

Evidence supporting predicted  
metabolic pathways for  
*Vibrio cholerae*

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6/12/2006

# *Vibrio cholerae* causes cholera

- Untreated patients can be killed in 24 h.





# *Vibrio cholerae*



- Two distinctive lifestyles
  - a bacterium well adapted to aquatic habitats
  - a pathogen living in human intestine

# Objectives

- Predict the metabolic pathways for *V. cholerae*
- Validate the predicted pathways

# VchoCyc

<b>PGDB</b>	<b>Quantity</b>
Pathways	171
Compounds	656
Enzymes	639
Enzymatic Reactions	912
With enzymes in VchoCyc	654

How do we validate the  
predicted pathways in  
VchoCyc?

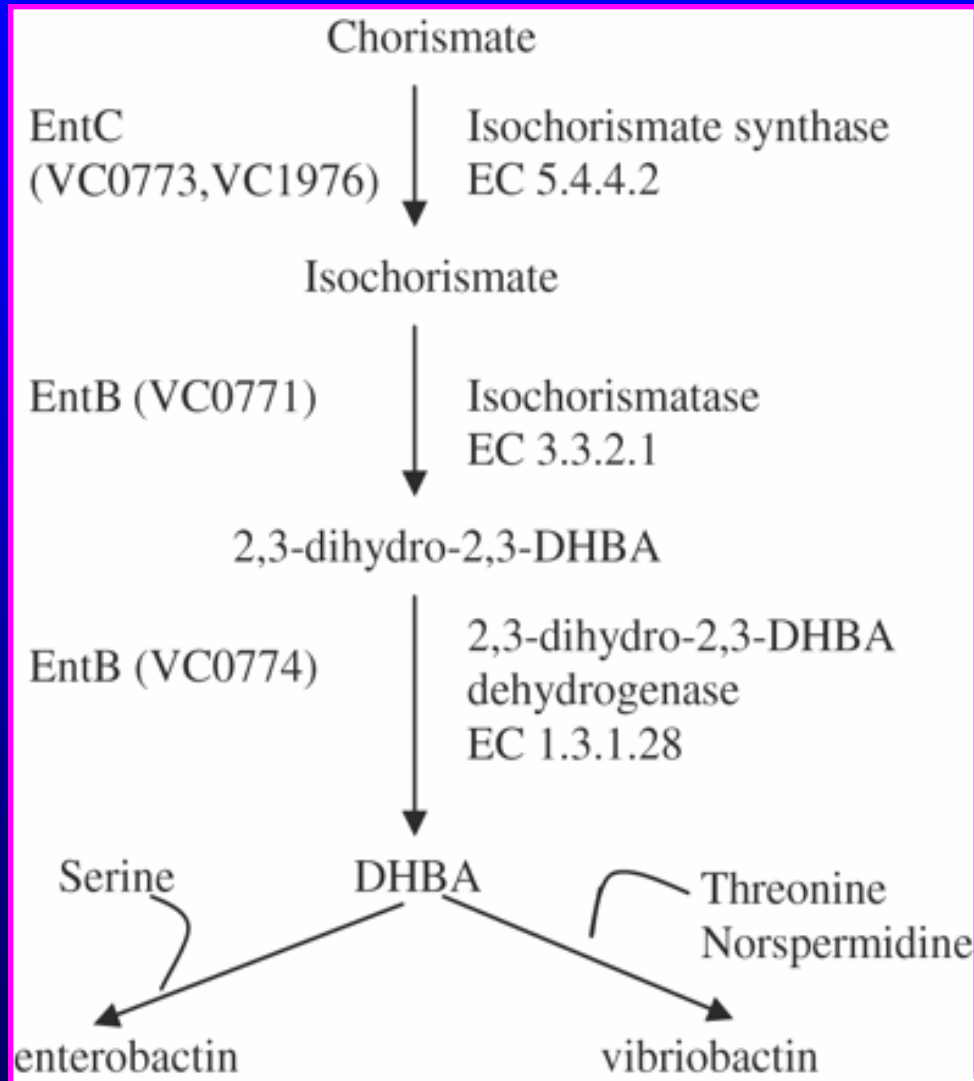
# Three types of evidence

- Previous literature
- Clinical tests
- Microarray expression data

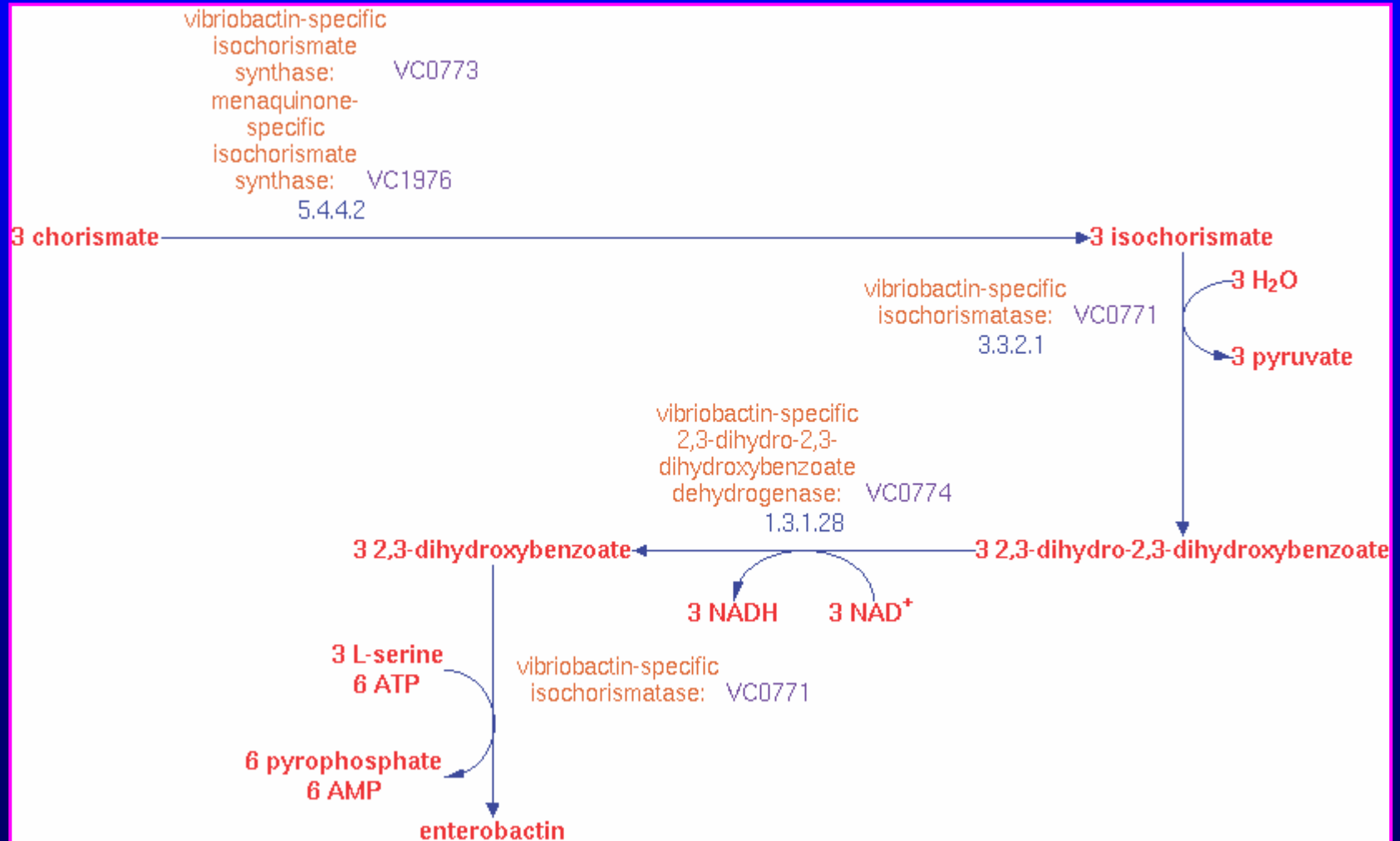


Using evidence from  
previous literature to  
validate predicted pathways

# Known biosynthetic pathways of enterobactin and vibriobactin



# Predicted biosynthetic pathways of enterobactin



Using evidence from clinical tests to validate predicted pathways

# Evaluating the pathways using clinical tests

- If a nutrient can support *V. cholerae* growth, the corresponding transporters and metabolic pathways/reactions should exist.
- Else, either no transporters or no metabolic pathways/reactions.

