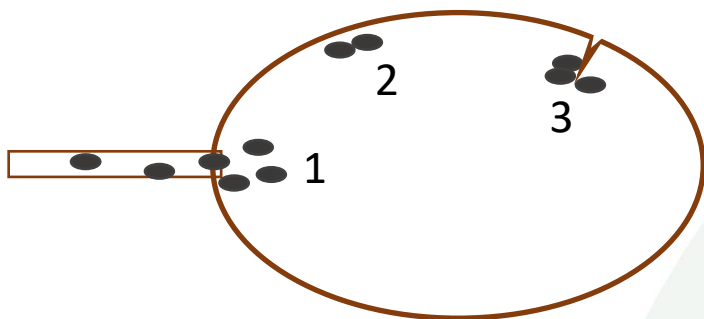
Soft rot



Introduction

Soft rot of potato tubers

Infection:



1. Stolons – cell wall disruption
2. Lenticels – cell wall disruption
3. Wounds



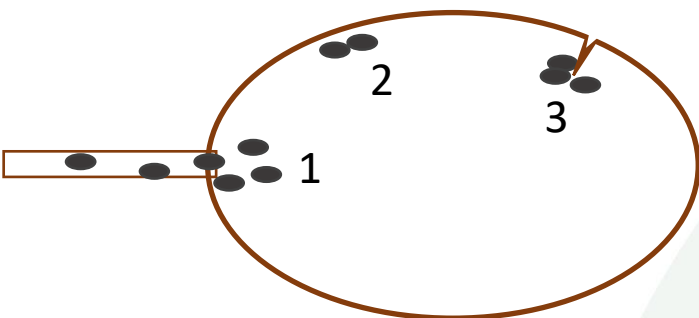
Type of stress:

- Abiotic - wounding
- Biotic - bacteria

Introduction

Soft rot of potato tubers

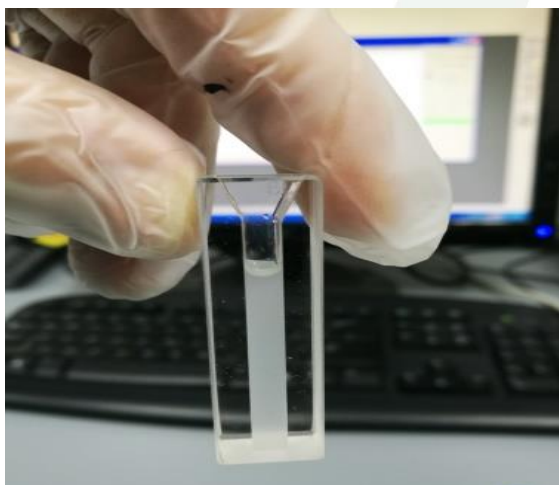
Infection:



1. Stolons – cell wall disruption
2. Lenticels – cell wall disruption
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Type of stress:

- Abiotic - wounding
- Biotic - bacteria



Introduction

Cultivar Irys



Lady Claire



Lady Rosetta



Highly susceptible



Medium resistant

Materials

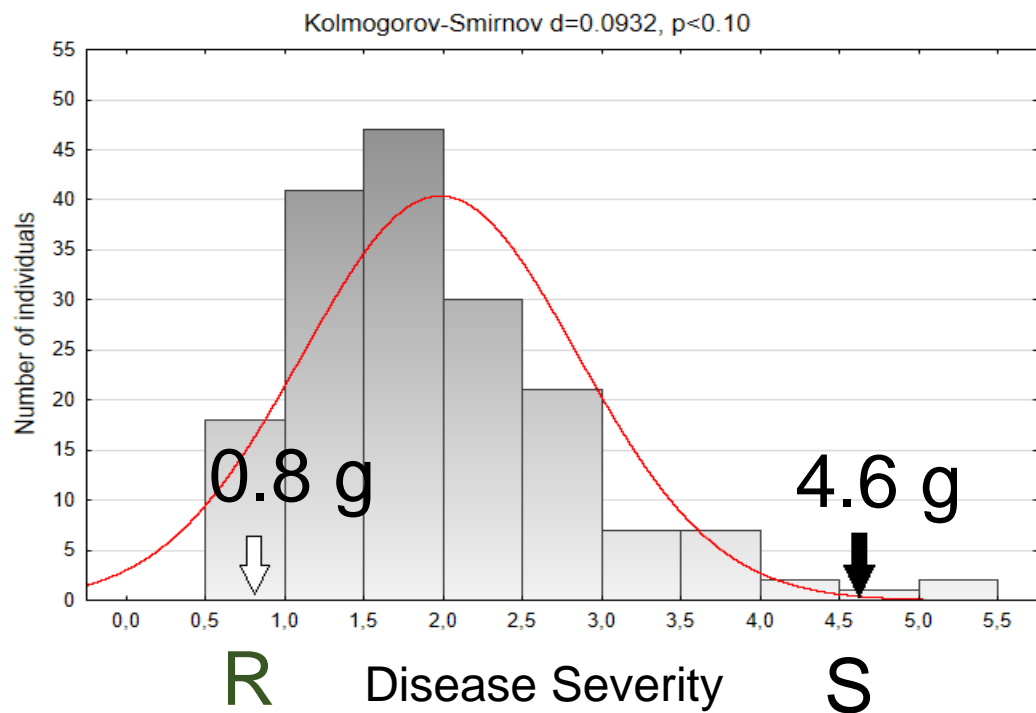
Diploid interspecific hybrids of *Solanum* spp.



