

Deep transcriptomic analysis of *Chromera velia* under Mercury-stress condition.

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*Poster Presenter

Introduction

- *Chromera velia* is an unicellular photosynthetic marine alga isolated from Australia.
- *C. velia* is the closest known relative of apicomplexan parasites.
- Mercury(Hg) is one of most toxic heavy metals in marine ecosystem.
- At higher concentration Hg leads to the disruption of water flow in higher plants, modulation of chloroplast structure and triggering of ROS effect.
- *C. velia* is more tolerant to Hg toxication when compared to plants and other related algae.
- RNA-seq is very useful tool for the identification of related gene and to elucidate the expression patterns in *C. velia*.

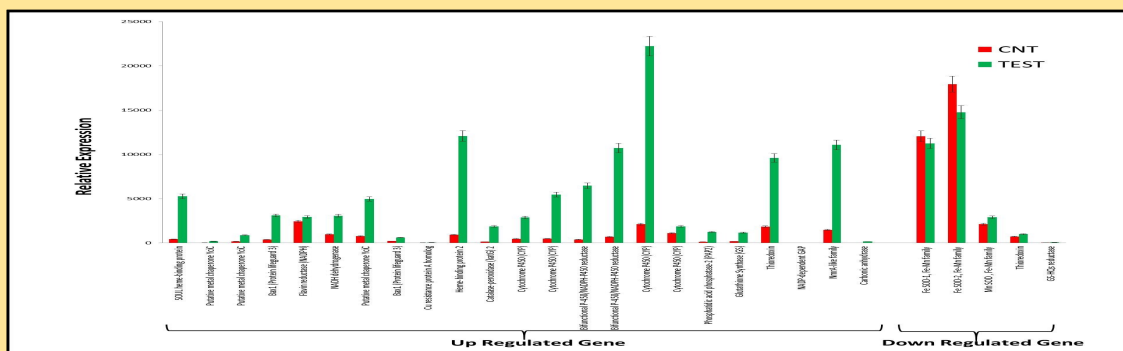
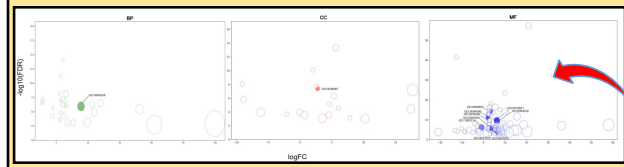
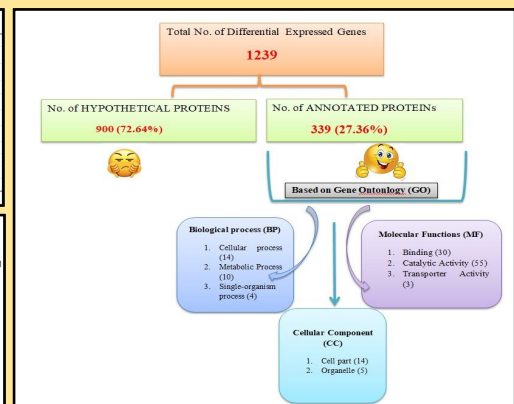
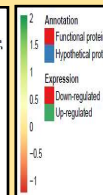
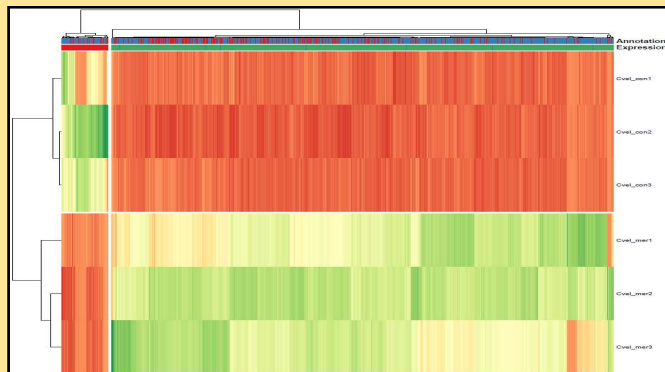
Methods

- *C. velia* was cultured in variable concentration of Hg.
- RNA isolation was followed by cDNA library construction.
- Transcriptome sequencing was done and followed by quantification of variable expression of genes.
- Identification of Differentially Expressed Gene's (DEG's)
- Real Time-qPCR analysis was done for validation of RNAseq results.

RESULTS

Sample name	Condition	Raw reads	Clean reads	Total mapped
Cvel_cont1	Control	590407.39	499612.65	435,130.77 (87.09 %)
Cvel_cont2	Control	602350.18	593301.55	450,098.77 (74.18 %)
Cvel_cont3	Control	539187.31	530589.42	466,393.73 (87.51 %)
	Subtotal	165,094.88	162,350.36	133,958.97 (82.51 %)
Cvel_mer1	Mercury	475722.8	467895.2	408,397.57 (87.28 %)
Cvel_mer2	Mercury	532108.78	523476.04	460,657.32 (87.23 %)
Cvel_mer3	Mercury	712047.9	642513.04	458,151.1 (66.52 %)
	Subtotal	147,903.237	145,388.428	126,523.540 (87.02 %)
	Total	312,997.725	307,738.790	

Data base	Number of Unigenes	Percentage (%)
Annotated in NRR	11173	9.09
Annotated in UniProt_blast	3639	2.96
Annotated in UniProt_blasts	16625	13.53
Annotated in PFAM	2854	2.32
Annotated in CryptoDB_blastX	38117	31.02
Annotated in CryptoDB_blastp	8806	7.17
InterPro	68713	56.36
Annotated in GO	10005	0.82
Annotated in at least one Database	52388	42.56
TrnIM4M	1283	0.05
SignalP	920	0.75
Total Unigenes	123274	100



ID	Description
GO:0045328	Cytochrome P450
GO:0030687	glutathione synthase
GO:0004784	Superoxide dismutase
GO:0038382	Flavin reductase [NADH]
GO:0031379	NADH dehydrogenase (plastoquinone)
GO:0045652	Kynurenine 3-monooxygenase
GO:0004936	Catalase_peroxidase
GO:0008865	Cytochrome b
GO:0018541	Bifunctional P-450(NADH-P450) reductase
GO:0004032	Aldehyde reductase
GO:1202334	Glutathione S-transferase
GO:0018715	UDP-glucosyltransferase
GO:0031072	Heat shock 70 kDa protein

CONCLUSION

- Deep Transcriptome analyses was done for *C. velia*
- Differential expression of various genes was observed under Hg stress in *C. velia*.

REFERENCES

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FUTURE DIRECTIONS

- ❖ Deciphering the molecular mechanism of *C. velia* causing the tolerance for Hg at higher concentration.
- ❖ The study can be focused on the de-toxication pathways genes used by *C. velia* and compared with other related organism important to humans, like *Plasmodium spp.* which causes malaria.

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