



24th Session International Poplar Commission

Transcriptional Profiling Analysis Of *Populus euphratica* In Response To Salt Stress


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Background




- Salinization is one of the major factors for degradation of land and water resources that causes environmental problems and limits the productivities of main food crops worldwide.
- Increasing salt tolerance of plants by genetic engineering is a efficient approach to improve the utilization of saline soil.
- Identification of stress-related genes, as well as elucidation of salt tolerance mechanisms response to salt stress, are the two key issues of tree genetics to increase salt tolerance of plants .



Objective

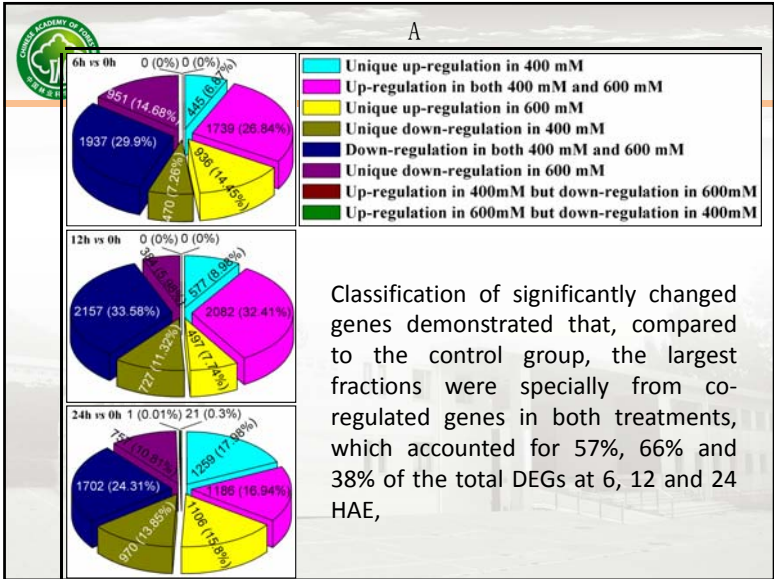
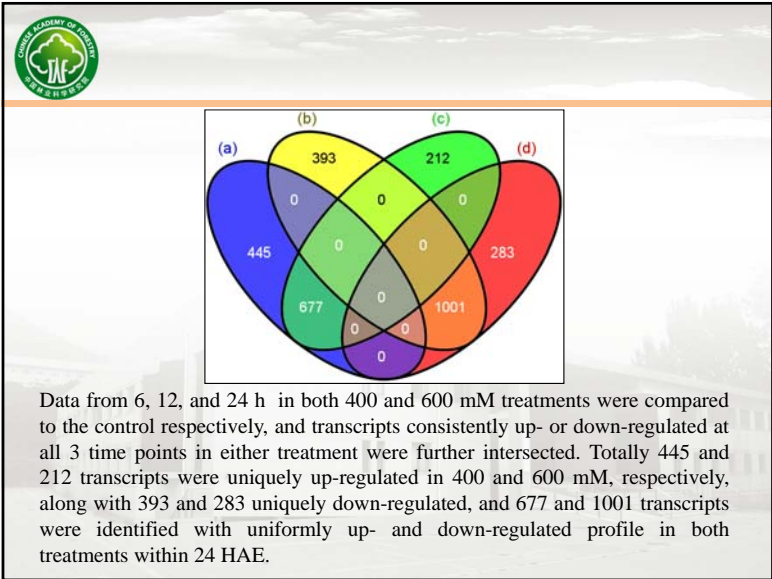
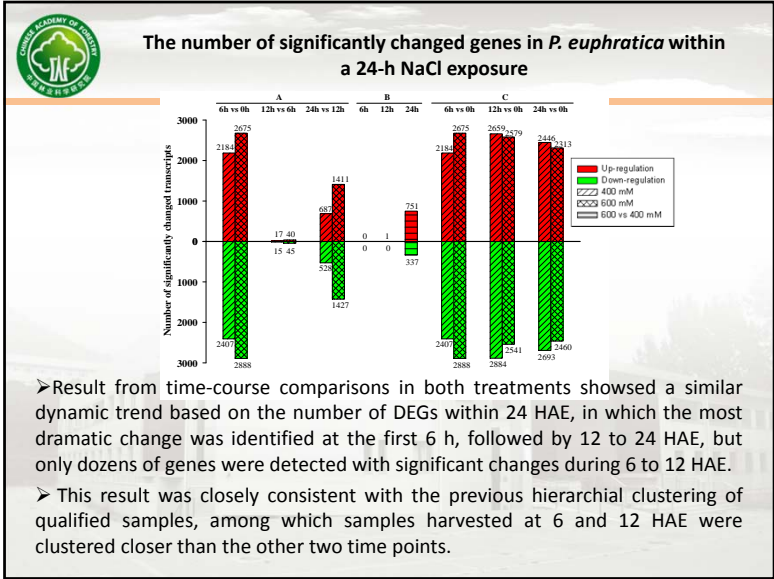
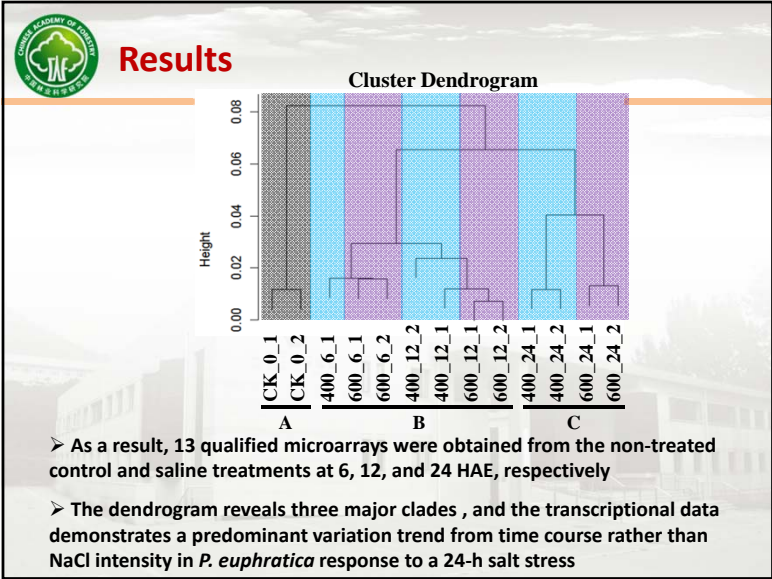