Reaction of potato tubers to inoculation with bacteria *D. solani* in the highly resistant parent (**R**) and the susceptible parent (**S**)

Materials

Frequency distribution of disease severity



Phenotypic variance of disease severity

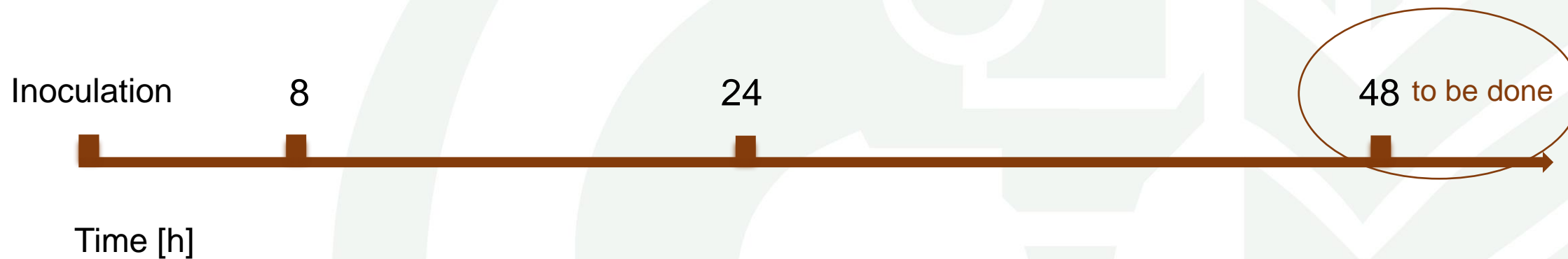
in the mapping population



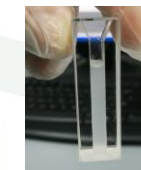
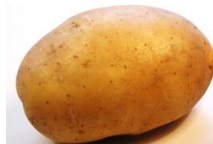
Three days after inoculation with bacteria *Dickeya solani*

Objectives

- To reveal differences in gene expression in resistant clones in comparison with susceptible ones in three different phases of infection.



