Perdeep K. Mehta, Ph.D.

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SUMMARY

Biotechnologist, biochemist, and programmer with 20 years bioinformatics experience and 28 publications. Research areas include molecular evolution, genomics, proteomics, infectious diseases, and cancer biology. Experience supervising a staff of 9 bioinformaticists in a hospital core facility. Strong teaching experience and presentation skills.

EDUCATION

Post-doctoral research fellow, European Molecular Biology Laboratory, Heidelberg, Germany, Biocomputing Division, January 1992 to December 1993. Developed a novel algorithm and implemented in C language for prediction of protein secondary structure from multiply aligned sequences.

Post-doctoral research fellow, University of Zurich, Switzerland, Institute of Biochemistry, January 1988 to December 1991. Finding evolutionary relationships among aminotransferases and related vitamin B_6-dependent enzymes.

Ph.D. in Biochemical Engineering & Biotechnology, Indian Institute of Technology, New Delhi, India, 1987.

M.S. in Biochemistry, N.D.R.I., University of Kurukshetra, India, 1980.

B.S. in Biology, Chemistry, and Physics, D. S. College, University of Kurukshetra, India, 1978.

SKILLS

Teaching: Biochemistry at undergrad level. Bioinformatics software to about 100 researchers annually for 11 years.

Programming: C, Perl, PHP, CGI, HTML, and XML.

PROFESSIONAL PROFICIENCY

Co-founder, President, and Research Scientist, Digital Genomics LLC, September 2013 to present. Provide customized bioinformatics support to analyze Affymetrix microarrays for expression, genotyping, drug-metabolism, and next generation sequencing data. Major areas of service include;

- Detect differentially expressed genes and involved pathways.
- Whole-genome *de novo* sequencing and re-sequencing.
- Identify genomic sequence variants like, SNPs, insertion-deletions (INDELs), and chromosomal copy number (CNVs).
- ChIP-Seq data peaks analysis.
- Whole transcriptome sequencing.
- Small RNA profiling and discovery.
- Quantitative proteomics using MaxQuant and protein homology modeling.
- Structure-function analysis of genes and gene products.
- Develop customized bioinformatics tools.

Bioinformatics research scientist, St. Jude Children's Research Hospital, Research Informatics, Information Sciences, April 2006 to November 2012. Provided bioinformatics support of in-house software suites, tools, assisted hospital researchers with analysis, and gave public presentations. Major projects have included;

- Analyzing Illumina short reads and developing tools to find retroviral integration sites in the rodent and primate genomes and their functional role for several groups in Hematology testing gene therapy vectors.
- Providing support for bioinformatics software suites, like CLC Bio Main and Genomics Workbench, DNA Star Lasergene, Vector NTI, and evaluated new bioinformatics tools, next gen sequencing short read aligners, such as BFAST, BWA, and CLC Bio.
- Analyzing and training in quantitative proteomics using MaxQuant, for Infectious Disease faculty, and taught Proteomics core staff to use MaxQuant for other clients.
- Developed algorithm and build web applications to support Proteomics core group and their Mass spectrum analysis users.
- Build a web application for homology modeling for Structural Biology.
- Provided computational, technical, and analysis support for St. Jude's first large-scale bird flu genome study. A total of 2,196 AIV genes were sequenced, assembled, and deposited to Genbank.

Bioinformatics group leader, St. Jude Children's Research Hospital, Hartwell Center for Bioinformatics and Biotechnology, March 2001 to March 2006. Managed a group of nine scientists in bioinformatics core, helped assign research projects, plan group budget, review manuscripts, recruit new staff, gave public presentations, and assisted hospital faculty and staff with analysis. Lead projects have included;

- Customizing computational support to researchers, e.g. Perl scripting to automate multiple batch Blast searches and identification of homologs among hundreds of sequences, i.e. Human-Mouse Ortholog database for gene expression profiling studies.
- PAARsnp database curation and annotation; therapy-related acute myloid leukemia; acute megakaryoblastic leukemia; and web interfaces to family profile analysis and protein secondary structure prediction programs.
- Developing meta-databases for current annotation of microarray data (cDNA & Affymetrix), Human-Mouse orthologs, and Gene Ontology.
- Provide training and teaching of several bioinformatics software suites.

Bioinformatics associate research scientist, St. Jude Children's Research Hospital, Hartwell Center for Bioinformatics and Biotechnology, July 2000 to February 2001.