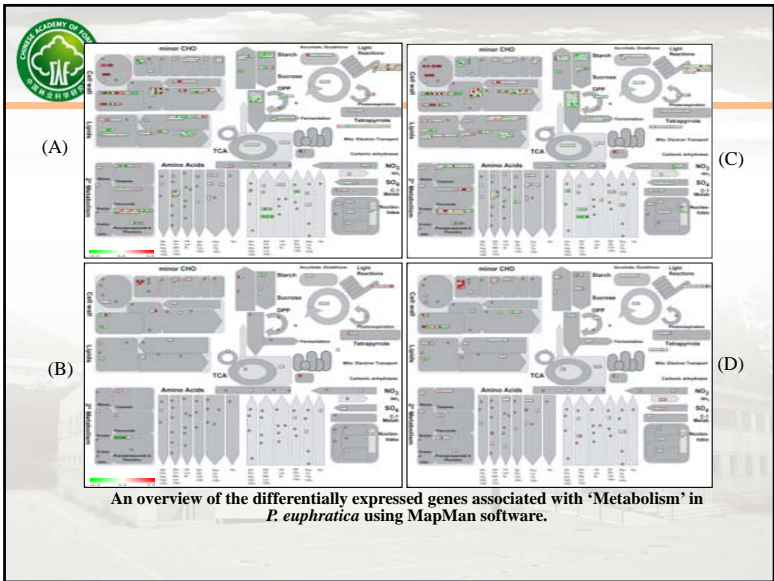
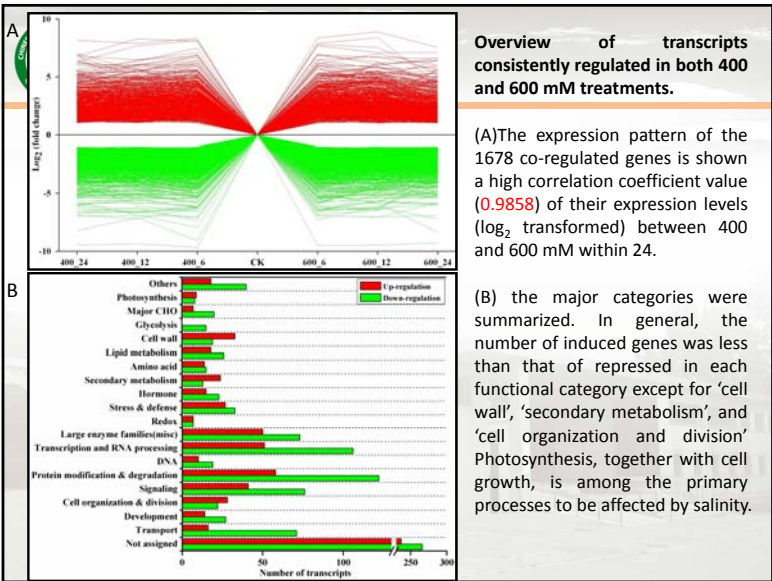
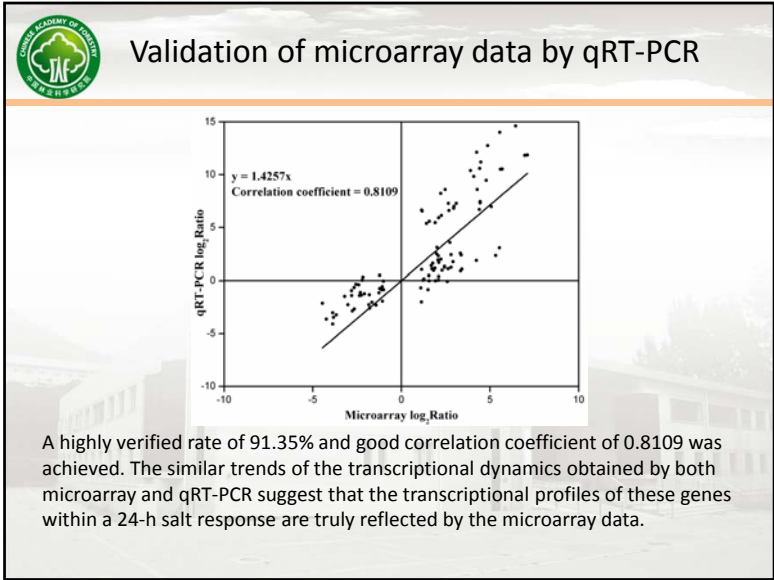
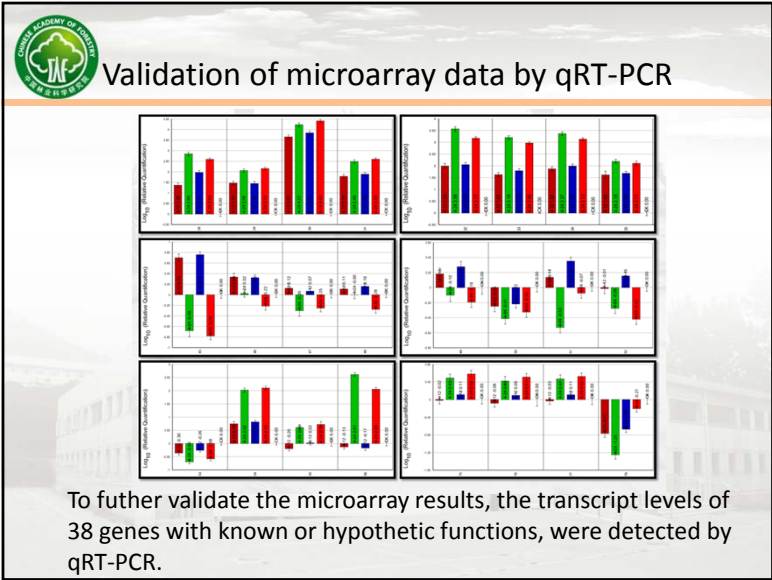
- *P. Euphratica* grows under a wide variety of temperature and soil conditions, such as high salt content in the soil and high temperatures in the air ,so it's a important genebank of stress tolerance of plant.
- Conducted a genome-wide transcriptional profiling analysis with the AffyMetrix GeneChip[®] Poplar Genome Array to get insight into the changes of gene expression in salt-tolerant woody plant *P. euphratica*. exposed to salinity



