SEVENTH FRAMEWORK PROGRAMME

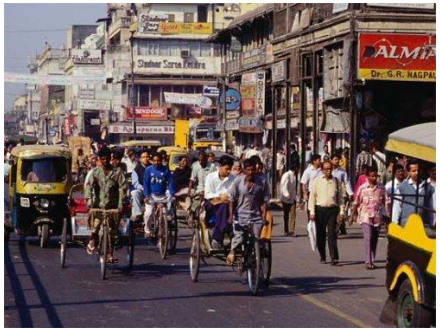
UNIVERSITY OF CAMBRIDGE

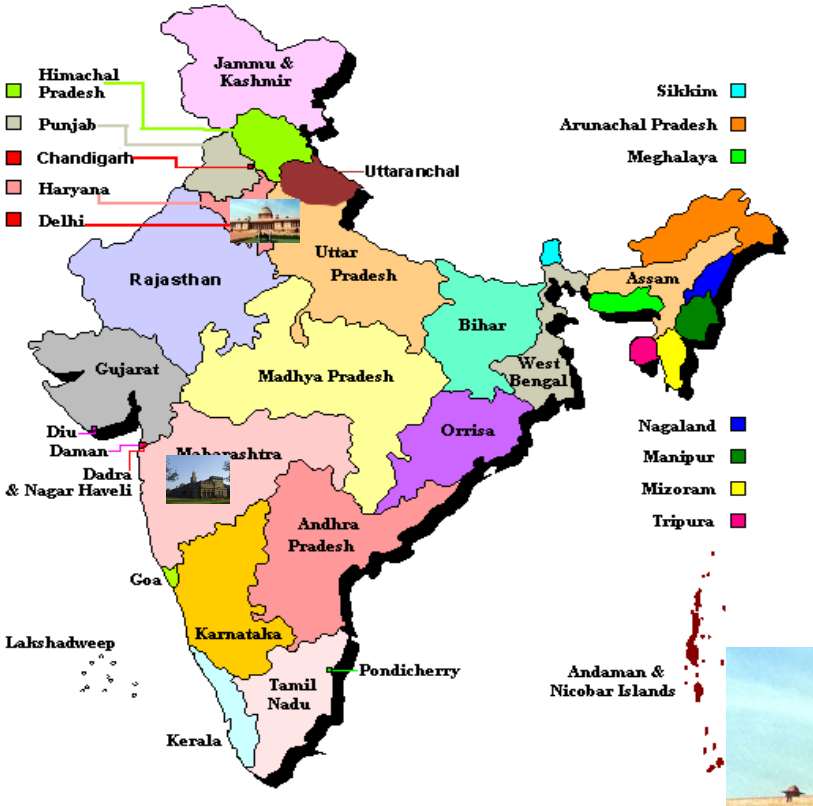
ESR: Priyanka Joshi
Supervisor: Prof. Michele Vendruscolo
Department of Chemistry
University of Cambridge, Cambridge, United Kingdom

IDPbyNMR

intrinsically disordered

Introduction





Integrated Masters in Biotechnology (Bachelors + Masters 5 Years programme)
(August 2006-May 2011)
Institute of Bioinformatics and Biotechnology
University of Pune
Pune, India

PhD in Chemistry (Structural Biology)
October 2011-
Department of Chemistry
Lensfield Road
Cambridge

Undergraduate thesis: Pathway Analysis of *Acinetobacter baylyi*
May 2008-May 2009
September 2009-March 2010

Identification of Potential Drug targets in *Acinetobacter baylyi* using Genomics approach
Genomic Medicine (The HUGO Journal)
P Joshi *et al.* (2009)
Volume 2, Numbers 3-4, 415-425,
DOI: 10.1007/s11568-009-9094-5

Journal of Bioinformatics and Sequence Analysis Vol. 1(3), pp. 041-045, October, 2009
Available online at http://www.academicjournals.org/jbsa

