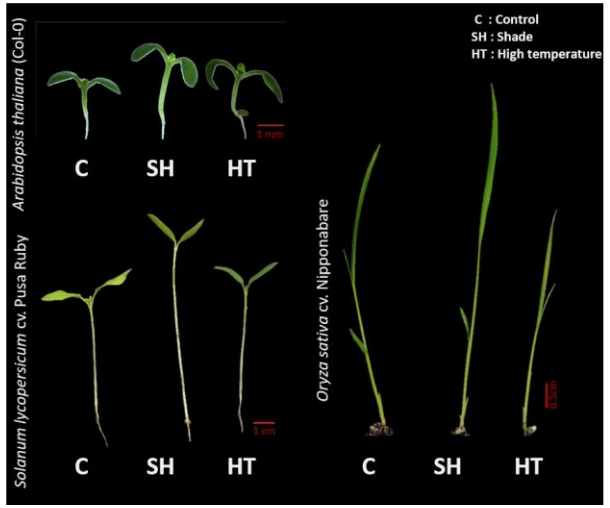
Comparative transcriptomics to understand light and temperature signalling across different plant species.

Aditi Dwivedi*, Kumud Saini, Aashish Ranjan (National Institute of Plant Genome Research, New Delhi)
*aditi.dwivedi11@nipgr.ac.in

We know : Arabidopsis hypocotyl elongates under shade (SH) and high temperature (HT) via shared signalling mechanisms.

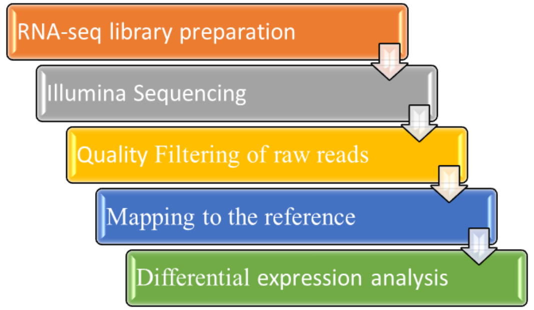
We asked : What are the similarities and dissimilarities in plant architecture and genes expression under shade and high temperature among Arabidopsis (*At*), tomato (*Sl*) and rice (*Os*) ?

I. Phenotypic response of Arabidopsis, tomato and rice under SH and HT



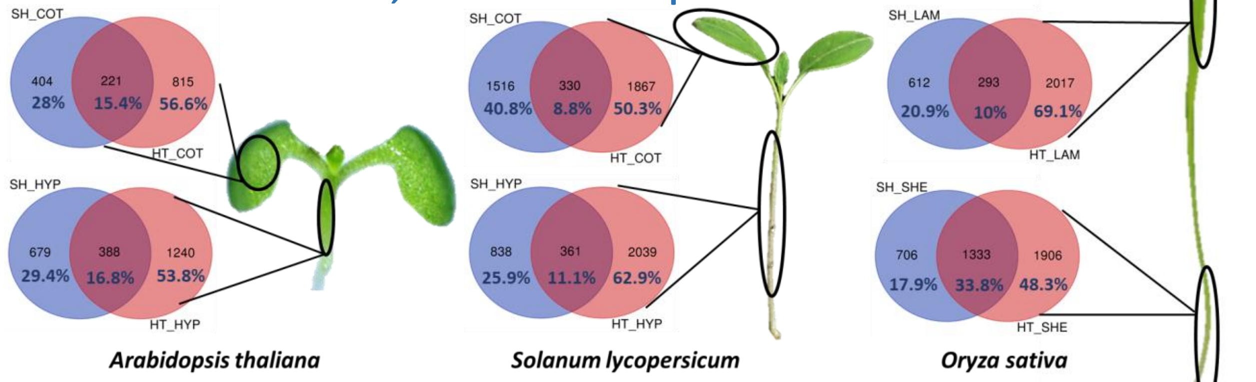
Shade (SH) response is common i.e. elongation, while a differential response of high temperature (HT) is seen among these three species.

II.



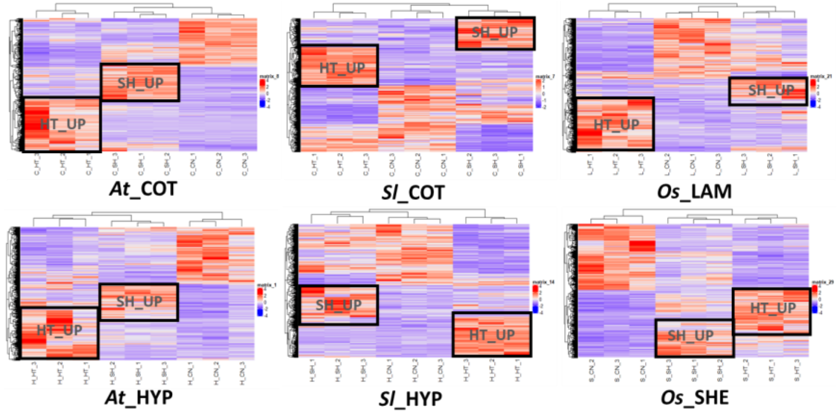
RNA-seq library preparation
Illumina Sequencing
Quality Filtering of raw reads
Mapping to the reference
Differential expression analysis