Methods



RNA sequencing

Not treated

Wounded + Water

Wounded + Bacteria

Resistant

NTR

WR

BR

Susceptible

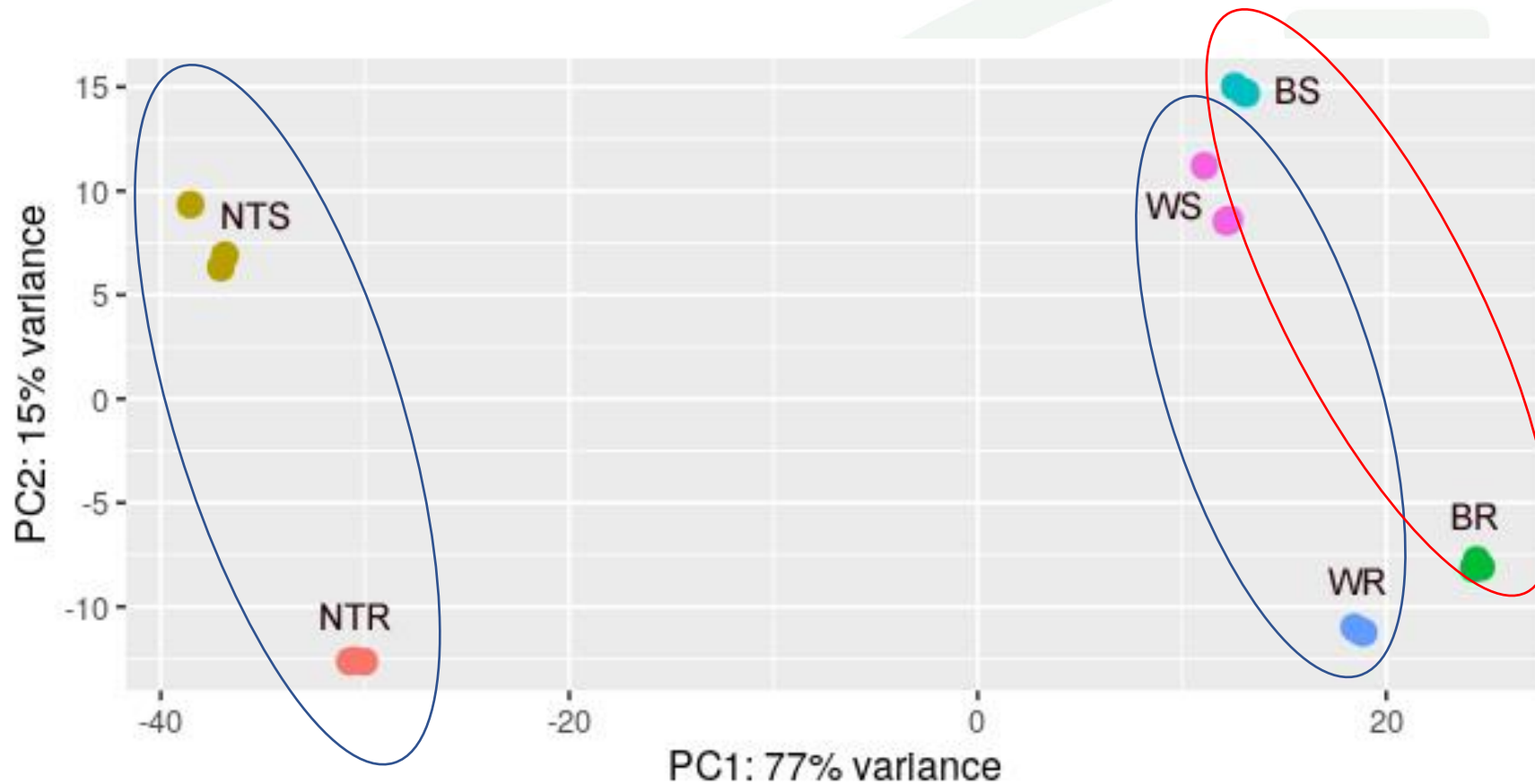
NTS

WS

BS

Results

Principal Component Analysis



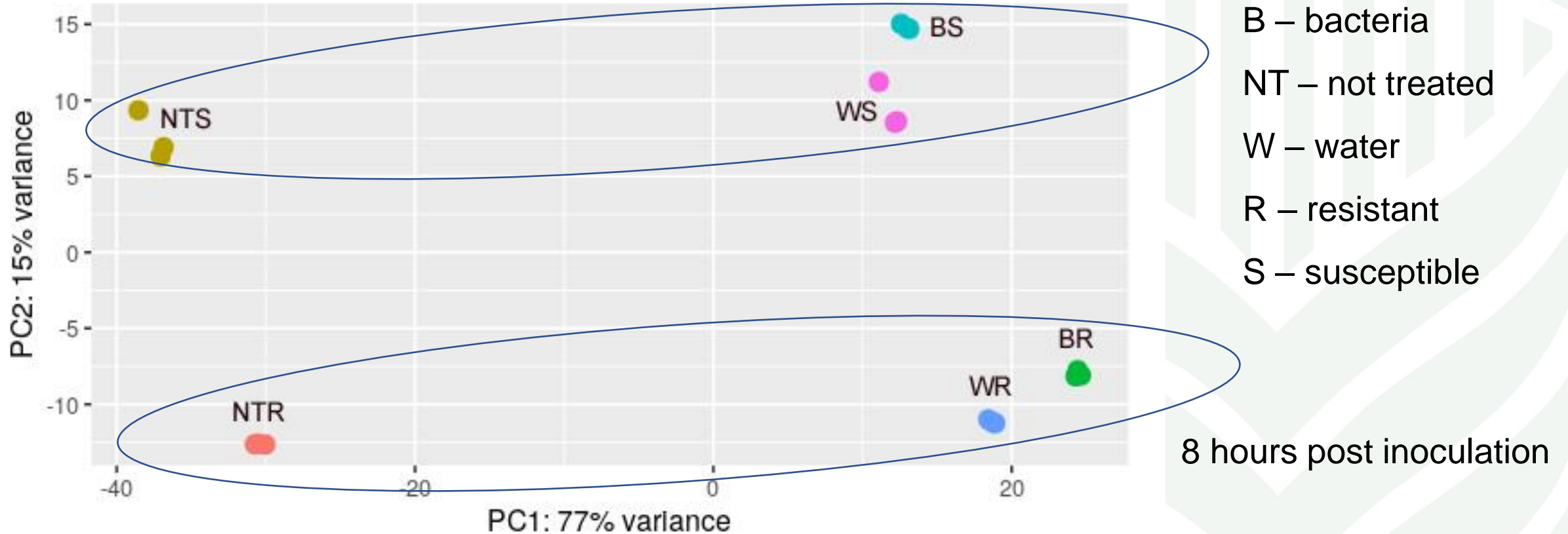
- B – bacteria
- NT – not treated
- W – water
- R – resistant
- S – susceptible

8 hours post inoculation

The most variation in gene expression is due to the treatment.

