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A systems-level study of the transcriptional changes of Dehalococcoides metabolism

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Islam, Ahsan, Elizabeth A Edwards, and Radhakrishnan Mahadevan. 2011. “A Systems-level Study of the Transcriptional Changes of Dehalococcoides Metabolism”. Loughborough University. https://hdl.handle.net/2134/13259099.v1.

New Insights into *Dehalococcoides* Metabolism from an Integrated Metabolic Transcriptomics Study

BioZone
Centre for Applied & Environmental Bioengineering Research

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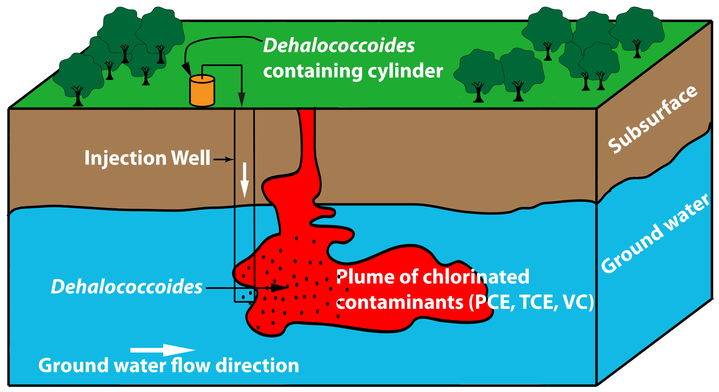
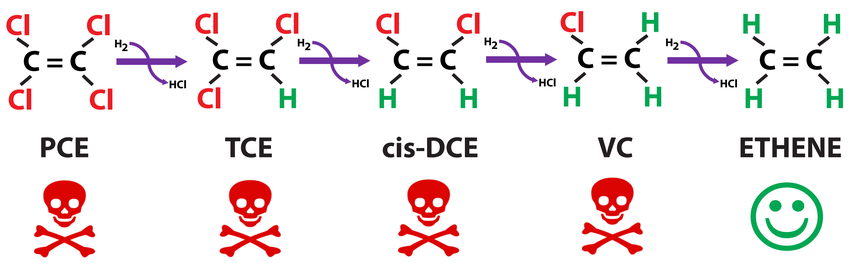
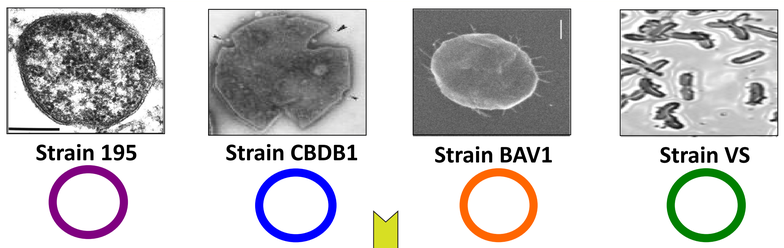
Bioremediation and *Dehalococcoides*