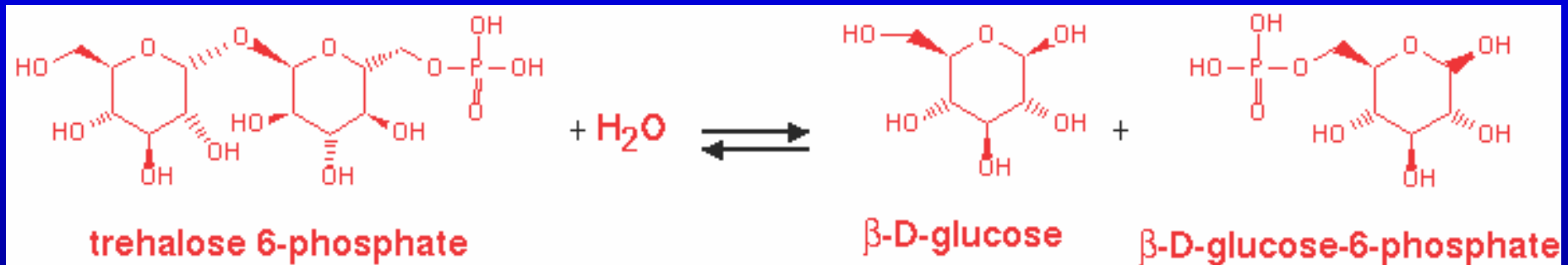
# Trehalose acid production clinical test for *V. cholerae*



If predicted pathway exists, we expect to find a transporter and enzymes for this test

# Trehalose, acid production (+)

EC 3.2.1.93



Found both enzyme and transporter: evidence supports the predicted pathway

# D-sorbitol acid production clinical test for *V.* *cholerae*

Clinical test for *V. cholerae* is negative for D-sorbitol acid production.

Should not find transporter and enzymes for this test

Neither a transporter nor a reaction was found.



# VchoCyc predictions are consistent with clinical tests

- 16 out of the total 17 clinical tests were consistent.
- 1 out of 17 was inconsistent: D-mannose with acid production (+).
  - the reaction to catalyze mannose was found but not the transporter for it.

Using evidence from  
microarray expression data  
to validate predicted  
pathways

When a “large” percentage of the reactions in a pathway are “active” simultaneously, we have expression evidence supporting this pathway.

# Microarray data

- Minimal media with Maltose or Lactate
- LB rich medium
- Patient stool samples

# Approach

Define the threshold of being "active"

