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Helicobacter pylori Homology Database: the case of tryptophan

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ABSTRACT

To study microorganisms it is necessary to evaluate phenotypes, which include biochemical and visual characteristic, and relation with its environment. Additionally the advance of sequencing technologies allow access to information about the organism's genome and how it is transcribed from multiple exemplars, that combined with its phenotype, results in a more complete picture of a microorganism. However, large quantities of genomes are being submitted every day at a pace challenging the capacities of analysis for those studying an organism. To date most searches for homology genes / proteins are done with the objective of find unknown function based on orthology or paraorthology to already known genes / proteins. This kind of searches are important to estimate the function of unknown proteins or genes. However many of the advantages of obtaining data from several clones from the same species are not being fully exploited at the moment, and if the researcher wants to take advantage of this homologies it need to rely on BLASTs or in a unanimous annotation of the genes of interested. The last is hardly achievable, leaving an tenuous and limited search through alignment. In order to show the advantages of genome / proteome information from several strains , we have developed a database using as model organism Helicobacter pylori. With the use of the database we have found that strains from H. pylori use tryptophan in proteins in a strain-specific way with potential changes in the function of membrane related and cation-binding proteins. We extended this analysis to other bacterial species adapting this database to their genome information, showing that it can be adapted to any microrganism of interest of which at least one complete genome is available in any genomic database together with several strains.

INTRODUCTION

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$$\mathrm{Ascorbate} + \mathrm{EDTA}\cdot\mathrm{Fe}^{3+} \rightarrow \mathrm{Oxidized\ ascorbate}$$

$$\mathrm{EDTA}\cdot\mathrm{Fe}^{2+} + \mathrm{H_2O_2} \rightarrow \mathrm{EDTA}\cdot\mathrm{Fe}^{3+} + \cdot\mathrm{OH} + \mathrm{OH}^{-}$$

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MATERIALS AND METHODS

Materials subsection one

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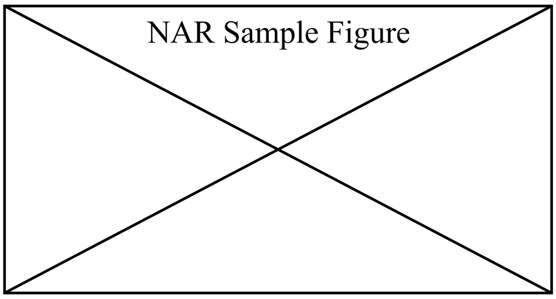

Figure 1. Caption for figure within column.

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$$\mathrm{LD}^r = \frac{\mathrm{LD}}{A_{\mathrm{iso}}} = 1.5S\left(3\cos^2\alpha_i - 1\right) \qquad (1)$$

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Materials subsection two

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$$\mathrm{LD}(t) = \sum_i a_i \exp\left(\frac{-t}{\tau_i}\right)$$

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RESULTS

Results subsection one

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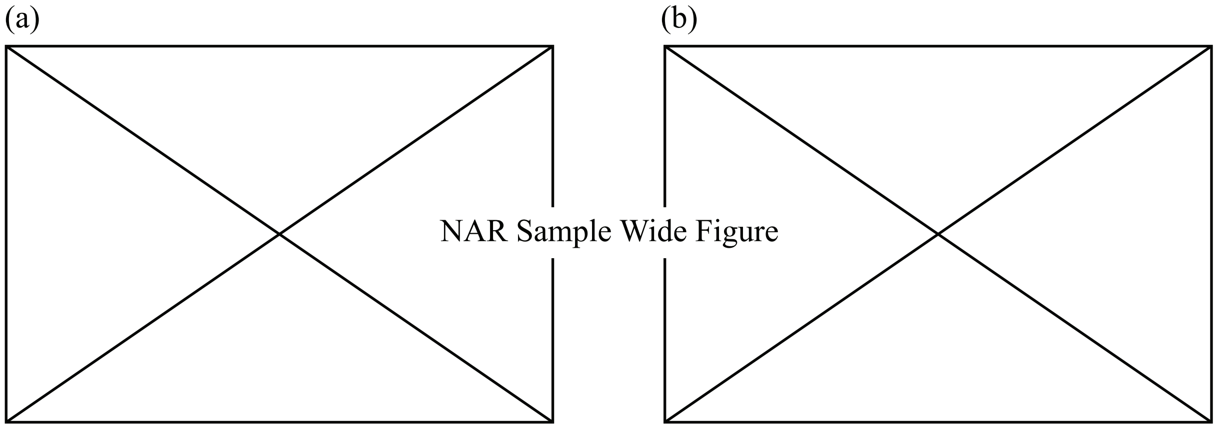

Figure 2. Caption for wide figure over two columns. **(a)** Left figure. **(b)** Right figure (see (a)).

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Results subsection two

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Text. Text (see Figure 2a).

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Table 1. This is a table caption

Col. head 1	Col. head 2 (%)	Col. head 3 (s^{-1})	Col. head 4 (%)	Col. head 5 (s^{-1})
Row 1	Row 1	Row 1	–	–
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Results subsection three

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DISCUSSION

Discussion subsection one

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Discussion subsection two

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Discussion subsection three

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CONCLUSION

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ACKNOWLEDGEMENTS

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Conflict of interest statement. None declared.

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