Role of sulfate-reducing bacterial enzymes in the processing of hydrogen sulfide associated with gastrointestinal tract diseases

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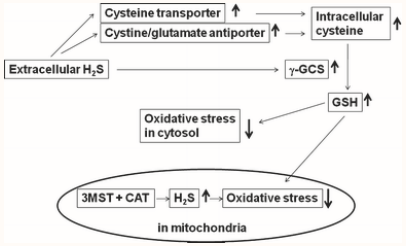
Abstract

In this project, we derived consensus sequences for use as primers in ***Polymerase Chain Reaction***, enabling further study of enzymes involved in the processing and production of ***hydrogen sulfide*** (H_2S) in the human gastrointestinal tract.

These enzymes are translated from three sources: mucosal epithelium cells, conserved ***sulfate-reducing bacteria*** (SRBs) and unique SRBs. The latter account for a small, but impactful percentage of the total 'gut flora' (bacteria that inhabit a persons gastrointestinal tract) and due to their ***aggregate and cooperate nature*** may play an important role in the control of disease in that region. (Kimura 2010) For this reason we used the database scouring tool BLAST to amass a personal library of bacteria that express our enzymes of interest.

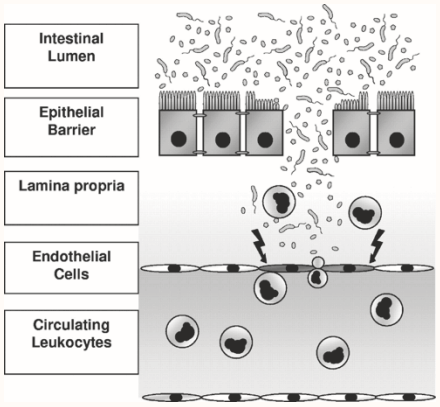


(Kimura)

Introduction

Oxidative stress has been directly linked to chronic irritation, which is correlated to cancer development. ***Reactive Oxygen Species (ROS)*** are regulated by many sources including processes that are catalyzed by enzymes expressed by SRBs. (Reuter 2010) All microbiomes are distinct: taxa are not conserved from one individual to the next.

SRB exist and operate cooperatively in aggregates, relying on each other to regulate ROS. Studies have shown distinct changes in microbiomes based on diet and other factors and linked them to disease. (Li 2008) (Lovely 2012) Our intention is to determine the microbial taxa that link those results, particularly the small subunit of the ***hydrogenase*** enzyme.



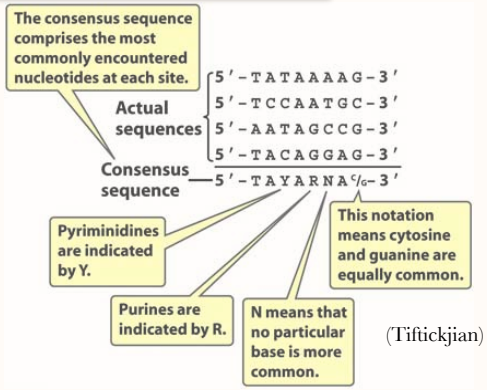
(Heidemann)

General coupled reaction catalyzed by hydrogenase (Vignais):

(1) $H_2 + A_{ox} \rightarrow 2H^+ + A_{red}$ (2) $2H^+ + D_{red} \rightarrow H_2 + D_{ox}$

Methods

1. Genomes of interest were found in genomic and metagenomic databases.
2. Corresponding sequences were then aligned using algorithms to ensure optimum consensus.
3. The derived consensus' were used to re-query the existing databases using BLAST

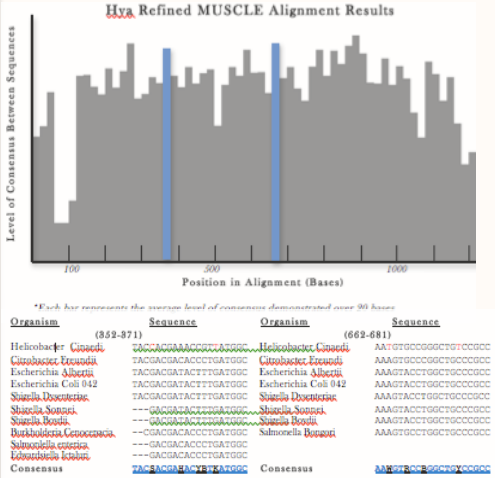


(Tiftickjian)

Genomic Databases:
- The Human Microbiome Project
- National Center for Biotechnology Information

Alignment Algorithms:
- ClustalW
- MUSCLE

Results/Discussion



- Varying the genomes compared allowed for optimum consensus
- Re-querying with BLAST using the generated consensus sequence greatly expanded the personal library
- Using BLAST resolved unconserved bases
- Hya Primers:

TACGACGATACTTTGATGGC
AAAGTACCTGGCTGCCCGCC

References

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