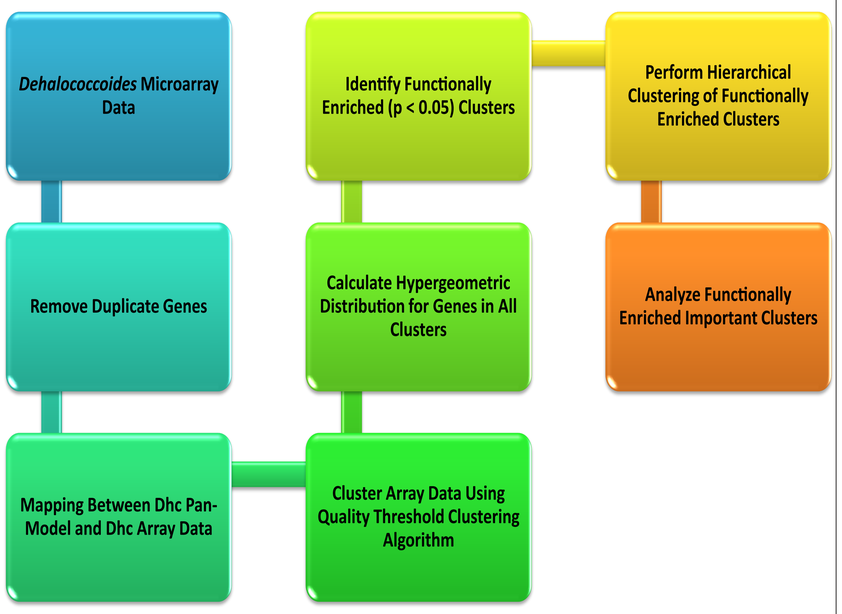




Dehalococcoides Metabolic Model

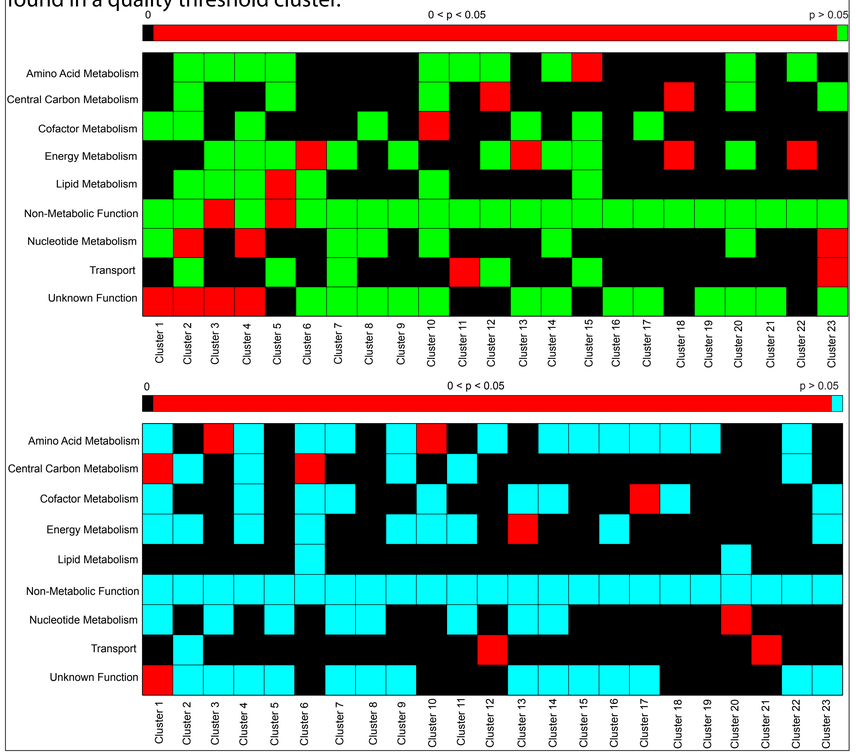


Data Analysis Work Flow

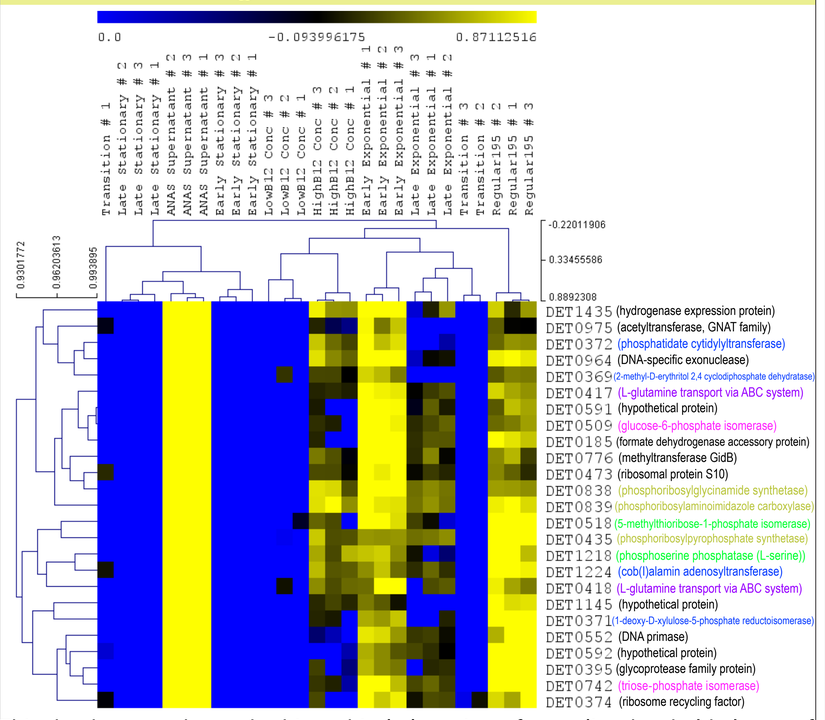


Clusters of Strain195 and Strain KB1

The top and bottom heat maps show functionally enriched ($p < 0.05$) clusters of strain 195 and strain KB1, respectively. Functional enrichment is determined by calculating the hypergeometric distribution of genes from each model subsystem or functional category found in a quality threshold cluster.

