In silico comparative analysis of conserved genes expressed in solanaceous plants under abiotic stresses

CSIR-CIMAP

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ABSTRACT

The gene expression data was studied in order to analyze genes involved in different abiotic stresses in solanaceous plants. Salt, temperature (heat & cold) and drought are the main abiotic stresses to the plants. Our findings suggest that a common set of genes are the key players in signaling pathway responsible for initiation of cascade of reaction in response to stress. The study will help to understand the mechanism of regulation of conserved differentially expressed genes with response to various abiotic stresses.

INTRODUCTION

Abiotic stress responses are important for plants to cope with environmental changes to survive. The idea was to analyze those differentially expressed genes, which show common expression in response to different abiotic stresses. Mitogen activated protein kinases (MAPK) are important mediators in signal transmission, connecting the perception of external stimuli to cellular responses. In plants, MAPKs play a major role in the signaling of abiotic stresses.

METHODS

The gene expression data of 7 solanaceous plants in 4 abiotic stresses were taken from GEO at NCBI.

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The expression value of probe ids were converted to hybridizing gene ids.

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The up & down regulated genes were taken above the cut off of 0.6 & -0.6 respectively.

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The common genes were selected showing expression in all the samples (time series) for each abiotic stress condition.

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The genes showing expression in atleast two abiotic stresses were listed.

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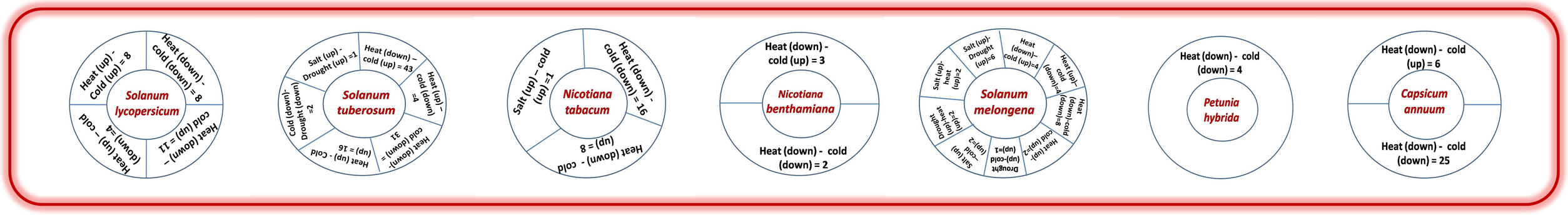
These conserved genes were studied for their role in MAP kinase pathway.

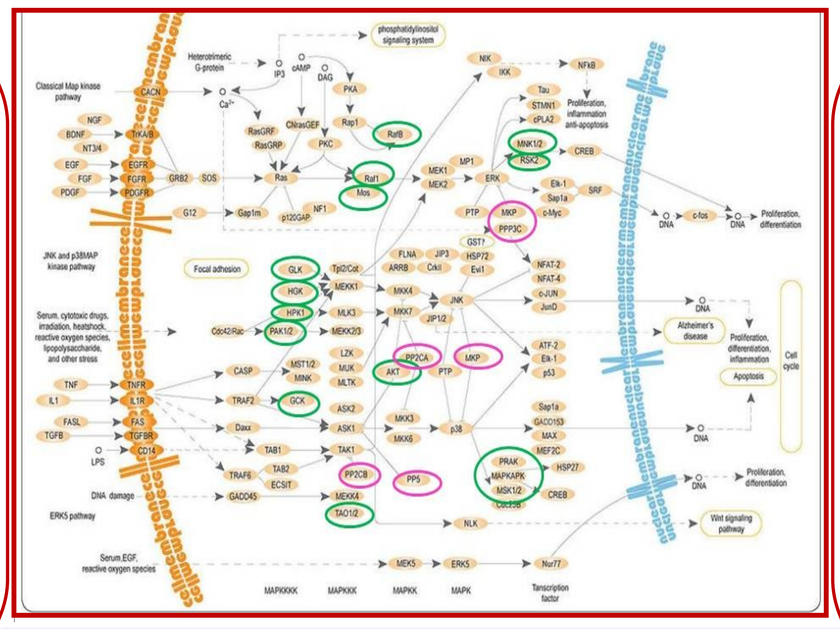
RESULTS



Conserved genes of 7 solanaceous plants that are regulated differentially (up/down) and common in atleast two type of abiotic stresses.