- Developed tools to detect single nucleotide polymorphisms (SNPs) in the human drug metabolizing genes.
- Structure-function analysis of genes and gene products.
- Provided support and help on new research tools, such as Sequence Retrieval System, GeneCards, and Family Profile Analysis etc.

Application support specialist, St. Jude Children's Research Hospital, Hartwell Center for Bioinformatics and Biotechnology, October 1999 to June 2000.

Projects with St. Jude researchers include structure-function analysis of genes and gene products that are involved in catastrophic diseases among children.

Research Scientist and lecturer, University of Zurich, Switzerland, Institute of Biochemistry, January 1994 to June 1999.

Analyzed remote/distant sequence relationships among proteins by implementing "Profile analysis" in a novel algorithm as family profile analysis. (Project coordinator: Prof. Philipp Christen).

RESEARCH EXPERIENCE

Bioinformatics

Developed application and custom programs in standard ANSI C (protein secondary structure prediction, pattern discrimination and family profile analysis), extension of knowledge in C++, Perl (HCNetDat, BGEM annotation pipelines, Viral insertion sites mapping), PHP (Web pages for QVviewer, PDZ domain proteins, and MASCOT search results), shell programming and programming constructs, html documents, server-side programming with CGI/Perl scripts.

Advanced biological database mining and search experience (Advanced Blast series and FastA, SRS, Entrez, ExPASy and several other tools on the web servers), maintained and used databases (GenEMBL, UniProt) in GCG software suite, EMBOSS package, and in-depth knowledge of several others, like 3D_ALI, DSSP, HSSP, PDB, SCOP, PRODOM, CATH, and InterPro. Analyzed gene and protein sequences (extensive experience with GCG package, DNA STAR's Lasergene, Vector NTI, CLC Bio Main & Genomics, EMBOSS, Sequence Retrieval System, and services of NCBI and EBI), phylogenetic programs (PHYLIP, ClustalW, ProfileWeight), and familiarity also with several molecular modeling packages (Biosym/MSI, Insight II, Homology, and 3D-profile).

Extensive use and sound knowledge of UNIX, LINUX Cluster, and Windows operating systems.

Expert on the manifold families of pyridoxal-5'-phosphate-dependent enzymes (listed in ExPASy, an EMB node in Switzerland; by Amos Bairoch), $(\beta)_8$-barrel enzymes, γ-trefoil proteins, globins, and hsp70/actin/hexose kinase ATPase domain etc.

Laboratory work

Extensive experience of various experimental techniques in enzymology, protein chemistry (purification, characterization, sequencing and kinetics), and analytical biochemistry (analytical centrifugation, electrophoresis, spectrophotometry, column chromatography, reverse-phase HPLC). Experienced in biotechnology research (lab scale bioreactors and immobilized enzyme reactors).

AWARDS AND HONORS

- Awarded Swiss National Science Foundation fellowship to work at the European Molecular Biology Laboratory in Heidelberg, Germany, January 1992 to December 1993.
- Post-doctoral research scholarship of SNSF, Switzerland, January 1988 to December 1988.
- Senior research assistantship from the Dept. of Non-conventional Energy Resources, India, October 1984 to July 1987.
- Research scholarship from the Department of Science and Technology, India, January 1981 to September 1984.