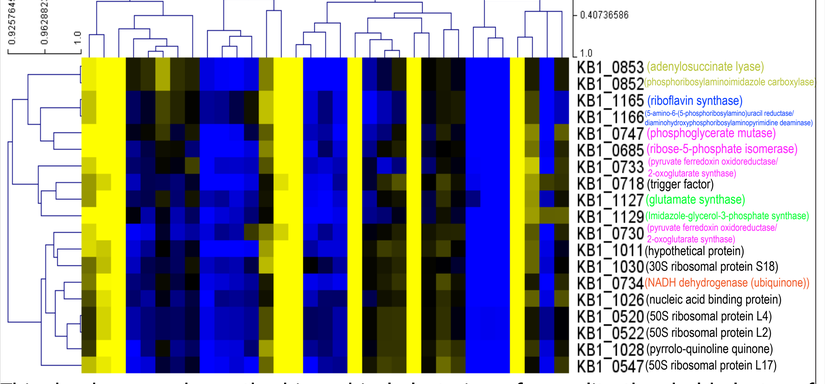


Dendrogram of Strain 195 Cluster 2



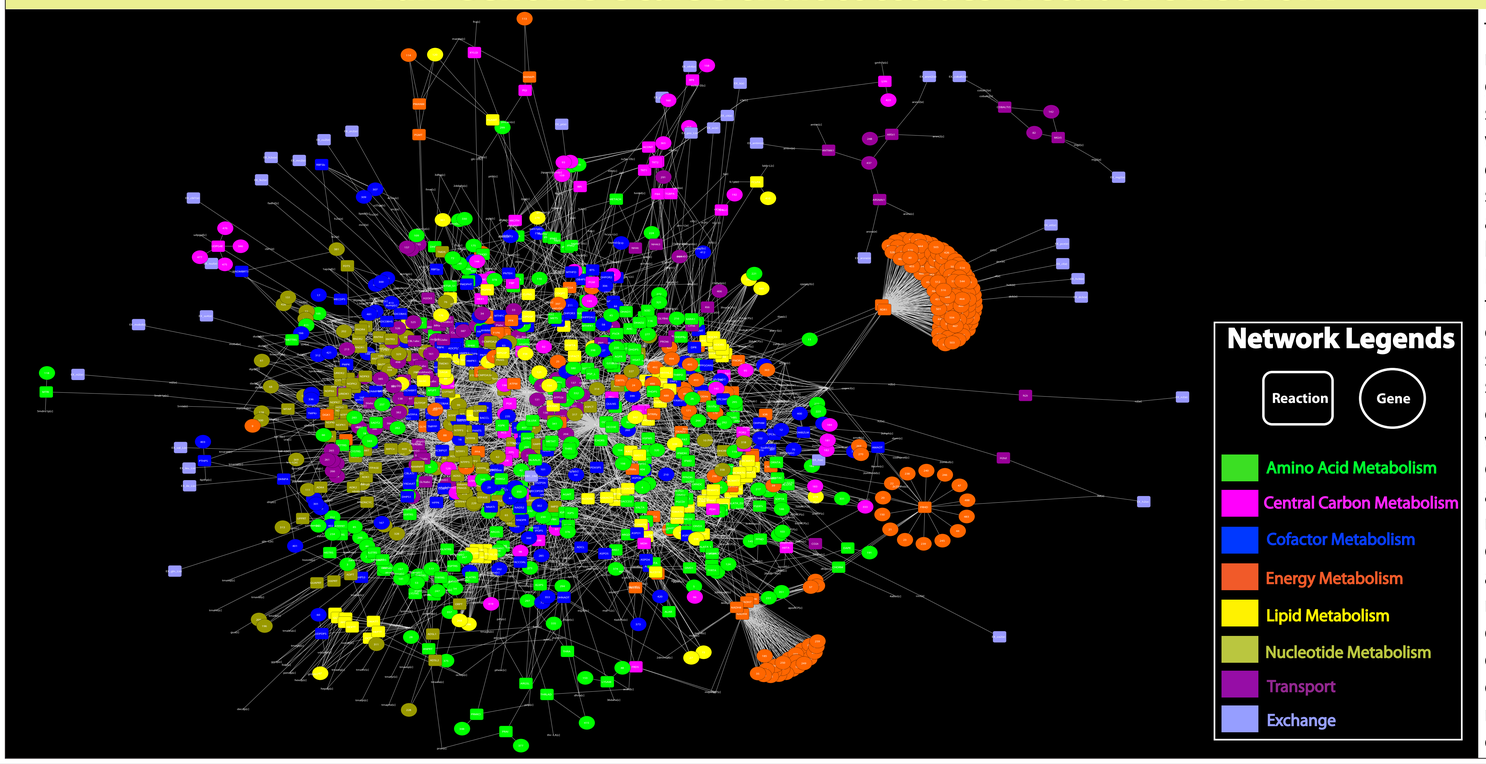
This dendrogram shows the hierarchical clustering of a quality threshold cluster of strain 195 genes. The cluster is functionally enriched with genes from nucleotide metabolism and unknown proteins as determined by hypergeometric distribution analysis of the quality threshold clusters. Annotations are color coded according to the model subsystems as depicted in *Dehalococcoides* metabolic network.

Dendrogram of Strain KB1 Cluster 1



This dendrogram shows the hierarchical clustering of a quality threshold cluster of strain KB1 genes. The cluster is functionally enriched with genes from central carbon metabolism and unknown proteins as determined by hypergeometric distribution analysis of the quality threshold clusters. Annotations are color coded according to the model subsystems as depicted in *Dehalococcoides* metabolic network.

Pan-Genome-Scale *Dehalococcoides* Metabolic Network



This cytoscape network represents the pan-genome-scale reconstructed metabolic network of *Dehalococcoides*. Genes are represented by circles and reactions are represented by round rectangles. Both genes and reactions are categorized according to the model subsystems and represented by different colors. Edges in the network are depicting gene-protein-reaction associations. Genes and reactions involved in energy metabolism such as, reductive dehalogenases, ferrodoxin hydrogenases, and NADH dehydrogenases are clustered together as represented by orange color.

Conclusions

1. Strain 195 seems to transport L-glutamine from the medium as L-glutamine transporters are upregulated during early exponential growth phase and in the autoclaved mixed culture (ANAS) supernatant experiments.

2. All genes in cluster 2 of strain 195 are upregulated with addition of autoclaved mixed culture (ANAS) supernatant.

3. Metabolism of riboflavin - a biomass precursor - plays important role in strain KB1 metabolism.

4. Genes involved in ribose metabolism including riboflavin synthesis, purine metabolism, and pentose phosphate pathway in both strains are co-regulated.

References

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Acknowledgements

1. Genome Canada and Ontario Genomics Institute.
2. Ontario Graduate Scholarship.
3. SERDP, University of Toronto, Natural Sciences and Engineering Research Council (NSERC), Canada