

A DEEP DIVE INTO THE ROLE OF NLRs IN SOLANACEAE

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Plants lack a mobile immune system, therefore they must recognize pathogens and deploy defence responses on a cell-autonomous level. This strategy engages resistance genes (R-genes).

R-genes encode for proteins, also known as NLRs, sharing common, highly conserved structures among species: the NB-ARC and a Leucine Rich Repeat domains.

R-genes can be directly involved in the defence response, culminating in the PAMP Triggered Immunity (PTI) or Effector Triggered Immunity (ETI). The macroscopic signature of the latter consists in the hypersensitive reaction, a consequence of cell death.

During the effector triggered immunity, cells march to their death in order to stop pathogen proliferation and trigger a transcriptome reprogramming for the downstream defence response.

In *Arabidopsis thaliana* ZAR1, a NLR belonging to the CC-NLR class, has been shown to form a pentameric structure, known as resistosome. The alpha-helices of ZAR1 are the main component of the pore function, and they harbour a high conserved N-terminal sequence: the MADA-motif.

A broad metadata analysis on transcriptome datasets of *Solanum lycopersicum* revealed a set of resistance genes always expressed at moderate levels: we define these genes as “core”. Core-genes were constitutively expressed in different experimental conditions (with and without pathogens).

A bioinformatic analysis on NLR distribution among species revealed that *Solanum lycopersicum* cv Heinze may express 232 NLRs, among which 28 harbour a MADA motif and 7 belong to the core-genes. Similar results emerged from

the other species taken into account.

The expression of this class of NLR orthologs is moreover supported by a novo RNA-seq assembly of *Solanum chilense* and *Solanum peruvianum* transcriptomes.

2 core-genes were conserved across species, suggesting their ancient role in plant defence and possible function in the resistosome assembly. One of these genes belongs to the same orthogroup of ZAR1. Another class of resistance genes, the NRCs, appear to perform as ZAR1, and they likely arose after the division between Rosids and Asterids.

These results suggest that a plant's response to biotic stress is controlled in part by a set of constitutively expressed genes. Their constitutive gene expression may pose an energetic cost therefore, dissecting their evolutionary history and regulatory pathways may lead to the development of new breeding strategies to ensure high resistance paired with low costs.