PUBLICATIONS

Refereed journals

- Zhao H., **Mehta P.K.**, Persons D.A. (2013). Gene Therapy for Canine Leukocyte Adhesion Deficiency with Lentiviral Vectors". Blood (in preparation).
- Greene M.R., Lockey T., **Mehta P.K.**, Kim Y-S., Eldridge P.W., Gray J.T., Sorrentino B.P. (2012). "Transduction of human CD34+ repopulating cells with SIN-Lentiviral vector for SCID-X1 produced at clinical scale by a stable cell line". Hum Gene Ther Methods. 23(5), 297-308.
- Pemble C.W., **Mehta P.K.**, Mehra S., Li Z., Nourse A., Lee R.E., White S.W. (2010). Crystal structure of the 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase-dihydropteroate synthase bifunctional enzyme from Francisella tularensis. *PLoS One*. 2010 Nov 30; 5(11):e14165.
- Zhao H., Pestina T.I., Nasimuzzaman Md., **Mehta P.K.**, Hargrove P.W., Persons D.A. (2009). Amelioration of Murine β-thalassemia Through Drug Selection of Hematopoietic Stem Cells Transduced with a Lentiviral Vector Encoding both γ-Globin and MGMT Drug Resistance Gene. Blood, 4; 113(23), 5747-56.
- Finkelstein, D.B., Mukatira, S., **Mehta, P.K.**, Obenauer, J.C., Su, X., Webster, R.G., and Naeve, C.W. (2007). "Persistent Host Markers in Pandemic and H5N1 Influenza Viruses." J. Virol. 81(19), 10292-99.
- Magdaleno S., Jensen P., Brumwell C.L., Seal A., Lehman K., Asbury A., Cheung T., Cornelius T., Batten D.M., Eden C., Norland S.M., Rice D.S., Dosooye N., Shakya S., **Mehta P.K.**, Curran T., (2006). "BGEM: an *in situ* hybridation database of gene expression in the embryonic and adult mouse nervous system." PLoS Biol. 4 (4), 497-500.
- Obenauer J.C., Denson J., **Mehta P.K.**, Su X., Mukatira S., Finkelstein D.B., Xu X., Wang J., Ma J., Fan Y., Rakestraw K.M., Webster R.G., Hoffmann E., Krauss S., Zheng J., Zhang Z., Naeve C.W., (2006). "Large-Scale Sequence Analysis of Avian Influenza Isolates." Science, 311 (5767), 1576-1580.
- Blanco J.G., Dervieux T., Edick M.J., **Mehta P.K.**, Rubnitz J.E., Shurtleff S, Raimondi S.C., Behm F.G., Pui C.-H., and Relling M.V. (2001). "Molecular emergence of acute myeloid leukemia during treatment for acute lymphoblastic leukemia." Proc. Natl. Acad. Sci. 98(18): 10338-10343.
- Ma Z., Morris S.W., Valentine V., Martin L, Herbrick J.-A., Cui X., Bouman D., Li Y., **Mehta P.K.**, Nizetic D., Kaneko Y., Chan G.C.F., Chan L.C., Squire J., Scherer S.W., and Hitzler J.K.

(2001). “Fusion of two novel genes, RBM15 and MKL1, in the t(1;22)(p13;q13) of acute megakaryoblastic leukemia.” Nature Genetics 28: 220-221.

- Salzmann D., Christen P., **Mehta P.K.**, and Sandmeier E. (2000). “Rate of evolution of pyridoxal-5’-phosphate-dependent enzymes.” Biochem. Biophys. Res. Commun. 270: 576-580
- **Mehta P.K**., Argos P., Barbour A.D., and Christen P. (1999). "Recognizing very distant sequence relationships among proteins by family profile analysis." Proteins: Structure, Function, and Genetics. 35: 387-400.
- Tormay P., Wilting R., Lottspeich F., **Mehta P. K.**, Christen P., and Boeck A. (1998) "Bacterial selenocysteine synthase: Structural and functional properties." Eur. J. Biochem. 254: 655-661.
- **Mehta P.K.**, Heringa J., and Argos P. (1995). "A simple and fast approach to prediction of protein secondary structure from multiply aligned sequences with accuracy above 70%". Protein Sci. 4: 2517-25.
- Alexander F.W., Sandmeier E., **Mehta P.K.,** and Christen P. (1994). "Evolutionary relationships among pyridoxal-5'-phosphate-dependent enzymes. Regio-specific alpha, beta and gamma families". Eur. J. Biochem. 219: 953-60.
- **Mehta P.K**. and Christen P. (1994). "Homology of 1-aminocyclopropane-1-carboxylate synthase, 8-amino-7-oxononanoate synthase, 2-amino-6-caprolactam racemase, 2,2-dialkylglycine decarboxylase, glutamate-1-semialdehyde 2,1-aminomutase and isopenicillin-N-epimerase with aminotransferases". Biochem. Biophys. Res. Commun. 198: 138-43.
- **Mehta P.K.** and Christen P. (1993). "A comment on: 'Homology of the family of proteins to a new class of pyridoxal phosphate-dependent enzymes', by Christos Ouzounis and Chris Sander (1993) FEBS Lett. 322, 159-164." FEBS Lett. 330: 241-42.
- **Mehta P.K.,** Hale T.I., and Christen P. (1993). "Aminotransferases: demonstration of homology and division into evolutionary subgroups." Eur. J. Biochem. 214: 549-61.
- **Mehta P.K.** and Christen P. (1993). "Homology of pyridoxal 5'-phosphate-dependent aminotransferases with the *cobC* (cobalamin synthesis), *nifS* (nitrogen fixation), *pabC* (p-aminobenzoate synthesis) and *malY* (abolishing endogenous induction of the maltose system) gene products." Eur. J. Biochem. 211: 373-76.
- **Mehta P.K**., Mishra S., and Ghose T.K. (1991). "Methanol biosynthesis by covalently immobilized cells of *M. trichosporium*: batch and continuous studies." Biotechnol. Bioengg. 37: 551-56.
- **Mehta P.K**., Hale T.I., and Christen P. (1989). "Evolutionary relationships among aminotransferases. Tyrosine aminotransferase, histidinol-phosphate aminotransferase, and aspartate aminotransferase are homologous proteins." Eur. J. Biochem. 186: 249-53.
- Kochhar S., **Mehta P.K**., and Christen P. (1989). "Assay for aliphatic amino acid decarboxylases by high-performance liquid chromatography." Anal. Biochem. 179: 182-85.
- **Mehta P.K.**, Mishra S., and Ghose T.K. (1989). "Growth kinetics and methanol oxidation in M. trichosporium NCIB 11131." Biotechnol. Appl. Biochem. 11: 328-35.

