High-Resolution Study of Wheat Transcriptomes in Response to Drought and Salinity

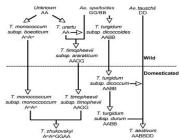
& Ontologies

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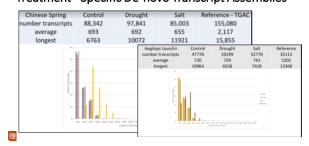


$Wheat \ lines \ being \ analyzed \ for \ their \ transcriptome \ sequencing, performance \ and \ genetic \ variation$

Plant ID	Species	Genome _type				Salt (150mM NaCl for 24hrs) treated -Replicates					
			R1	R2	R3	R1	R2	R3	R1	R2	R3
PI542274*		88	0	1	-1	1	1	1	1	1	1
P1542263*			-1	1	-1	1	1	1	0	1	0
P1574466	Aegilops spetbides		1	- 1	0	1	0	1	0	0	0
1560748	Augrops spectroes		0	1	- 1	1	1	1	0	0	0
PI580751			- 1	- 1	- 1	1	1	1	0	0	0
1542259			1	1	- 1	1	0	1	0	1	٥
1428564		DD	0	1	- 1	1	1	0	0	0	0
T1859*			-1	- 1	- 1	1	1	1	1	1	- 1
1220641	Aegilops tauschii		1	1	-1	1	1	1	0	0	0
PI508261*	1		0	1	- 1	1	1	1	1	1	1
1486270	i		1	0	- 1	1	1	1	0	0	0
IMDV92		AA	0	1	- 1	0	1	0	1	0	0
PI167625*	Triticum manacaccum		- 1	1	- 1	1	1	- 1	1	1	- 1
MG3116	тивсим жинососсим		1	- 1	0	0	1	0	1	0	0
4362610°			-1	-	٥	1	1	0	1	1	-
Caseberg*	Triticum aealivum	AABBOD	- 1	-1	- 1	1	1	1	1	1	1
add*			- 1	1	- 1	1	1	1	1	1	1
Rosalyn*			1	1	-1	1	1	1	1	1	- 1
Sobtail*			-1	-	0	1	- 1	1	1	- 1	1_
thinese Spring*			- 1	- 1	- 1	1	1	1	1	1	1

The mRNA from 89-samples (colored cells) from 11 wheat lines marked with ", were processed for 150bp paired-end RNA-Seq sequencing on illumina H-Seq 3000. Wheat plants were grown in the <u>OSU green houses</u> under normal 12H-day/12h-night photoperiod cycle a 72B temperature. When the plants reached <u>Deoting stage</u>, the treatments were given and only the toppost leaf was harvested for solating the <u>mRNA</u>. The plants continued to complete their lifecycle under normal conditions after the treatment and were observed for yield traits like average grain number and weight, after undergoing stress shock during their reproductive phase. Ideally stress during reproductive phase would negatively impact the yield.

Treatment – Specific De-novo Transcript Assemblies



An Example of Differentially Spliced Transcript Isoforms Under Different Treatments



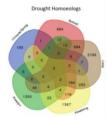
Number of Homeologous Genes Expressed Under Salt and Drought Conditions

	Drought	Salt
Chinese Spring	181	52
Bobtail	1726	365
Ladd	3407	60
Kaseberg	1971	12
Rosalyn	1410	2278
Total number of ho	moeologs in Gramene Database: 86,923	

Common & Treatment-Specific Homeologues in Hexaploid Accessions



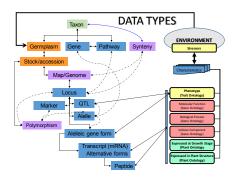
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SNP Identification and Their Consequences

		V	ariety		
consequence type	ChineseSpring	Bobtail	Ladd	Kaseberg	Rosalyn
3_prime_UTR_variant	4728	39291	45503	40772	47157
5_prime_UTR_variant	2601	10163	12178	11204	1216
coding_sequence_variant	418	308	295	304	432
downstream_gene_variant	15791	66091	76527	69227	83927
frameshift_variant	112	367	588	566	546
inframe_deletion	48	277	356	351	398
inframe_insertion	2	103	110	111	114
intergenic_variant	6215	27405	33849	30448	32990
intron_variant	16615	57402	71401	62901	70908
missense_variant	7695	44072	52417	47804	51757
protein_altering_variant	0	15	15	19	12
splice_acceptor_variant	3093	2705	2935	3057	3230
splice_donor_variant	5729	5024	4784	5088	5349
start_lost	15	31	47	46	43
stop_gained	99	431	508	472	526
stop_lost	43	163	167	174	189
stop_retained_variant	11	. 66	75	76	96
synonymous_variant	9893	54876	64175	59899	66426
upstream gene variant	10059	43881	51773	46248	53802





Planteome: Reference Ontologies for Plants

	Environment Ontology (ENVO)						
É	Plant Environmental Conditions (EO)						
GRANUL)	Plant Taxonomy	omy NCBI Taxonomy		Phenotypic Quality (PATO)	Biological Process (GO)		
ı	Anatomy	Plant Anatomical Entity Plant Ontology (PO)	Plant Ontology (PO) Plant Cell (PO) Cell (CL) Cellular Component (GO) Molecular Entity (ChERL PR)		Plant Structure		
ı	Cell			Plant Trait Ontology (TO)	Developmen Stage (PO)		
ı	Cellular Component	Cellular Component (GO)					
	Molecule			Molecular Function (GO)	Molecular Process (GO)		

Key: Yellow: Ongoing Planteome development; Blue: Collaborator ontologies with plant enrichment Pink: New ontology to be developed

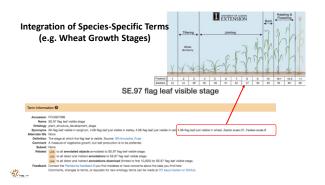
Planteome Ontologies Maintained on the GitHub

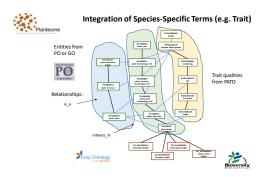


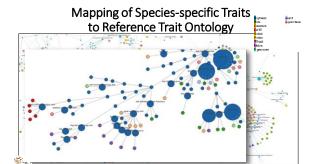
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https://github.com/Planteome









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