Full Length Research Paper

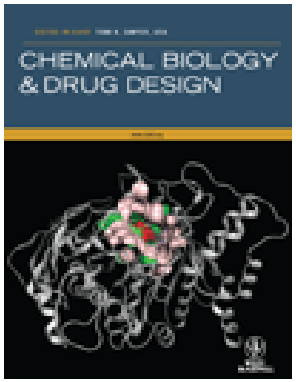
Choke point analysis of the metabolic pathways of *Acinetobacter baylyi*: A genomics approach to assess potential drug targets

Shailza Singh*, Priyanka Joshi and Balu Ananda Chopade

Institute of Bioinformatics and Biotechnology, University of Pune, Pune-411007, India.

Accepted 14 September, 2009

Numerous species of the genus *Acinetobacter* have been known to cause various nosocomial infections. An insight into the pathogenesis of *Acinetobacter baylyi* reveals that it is a potent organism



Chem Biol Drug Des 2011
Research Letter

doi: 10.1111/j.1747-0285.2011.01191.x

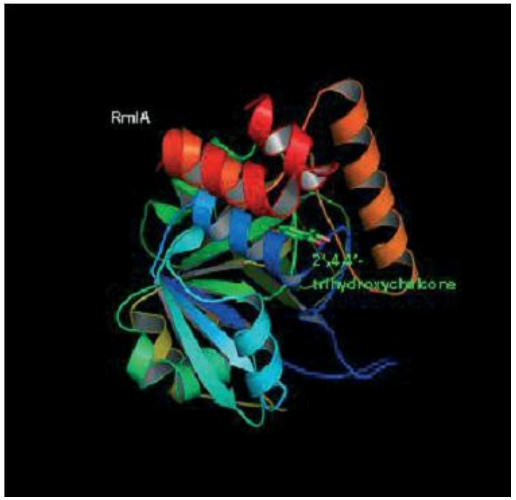
Pathway Analysis of *Acinetobacter baylyi*: A Combined Bioinformatic and Genomics Approach

Shailza Singh[1,*], Priyanka Joshi[2] and Balu A. Chopade[2]

[1]*National Centre for Cell Science, NCCS Complex, Pune University Campus, Pune 411007, India*
[2]*Institute of Bioinformatics and Biotechnology, University of Pune, Pune 411007, India*
**Corresponding author: Shailza Singh, shailza_iitd@yahoo.com; singhs@nccs.res.in*

Acinetobacter* spp., source of numerous nosocomial infections, deserves a close attention as various multidrug resistance strains are being discovered worldwide. *Acinetobacter baylyi* is chosen because of its high competence for natural transformation, and its ability to undergo direct homology-based recombination. An *in silico* comparative analysis of the metabolic pathways of the host *Homo sapiens* and the pathogen *Acinetobac-

Acinetobacter spp., these gamma-proteobacteria are classified in the order Pseudomonadales and in the family Moraxellaceae. They are ubiquitous in their distribution and are found in water, soil, living organisms, and even on human skin. These gram-negative bacteria can be distinguished from the other genera by the following characteristics: they are oxidase negative, catalase positive, strictly aerobic, and possess a strict respiratory metabolism; they are immobile with no flagella, do not form spores, and appear as cocci under the microscope or as short bacilli, often in pairs or assembled into longer chains. Their capability of utilizing a vast range of compounds as sources of carbon and energy gives them a high capacity for adaptation that explains why they can be found in diverse environments (1). Because of their robust metabolism, they are a potential source of use in biotechnological and environmental applications (2). This robust metabolism makes it easier for them to sustain themselves in varying environments at a variable pH and



Indian Academy of Sciences Fellowship
(2009, 2011)