Results

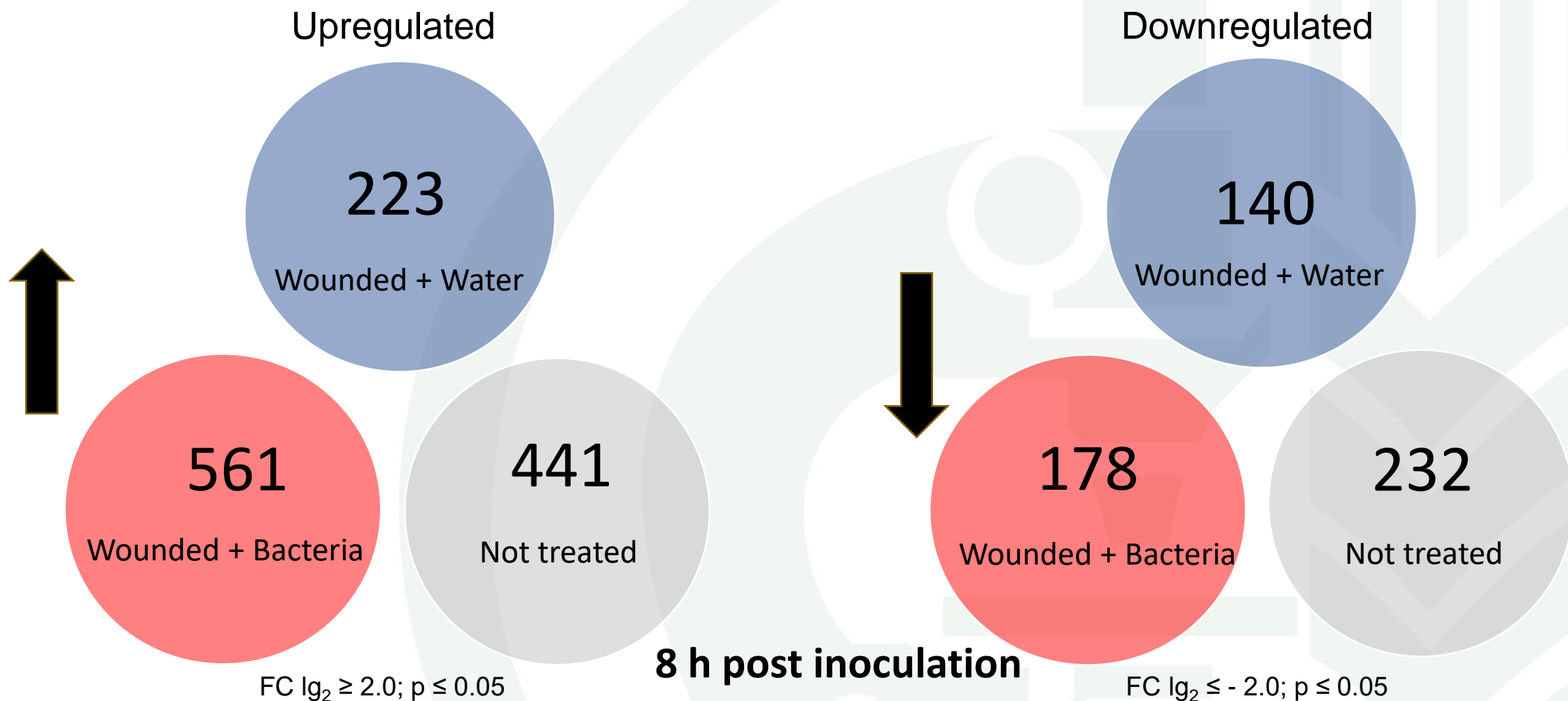
Principal Component Analysis



The second principal component showed gene expression variation due to the resistance level.