Plant material and salt treatment

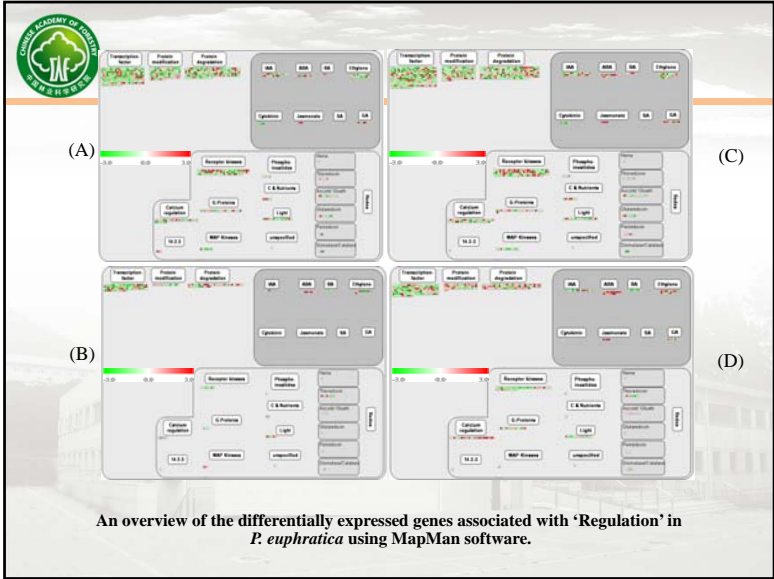
- In July 2009, well-grown 1-meter-high *P. euphratica* seedlings individually planted in 10 L pots containing local loam soil were employed for salt treatment at Yuli, Xinjiang Uygur Autonomous Region of China
- For salt treatment, 2 L Sodium Chloride (NaCl) solution, concentration in 400 mM and 600 mM respectively, was irrigated to each potted plants and equal amount of solution without NaCl was set as control.
- Apical buds with the top 5 young leaves were harvested at 0, 6, 12, and 24 h after salt exposure (HAE)





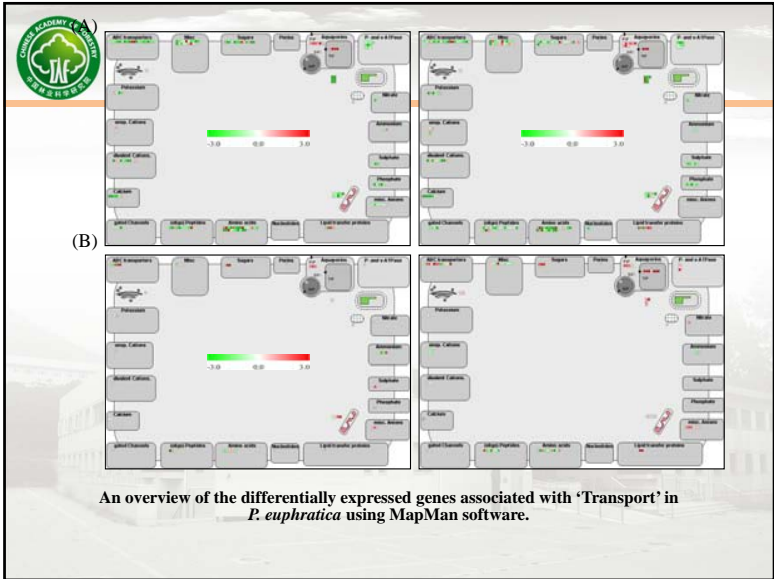
➤Concerning genes involved in amino acid metabolism, the largest fraction was from genes associated with **aspartate** family, in which 1 transcript responsible for asparagine synthesis, 2 transcripts related to lysine degradation, 3 transcripts encoding aspartate aminotransferases, and 10 transcripts pertained to 5 functional categories associated with methionine synthesis were found to be induced or repressed.