Cloning and Bioinformatics analyses of Aquaporins from *Leishmania donovani*

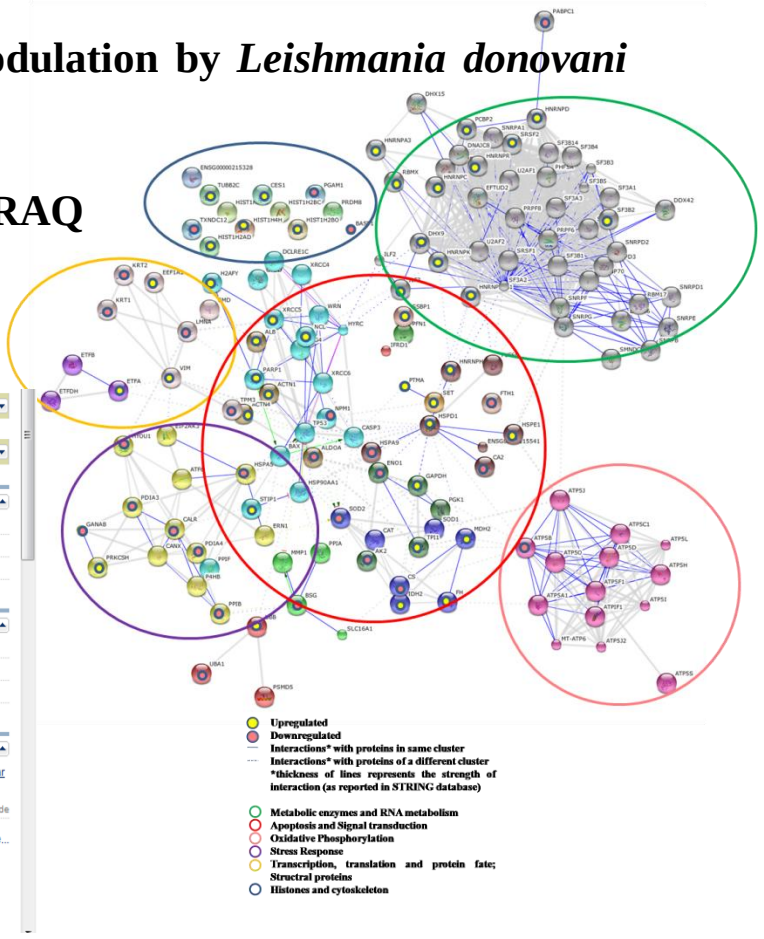
May-July 2009; Supervised by Prof. R. Madhubala, School of Life Sciences, Jawaharlal Nehru University, New Delhi, India

A proteomics approach to study the host proteome modulation by *Leishmania donovani* infection

May-September 2011

Proteins (post infection 12 hrs and 24 hrs) labelled using **iTRAQ**

Supervised by Prof. R. Madhubala, School of Life Sciences, Jawaharlal Nehru University, New Delhi, India



Visiting Research Student at EMBL, Heidelberg (June-August 2010)
Study of Structural Variations in the Yeast Genome
Supervised by Dr. Jan Korbel, European Molecular Biology Laboratory, Heidelberg, Germany

Motivation: Structural variations may contribute to genetic instability
Methodology: Next-Gen short sequence reads from bottleneck studies on yeast, Comparative genome analysis to identify Indels.

Entrepreneurial Research Concept
Research Based Business Concept: **Minicell Based Oral Insulin Delivery System**
Awarded a Prize of $4500 USD and funding from Department of Biotechnology, Government of India

ABLE Association of Biotechnology Led Enterprises
The collective face of the Indian Biotech Industry

MINULIN
NO MORE PRICKS...

