

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

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## 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*.

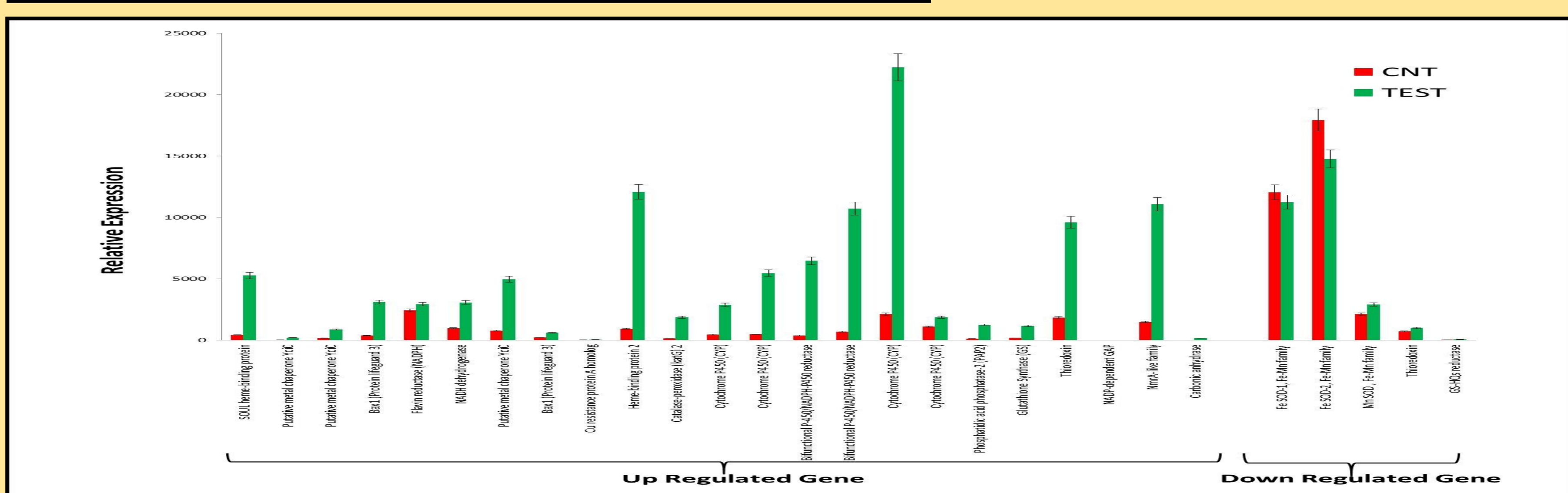
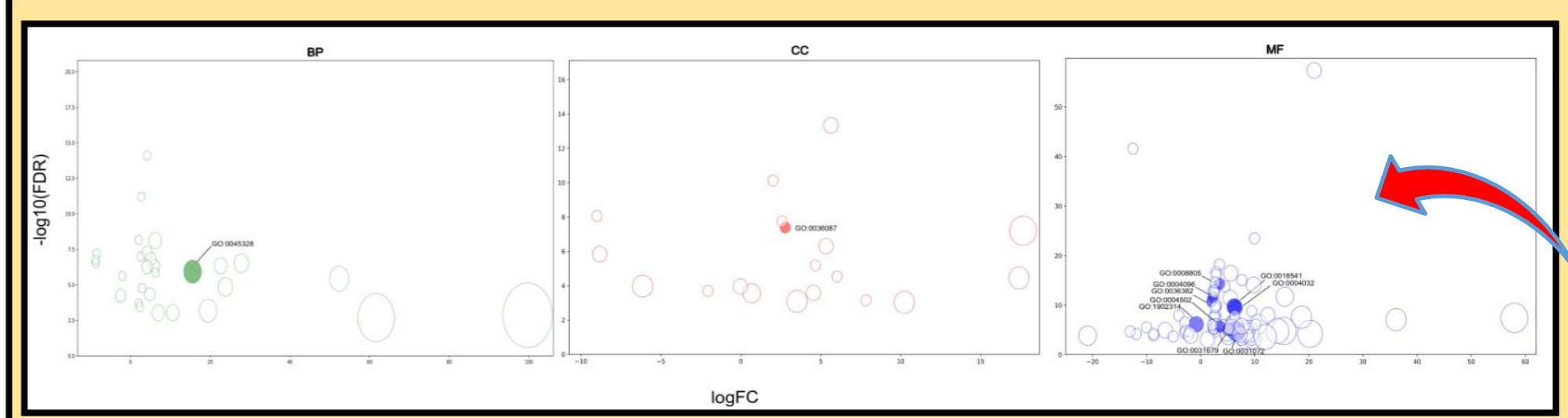
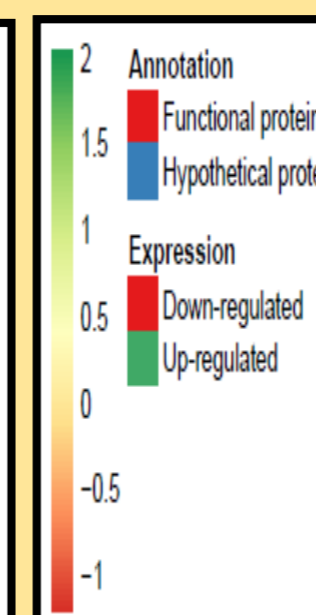
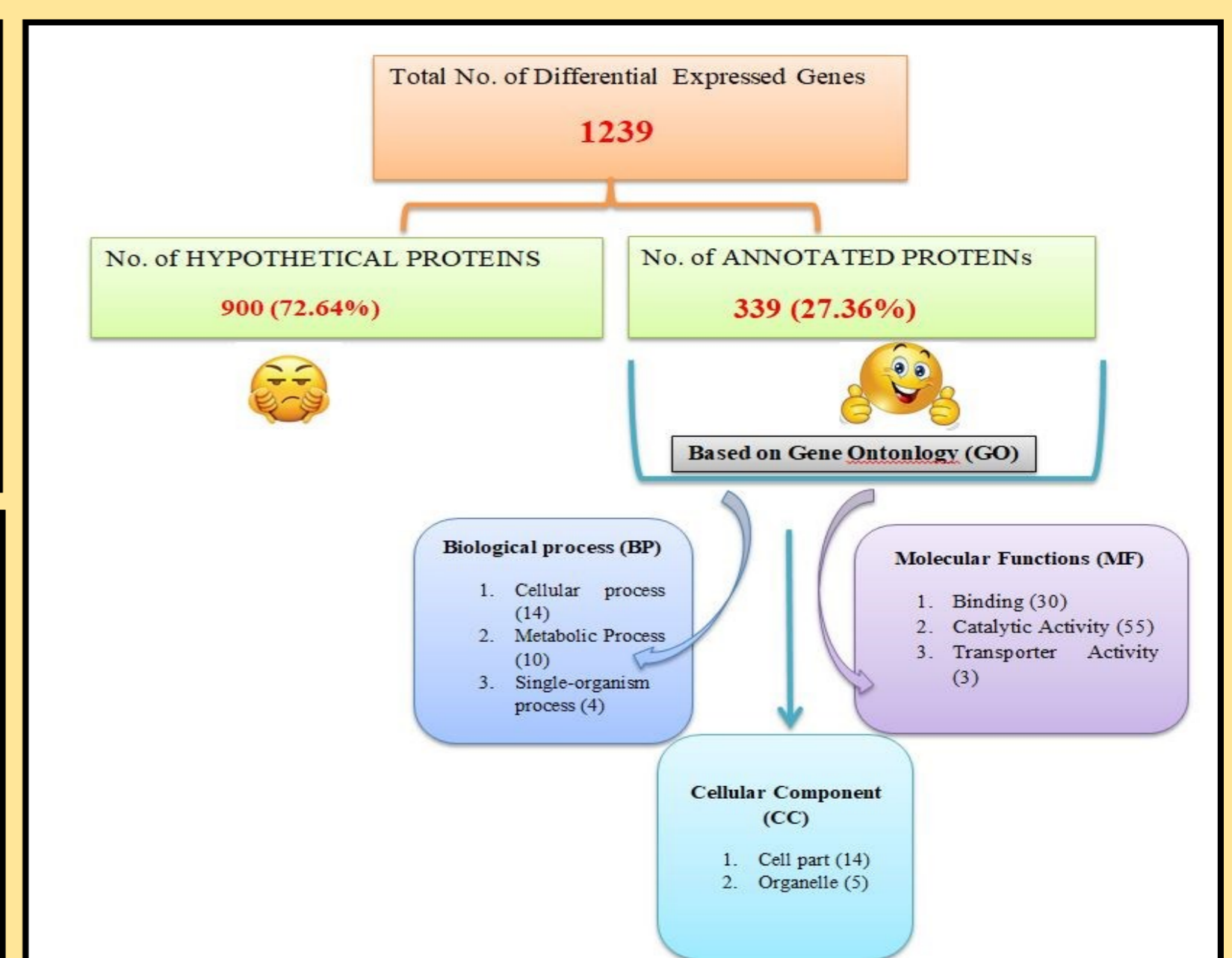
## Methods