Results

Number of differentially expressed genes - Susceptible vs Resistant

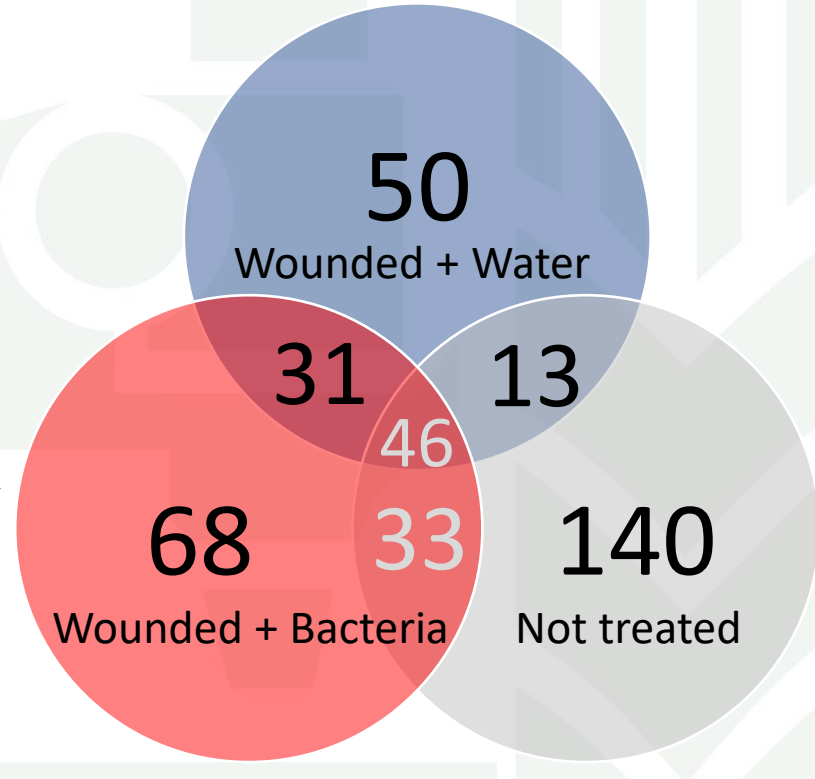
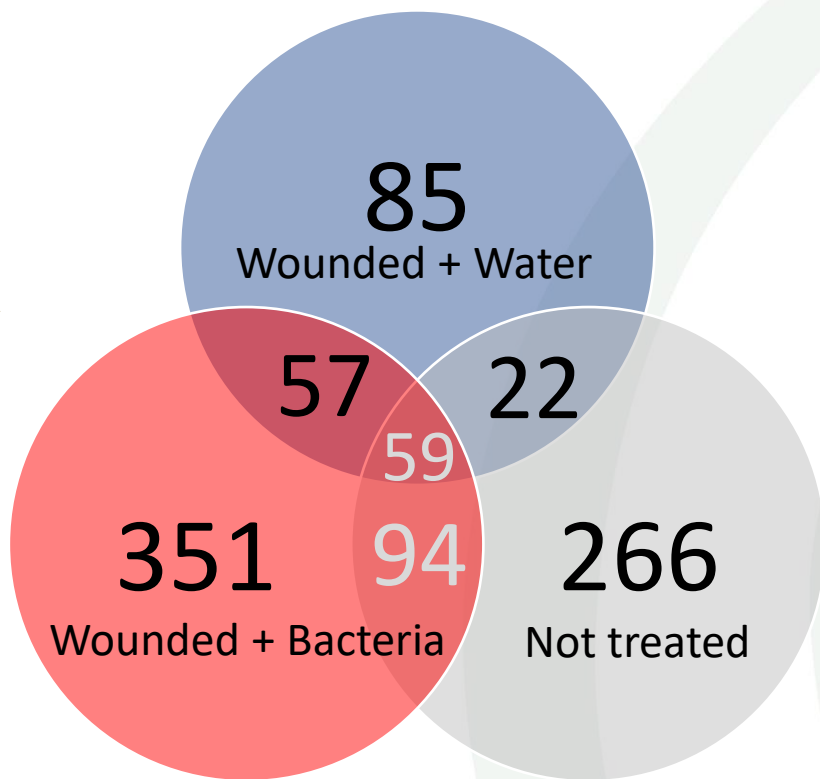


