Quantitative analysis of oyster larval proteome provides new insights into the effects of multiple climate change stressors

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Outline
The metamorphosis of planktonic larvae of the Pacific oyster (Crassostrea gigas) underpins their complex life-history strategy by switching on the molecular machinery required for sessile life and building calcite shells. The use of quantitative proteomics in conjunction with the annotated genome of the C. gigas has allowed us to construct a detailed proteomic profile of oyster larvae under multiple climate change stressors: decreased pH (pH 7.4), increased temperature (30°C), and reduced salinity (15 psu), which enabled us to make predictions about the differential susceptibility of molecular pathways and their importance in determining an individual’s physiological response to stress. In this study, we investigated multiple stressors on the Pacific oyster (C. gigas) as a model to address the following questions: How does the larval proteome respond to multiple stressors? Do multiple stressors act independently or synergistically on the proteome?

Methods
Experimental Design: The fertilized embryos were raised under different climate change stressor conditions in 50 L plastic culture tanks with biological replicates iTRAQ labeling: Proteomics samples were collected from the pediveliger larvae from each treatment were digested, desalted prior to 8-plex iTRAQ labeling LC MS/MS analysis and protein identification: The SCX fractionated peptides were analyzed using LTQ-Orbitrap Velos. Protein identification was carried out using Sequest HT search algorithm against 27900 C. gigas annotated protein sequences Metabolic pathway analysis: The differentially expressed proteins were subjected to protein-protein interaction analysis using Cytoscape 3.0 ClueGO to identify pathways contributing to oyster stress and resilience

Results
1300 proteins
Hierarchical clustering shows down-regulation of P, SP and TP and up-regulation of TS and TSP treatments

Conclusion
The proteome of C. gigas larvae from Yellow Sea show phenotypic plasticity to survive multiple climate stressors, but with physiological costs

Proteomics cum bioinformatics analysis revealed that multiple stress impair protein processing, cell signaling, energy production, growth and development and induces amino acid, fatty acid and nucleotide metabolism as an alternative energy sources to compensate the energy requirements during multiple stresses

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