- 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	509407.39	499612.65	435,130,47 (87.09 %)
Cvel_cont2	Control	602350.18	593301.55	440,098,77 (74.18 %)
Cvel_cont3	Control	539187.31	530589.42	464,339,73 (87.51 %)
	<b>Subtotal</b>	<b>165,094488</b>	<b>162,350362</b>	<b>133,956,897 (82.51 %)</b>
Cvel_mer1	Mercury	475722.8	467895.2	408,397,57 (87.28 %)
Cvel_mer2	Mercury	532104.78	523476.04	456,650,32 (87.23 %)
Cvel_mer3	Mercury	47120.479	462513.04	400,187,51 (86.52 %)
	<b>Subtotal</b>	<b>147,903237</b>	<b>145,388428</b>	<b>126,523,540 (87.02 %)</b>
	<b>total</b>	<b>312,997725</b>	<b>307,738790</b>	

Data base	Number of Unigenes	Percentage (%)
Annotated in NR	11173	9.09
Annotated in UniProt_blastp	3639	2.96
Annotated in UniProt_blastx	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
Annotated in GO	1005	0.82
Annotated in at least one Database	52388	42.36
TmHMM	1283	1.05
SignalP	920	0.75
<b>Total Unigenes</b>	<b>122874</b>	<b>100</b>



ID	Description
GO:0005118	Cytoplasm
GO:0005197	Cytoplasmic Part
GO:0005977	glutathione synthase
GO:0004784	Superoxide dismutase
GO:0003632	Flavin reductase (NADH)
GO:00031679	NADH dehydrogenase (plastoquinone)
GO:0004502	Kynurenine 3-monooxygenase
GO:0004096	Catalase_peroxidase
GO:0008805	Cytochrome b
GO:0018541	Bifunctional P-450/NADPH-P450 reductase
GO:0004032	Aldose reductase
GO:1902214	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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- Chen, T., Li, F., & Chen, B.-S. (2009). Cross-talks of sensory transcription networks in response to various environmental stresses. *Interdisciplinary Sciences: Computational Life Sciences*, 1(1), 46–54.

## 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.

## ACKNOWLEDGEMENTS

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