E.C No. 2.7.11.1

S. lycopersicum (21)	*S. tuberosum (79)*	*N. tabacum (21)*	*N. benthamiana (4)*	*S. melongena (29)*	*P. hybrida (4)*	*C. annuum (25)*
BQ116964 BQ515871 BQ120283 BQ515870 BQ112095 BQ113773 BQ120282 BQ113774 BQ114591 BQ111743 BQ118735 BQ111344 BQ114590 BQ111343 BQ115201 BQ114001 BQ114552 BQ111742 BQ114551 BQ504636 BQ115200	BQ110556 BQ112265 BQ112264 BQ510464 BQ518081 BQ513122 BQ112708 BQ513757 BQ512271 BQ506104 BQ513756 BQ512272 BQ508930 BQ513121 BQ510465 BQ518080 BQ515378 BQ508892 BQ119821 BQ121482 BQ515342 BQ118917 BQ117705 BQ515379 BQ118916 BQ508891 BQ119820 BQ504944 BQ117704 BQ115546 BQ111344 BQ515274 BQ513172 BQ111343 BQ115673 BQ504943 BQ506305 BQ115674 BQ518043 BQ111456	BQ51804 2 BQ11428 3 BQ51664 7 BQ51770 9 BQ51265 8 BQ12028 3 BQ51901 1 BQ51664 6 BQ51901 2 BQ12173 7 BQ51864 8 BQ50787 1 BQ12127 7 BQ51894 0 BQ51569 5 BQ51885 5 BQ12190 0 BQ51229 1 BQ12173 8 BQ51298 4 BQ12067 4 BQ51826 3 BQ51587 3	BQ112095 BQ119220 BQ111344 BQ111343	BQ12056 2 BQ51844 0 BQ11955 6 BQ12056 3 BQ51843 2 BQ11955 6 BQ51843 2 BQ11955 6 BQ51843 2 BQ51414 1 BQ11955 6 BQ11955 6 BQ51046 4 BQ11955 6 BQ51098 5 BQ50548 3 BQ51098 6 BQ51537 9 BQ11134 4 BQ11134	BQ12036 8 BQ50467 9 BQ12036 7 BQ11965 2	BQ512867 BQ113430 BQ507869 BQ507870 BQ113431 BQ512866 BQ114084 BQ118225 BQ512361 BQ121482 BQ517719 BQ517070 BQ508195 BQ517720 BQ513959 BQ111344 BQ508194 BQ111343 BQ112252 BQ114516 BQ115201 BQ112251 BQ512362 BQ114889 BQ115200



Reference Mitogen Activated Protein kinase pathway

EC No. : 3.1.3.16

S. lycopersicum (24)	*S. tuberosum (81)*	*N. tabacum (22)*	*N. benthamiana (4)*	*S. melongena (30)*	*P. hybrida (4)*	*C. annuum (21)*
BQ510464 BQ508767 BQ112919 BQ513259 BQ508768 BQ510465 BQ515885 BQ515306 BQ515307 BQ507633 BQ115673 BQ507634 BQ111457 BQ111456 BQ115246 BQ120283 BQ117132 BQ112096 BQ112095 BQ517715 BQ508580 BQ505033 BQ517716 BQ120282	BQ119556 BQ112265 BQ112264 BQ510464 BQ518081 BQ513122 BQ112708 BQ513757 BQ512271 BQ506104 BQ513756 BQ512272 BQ508930 BQ513121 BQ510465 BQ518080 BQ515378 BQ508892 BQ119821 BQ121482 BQ515342 BQ118917 BQ117705 BQ515379 BQ118916 BQ508891 BQ119820 BQ504944 BQ117704 BQ115546 BQ111344 BQ515274 BQ513172 BQ111343 BQ115673 BQ504943 BQ506305 BQ115674 BQ518043 BQ111456	BQ116964 BQ515871 BQ120283 BQ515870 BQ112096 BQ112095 BQ120282 BQ114002 BQ114591 BQ111743 BQ118735 BQ114590 BQ514119 BQ111343 BQ115201 BQ114001 BQ514118 BQ114552 BQ111742 BQ114551 BQ504636 BQ115200	BQ112096 BQ112095 BQ119220 BQ111343	BQ12056 2 BQ51844 0 BQ11955 6 BQ51844 1 BQ12056 3 BQ51843 2 BQ11955 6 BQ51843 2 BQ11955 6 BQ51843 2 BQ51414 1 BQ11955 6 BQ11955 6 BQ11955 6 BQ51537 8 BQ51098 5 BQ50548 3 BQ51098 6 BQ51537 9	BQ12036 8 BQ50467 9 BQ12036 7 BQ11965 2	BQ51286 7 BQ11343 0 BQ50787 0 BQ51286 6 BQ11408 4 BQ11822 5 BQ12148 2 BQ51771 9 BQ11489 0 BQ51707 0 BQ50819 5 BQ51395 9 BQ50970 9 BQ50819 4 BQ11134 3 BQ11520 1 BQ11225 1 BQ11488 9 BQ11520 0 BQ51175 8

DISCUSSION

- The genes showing differential expression (up/down) in any two types of abiotic stresses may representing conserved genes.
- A total of 51 enzymes are reported in reference MAP kinase pathway.
- These selected conserved genes showing functional similarity with 20 enzymes of *Arabidopsis thaliana* which belong to only two enzyme families.

CONCLUSION

- Osmotic (salt & drought) and temperature (heat & cold) stresses are largely regulated by highly conserved different sets of genes.
- The mechanism of regulation of these genes may help to develop a strategy for stress resistance in plants.
- Conserved genes belong to two enzyme families - non-specific serine/threonine protein kinase & phosphoprotein phosphatase.

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