Results

Number of differentially expressed genes - Susceptible vs Resistant

Upregulated

Downregulated



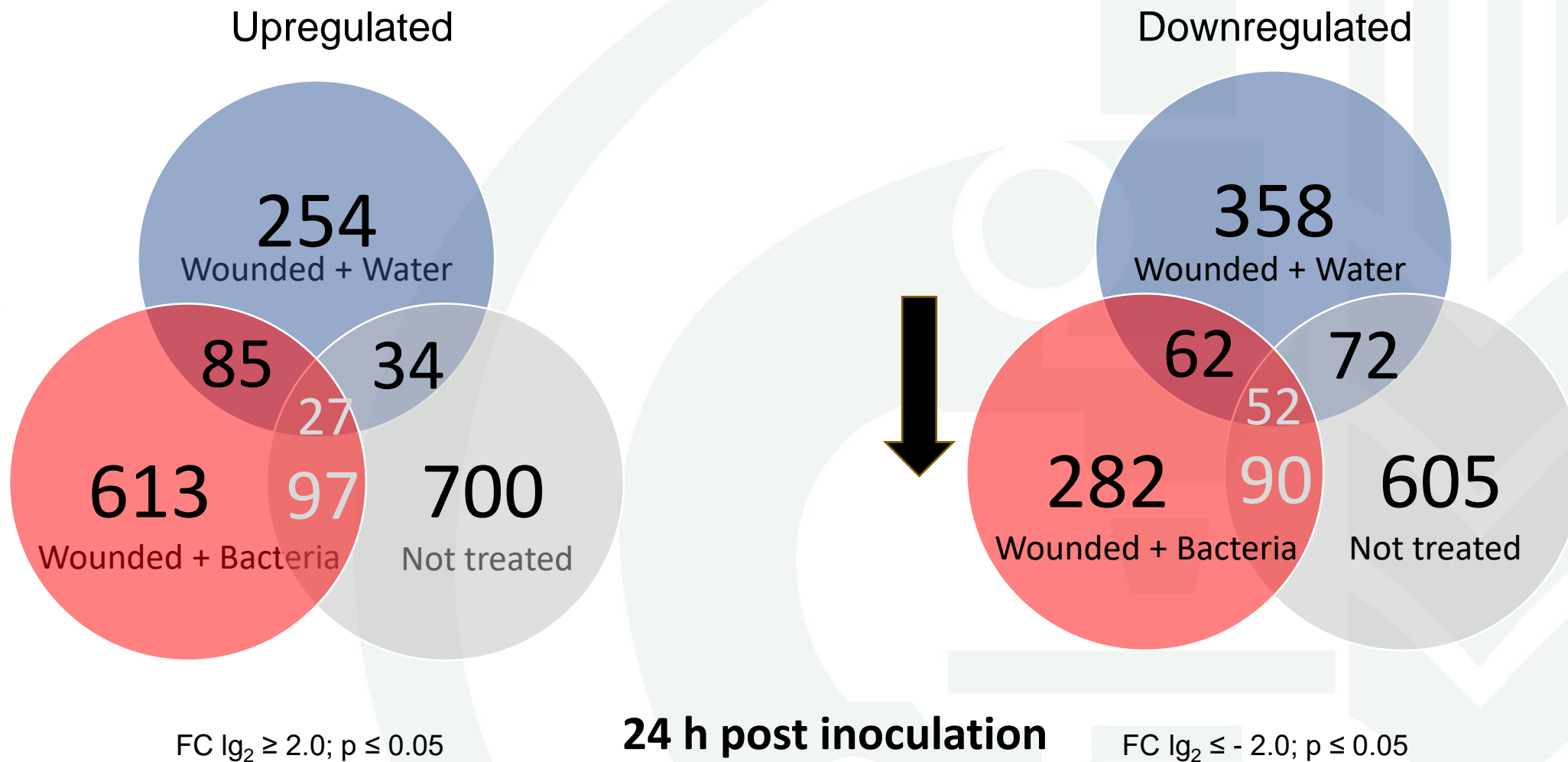
FC $\lg_2 \geq 2.0$; $p \leq 0.05$

FC $\lg_2 \leq -2.0$; $p \leq 0.05$

8 h post inoculation

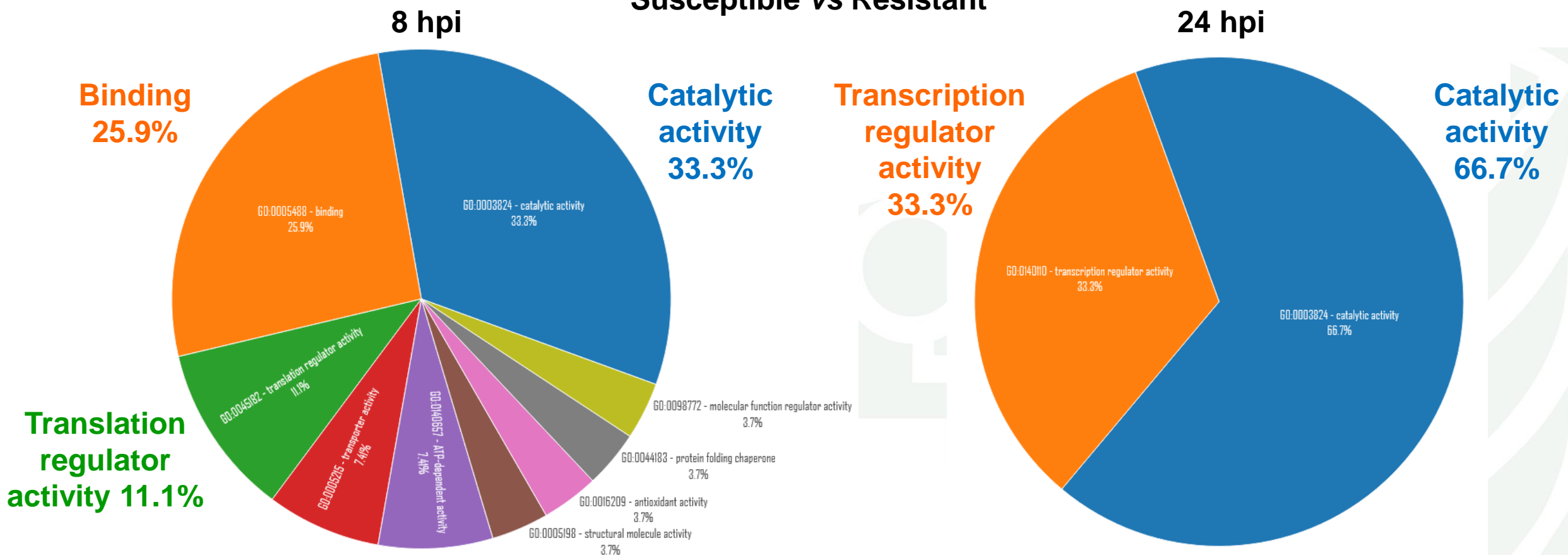
Results

Number of differentially expressed genes - Susceptible vs Resistant



Results

GO enrichment analysis, Molecular Functions in „Wounded + Bacteria” Susceptible vs Resistant