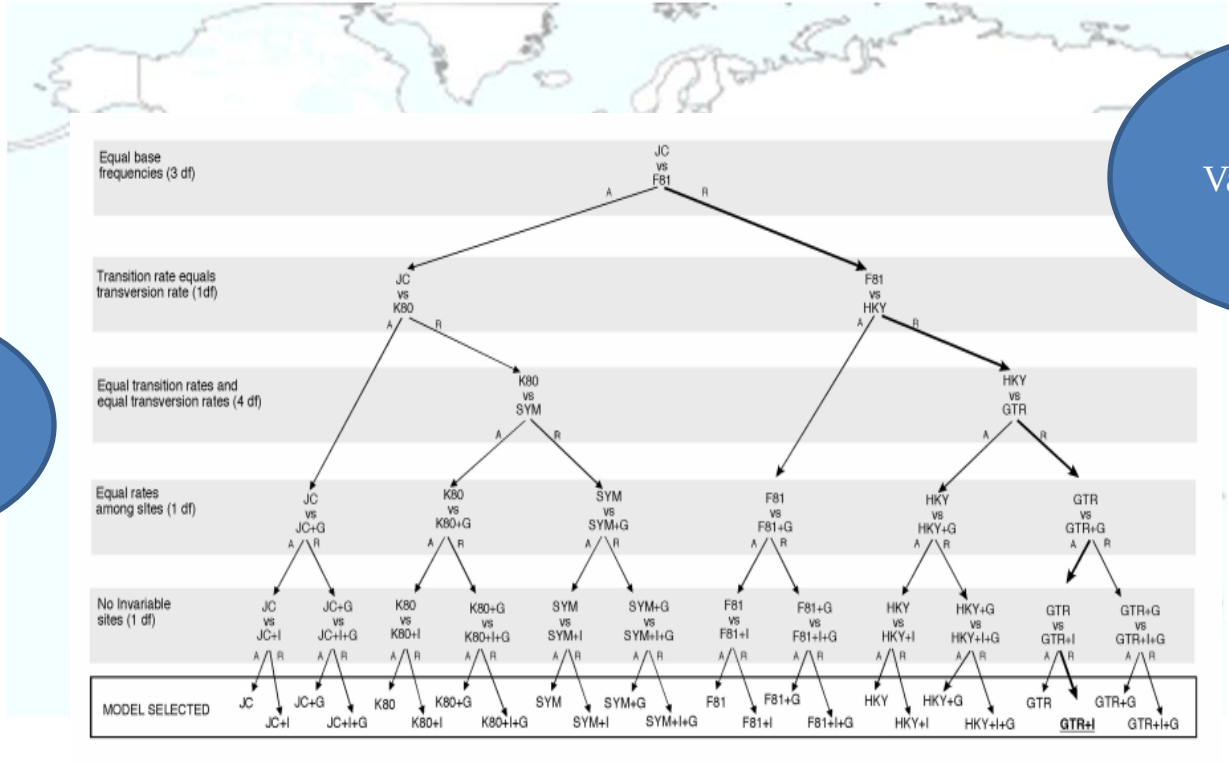
Masters Thesis
Jan-May 2011

Phylogenetic analysis of HIV-1 subtype C

Dr. Somdatta Sinha
Group Leader
Mathematical Modeling and Computational Biology Group
Centre for Cellular and Molecular Biology (CSIR), Hyderabad

Gene	no. of CTL epitopes	HLA
env	25	B44, B*3501, B35, A*01, B*0702, B7, A29, A3, A*2902, Cw8, Cw*0602, B27, B18, A11, A*0201, A82402, A*0205
gag	0	-
pol	0	-
tat	26	A*1103, A*2402, B*1402, B*1501, Cw*0802, B35, A3, A68, A*2902
rev	21	B*5701, B*5801, B*5703, B57, B63, A*0101, A1, A*0301, Cw*0501, Cw5, Cw8
nef	42	A*2501, A24, A*2402, A2, A*0201, A1, A11, A33, B51, B35, B52, B*1503, B*15, B8, B*0702, B*1801, B27, B*5801, B7, B*4001, B40, Cw4, Cw8
vpr	4	A2, A*2501, A*6801, A68, A*11, A*0201
vpu	2	Cw*1801, Cw18
vif	3	B57, B7, B*1503

Maximum Likelihood Methods



Selection pressure Variable Codon substitution model

IDPbyNMR

Early Stage Researcher (towards a PhD)
Start: October 2011

Rational drug design on IDPs using NMR-derived structural ensembles

- Developing computational methods to enable screening of compounds for IDPs (conformations derived from NMR measurements)

- Applications focused on alpha-synuclein, Abeta and tau.

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Thank you for your attention!