➤ The following fraction contained 6 transcripts encoding **enzymes functioning in synthesis and degradation of aromatic amino acids**. Besides, a transcript homologous to AtP5CS (AT2G39800), a known gene responsible for the proline synthesis in plant, was found to be repressed.



➤The most abundant transcripts of those differentially expressed regulatory genes involved in signal transduction categories were observed to be **calcium-related signaling, G-proteins, MAP kinases, and receptor kinases mainly including leucine rich repeat family, DUF 26, and S-locus glycoprotein like** .

➤Many hormone-related genes invovled in **abscisic acid (ABA), auxin, cytokinin, ethylene, and gibberelin** metabolism were also broadly observed to be significantly co-regulated under the tested regimes





- In terms of transport factors, surprisingly, the **co-repressed** transporters were widely identified including **nitrate, ammonium, sulphate, phosphate, metabolite, potassium, calcium and H⁺-transporting pyrophosphatase**,
- as well as most of the members from categories including sugars, amino acids, peptides and oligopeptides and ABC transporters with several exceptions.
- members from three subfamilies **PIP, TIP and NIP** belonged to aquaporin were observed to be consistently induced.



In the stress-related category, the most fraction enriched in the class of **disease resistance proteins and dehydration-responsive family protein**, with known functions in response to physiological dehydration that could be induced by cold, drought or **salt stress**, were observed to be significantly co-regulated in our tested treatments.




Expression of targets regulated by stress-related miRNAs

- In *Populus*, previous publications have proven that most of the known *P. trichocarpa* miRNAs were broadly employed to response to adverse environments, such as drought, salt, and other stresses.
- Collected known and candidate miRNAs from database and publications of *P. trichocarpa* and *P. euphratica*, constituting a non-redundant dataset of **479** poplar miRNAs.
- Among the 11705 differentially expressed transcripts, **366 non-redundant transcripts** were identified as putative targets of 331 miRNAs



Expression of targets regulated by stress-related miRNAs


Confirmed targets including squamosa promoter binding protein-like (**SPL**), NAC domain-containing proteins (**NAC**), homeobox transcription factor (**HB**), CCAAT box binding factor, polyphenol oxidase (**PPO**), plantacyanin, laccase (**LAC**) and disease resistance proteins (**NBS-LRR**), which were proved to be targeted by miR156, miR164, miR166, miR169, miR1444, miR408, miR397, mi472 and miR482 family, were also identified as DEGs in *P. euphratica* within 24 HAE



Comparison with published stress-responsive transcriptome of *P. euphratica* revealed by microarray


Compared with the published papers involved in salt tolerance of populus, **41.3%, 72.7%, 53.7%, and 75%** of the significantly changed transcripts from these publications were also detected in our results

The intersections and differences between publications and our result can be beneficial to the elucidation of molecular response mechanism of *P. euphratica* under different types and degrees of stresses, especially salinity and drought.



Conclusions

- 677 up- and 1001 down-regulated transcripts were consistently remarked from all three time points in both treatment.
- 939 putative transcription factors belonged to more than 30 families, which were primarily involved in AP2/ERF, bHLH, bZIP, HD-ZIP, MYB, WRKY, NAC *et al.*, were identified with different profiling within 24 AE.
- Function classification revealed that many of these genes were involved in metabolism, cellular response, transport, and specially regulation such as transcription, hormone *et al.*.
- Genes identified with different expression patterns between diverse salinization level are desired candidates for further function verification to understand more complicated molecular mechanisms of saline differences in plant salt response.



Thanks for your attention!