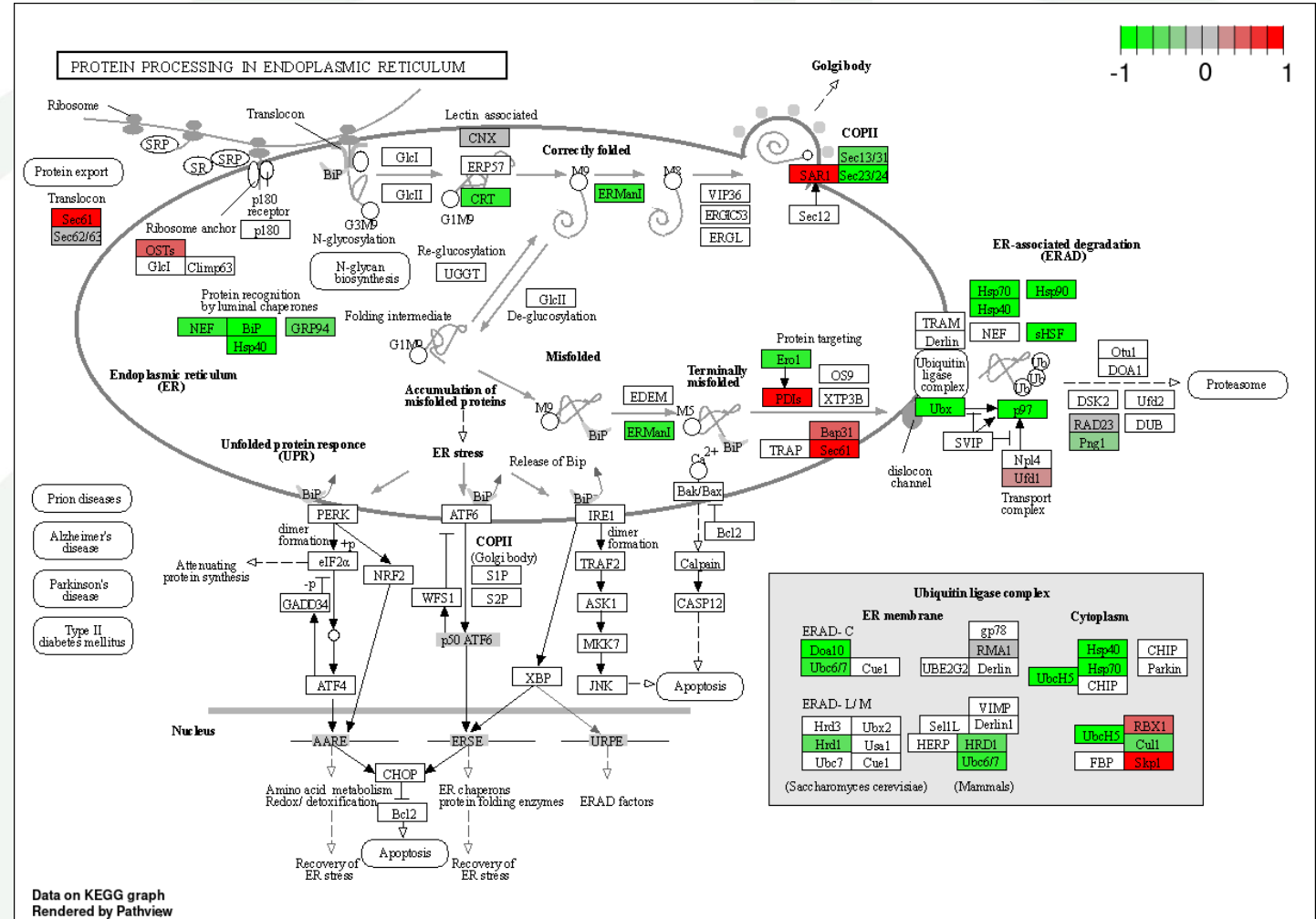


There are differences in over-represented GO terms, molecular functions, at the early phase of the infection (8 hpi) and later stage of infection (24 hpi).

Results

Protein processing in endoplasmic reticulum 24 hpi is the significant pathway in both wounded and wound-inoculated samples.