III. HT showed more pronounced impact on the transcriptional profile of *At, Sl* and *Os* as compared to SH



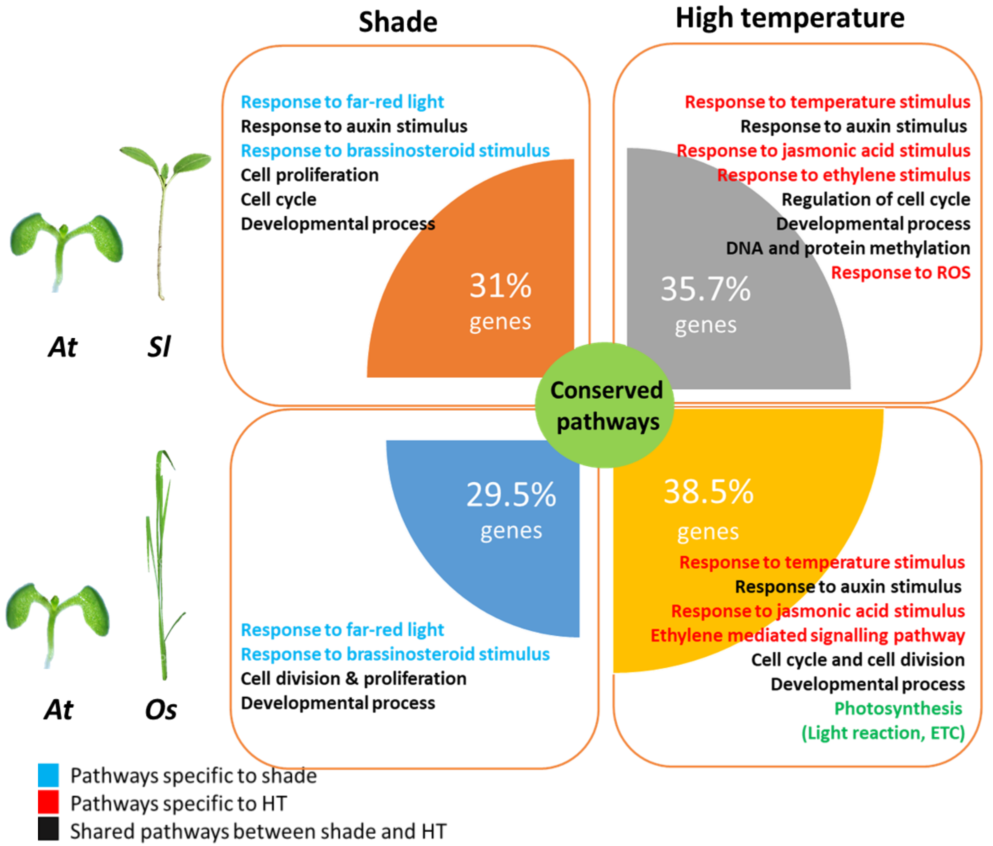
25-30% DEGs- unique to shade . **50-60% DEGs** – unique to HT.
10-15% DEGs- shared between SH and HT.

IV. Hierarchical clustering to obtain clusters that are shared and unique between SH & HT



Tissue and treatment specific clusters were obtained and biological processes like hormone stimulus, cell cycle, leaf development etc. were enriched. Gene networks are being prepared using these clusters.

V. Detection of conserved processes involved under SH and HT



Response to far-red light
Response to auxin stimulus
Response to brassinosteroid stimulus
Cell proliferation
Cell cycle
Developmental process

Response to temperature stimulus
Response to auxin stimulus
Response to jasmonic acid stimulus
Response to ethylene stimulus
Regulation of cell cycle
Developmental process
DNA and protein methylation
Response to ROS

Response to far-red light
Response to brassinosteroid stimulus
Cell division & proliferation
Developmental process

Response to temperature stimulus
Response to auxin stimulus
Response to jasmonic acid stimulus
Ethylene mediated signalling pathway
Cell cycle and cell division
Developmental process
Photosynthesis
(Light reaction, ETC)

🟦 Pathways specific to shade
🟥 Pathways specific to HT
⬛ Shared pathways between shade and HT

Orthology overlap between DEGs of *At - Sl* and *At - Os* was performed to identify the conserved biological processes.

Summary : Phenotypic response of SH is common while HT is different across *At, Sl* and *Os.* 30-35% DEGs are conserved across these species. Response to auxin and cell division seem to be the most conserved pathways under SH and HT in all the species while response to brassinosteroid seems to be SH specific and response to jasmonic acid and ethylene seem to be HT specific.