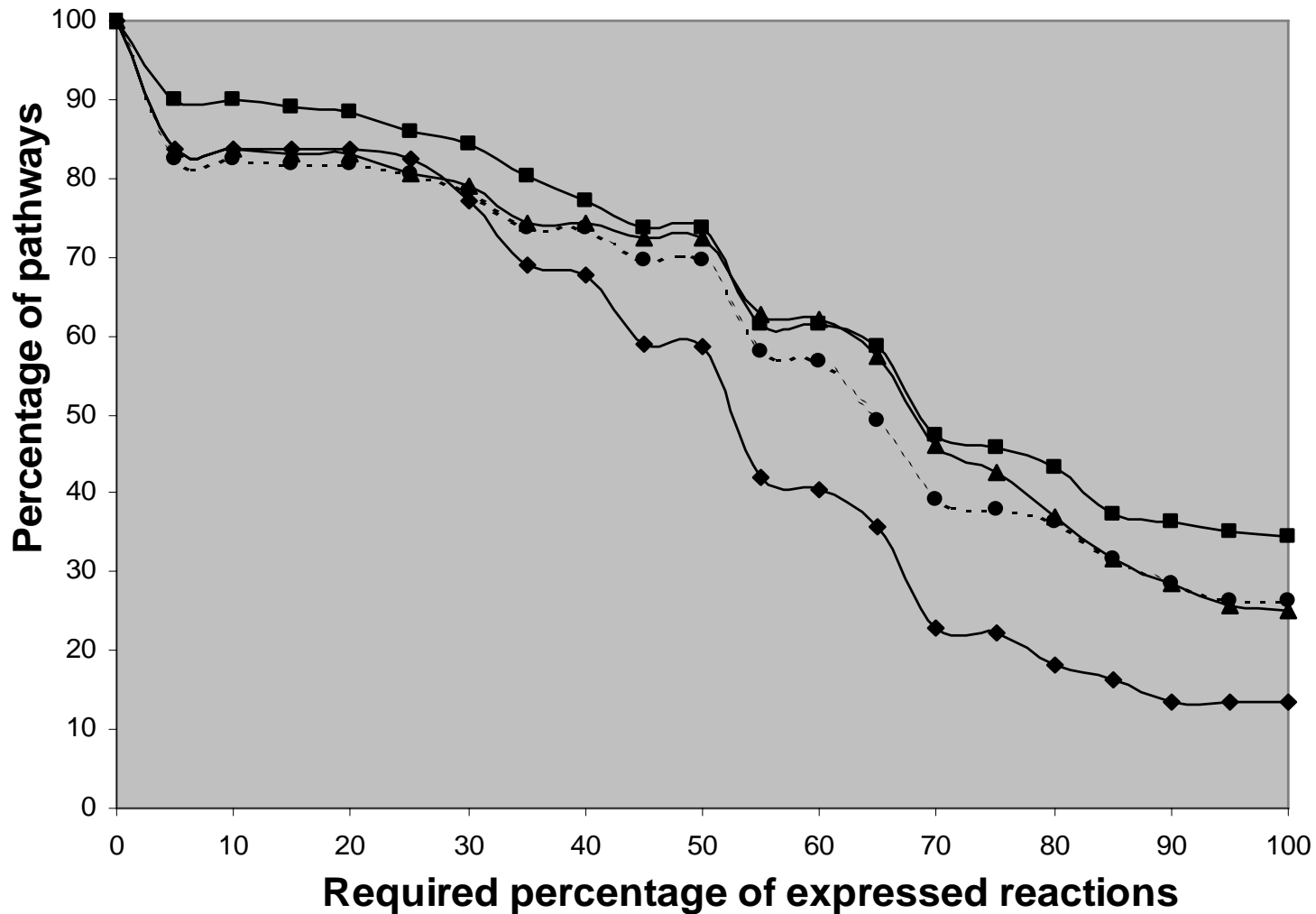


Determine the "active" genes



Calculate the percentage of "active" reactions for each pathways

For a given proportion of expressed reactions in a pathway, how much percent of pathways have supporting evidence?



# Example pathways with strong evidence from microarray data

Pathway name	Minimal medium + lactate	Minimal medium + maltose	LB	Patient
aspartate biosynthesis and degradation	100	100	100	100
fatty acid elongation -- saturated	100	100	100	100
fatty acid elongation -- unsaturated	100	100	100	100
glycine biosynthesis I	100	100	100	100
glycine cleavage	100	100	100	100

# Example pathways with no evidence from microarray data

Pathway name	Minimal medium + lactate	Minimal medium + maltose	LB	Patient
4-hydroxyproline degradation	0	0	0	0
Entner-Doudoroff pathway	0	0	0	0
L-idonate degradation	0	0	0	0
tyrosine biosynthesis II	0	0	0	0



# Different media provide evidence for different pathways

- In patient data, there is evidence for the amino acid biosynthesis pathways. Consistent with Merrell et al, 2002.
- In LB medium, there is evidence for degradation pathways of amino acids.

# Summary

- We constructed VchoCyc
- We used three sources of evidence to support the predicted pathways in VchoCyc
  - Previously known pathways in literature
  - Consistency with clinical tests
  - Consistency with microarray data

# Acknowledgements

- Peter Karp
- Pedro Romero
- Gary Schoolnik
- Alfred Spormann
- Ellen Baron
- Michelle Green
- Ron Caspi
- Nadia Dolganov
- Stan Cohen
- Michael Walker
- Stanford Graduate Fellowship