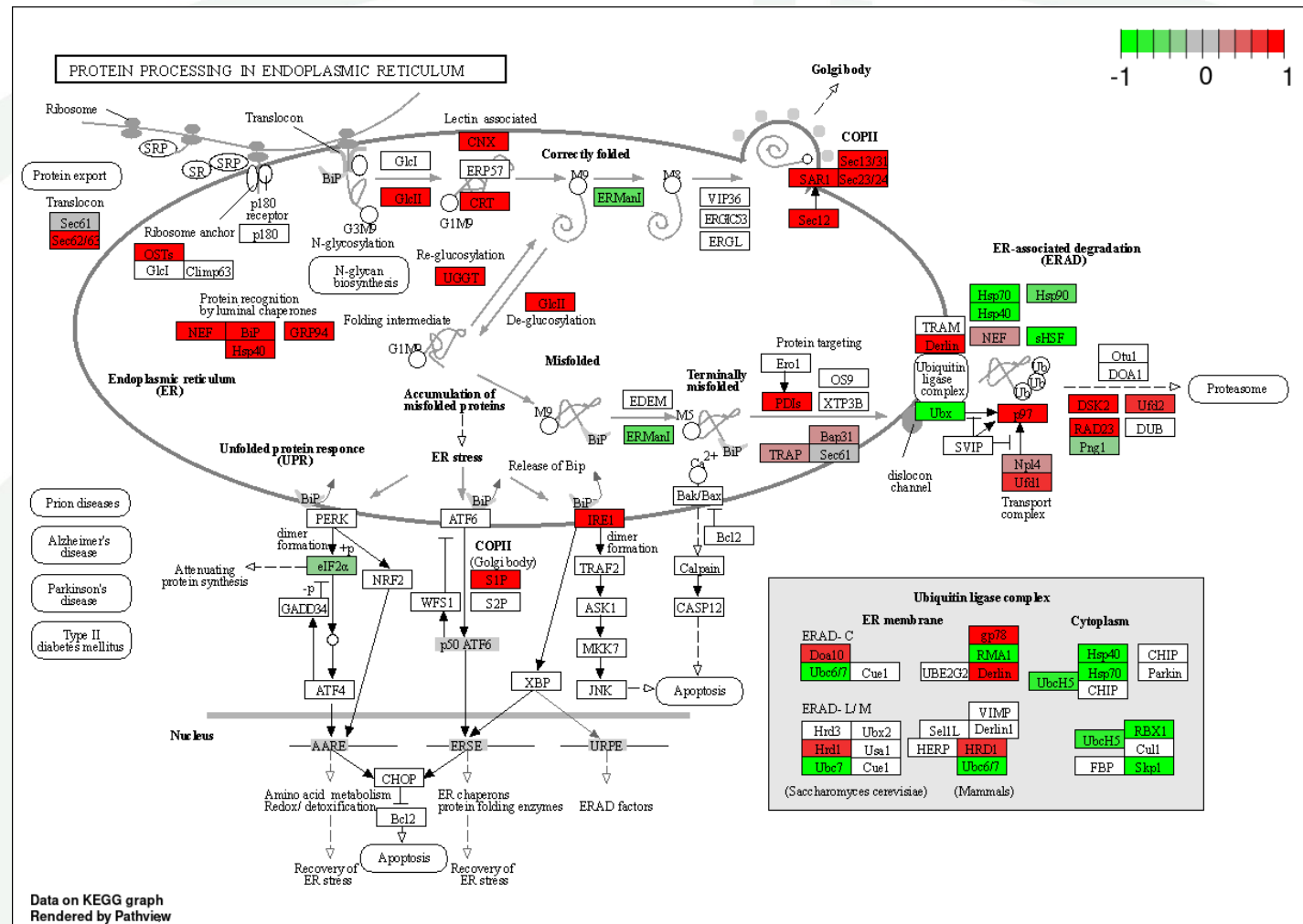
Wounded + Water – Susceptible vs Resistant



Results

Protein processing in endoplasmic reticulum 24 hpi is the significant pathway in both wounded and wound-inoculated samples.

Wounded + Bacteria – Susceptible vs Resistant



Conclusions

- ❑ The first principal component separated not treated potato tubers from wounded and wound-inoculated tubers (77% and 68%, 8 and 24 hpi respectively). The second component separated samples due to the level of resistance to *Dickeya solani* (15% and 18%, 8 and 24 hpi respectively).
- ❑ The number of differentially expressed genes between resistant and susceptible bulks increased with time after inoculation with *Dickeya solani*.
- ❑ The gene ontology analysis showed that the resistance to soft rot bacteria was enriched in DEGs associated with the Krebs Cycle and protein processing in the endoplasmic reticulum (24 hpi).

Acknowledgments

Katarzyna Szajko
Anna Grupa-Urbańska
Dorota Sołtys-Kalina

Thank you for your attention.

The Plant Breeding and Acclimatization Institute (IHAR) - National Research Institute

Radzików
05-870 Błonie, Poland
tel. 22 733 45 00
NIP-PL: 5290007029
REGON: 000079480
e-mail: postbox@ihar.edu.pl
www.ihar.edu.pl



First and last name: Renata Lebecka

Contact information:

IHAR-PIB, 05-831 Młochów, Poland

Tel.: 22 729 92 48 w 207

e-mail: r.lebecka@ihar.edu.pl