- **Mehta P.K**., Mishra S., and Ghose T.K. (1987). "Methanol accumulation by resting cells of M. trichosporium." J. Gen. Microb. 33: 221-29.

Presentations

- Greene M.R., **Mehta P.K.**, Sorrentino B.P. (2012). Illumina platform sequencing provides adequate read lengths to map lentiviral vector insertion sites in human cells and uncovers both mis-mapped and false positive reads from traditional LAM-PCR and nrLAM-PCR products.
- Magdaleno S, Jensen P, Rice DS, Asbury A, Seal A, Lehman K, Cheung T, Dosooye N, **Mehta PK**, Curran T (2004) High Throughput gene expression mapping in the developing nervous system. Presented at Soc. Neurosci. Ann. Meeting, San Diego, CA, Oct. 23-28.
- **Mehta P.K**. and Christen P. (1996). "Family profile analysis: detection and evaluation of evolutionary relationships among protein families." In fourth internatl. conference on 'Intelligent systems for molecular biology' (ISMB96) June 12-15, St. Louis.
- **Mehta P.K.**, Heringa J., and Argos P. (1993). "Secondary structure predictions using residue exchange statistics in multiple sequence alignments." In Macromolecules, Genes, and Computers - Chapter III, Aug. 17-22, New Hampshire.
- **Mehta P.K.** and Christen P. (1992). "Division of aminotransferases into evolutionary subgroups", In Modern Enzymology: Problems and Trends, Sep. 9-13, St. Petersburg.
- **Mehta P.K.**, Hale T.I., and Christen P. (1991). "Evolutionary relationships among aminotransferases." In 15th Internatl. Congress Biochem., Aug. 4-8, Jerusalem.
- **Mehta P.K.** and Christen P. (1990). "Evolutionary relationships among pyridoxal phosphate-dependent enzymes." In 20th FEBS Meeting, Aug. 19-24, Budapest.
- **Mehta P.K.,** Hale T.I., and Christen P. (1989). "Evolutionary relationships among aminotransferases." In 21st Ann. Meeting Swiss Soc. Exptl. Biol., Experientia 45: A52.
- **Mehta P.K.**, Mishra S., and Ghose T.K. (1988). "Continuous methanol biosynthesis by covalently immobilized cells of M. trichosporium." In VIIIth Internatl. Biotechnology Symposium, July 17-22, Paris.

Reviews:

- Christen P, **Mehta PK**. (2001). "From cofactor to enzymes. The molecular evolution of pyridoxal-5'-phosphate-dependent enzymes." In Chem. Rec., 1, (Eds. H. Yamamoto and B. Johnson), pp 436-47.
- **Mehta PK** and Christen P (2000). "The molecular evolution of pyridoxal-5’-phosphate-dependent enzymes." Advances in Enzymology. 74: 129-184.
- Christen P, **Mehta PK**, and Sandmeier E. (1994). "Molecular evolution of pyridoxal 5'-phosphate-dependent enzymes. In Biochemistry of Vitamin B_6 & PQQ, (Eds. G. Marino, G. Sannia and F. Bossa), pp 9-13.
- **Mehta PK**, Hale TI, and Christen P (1991). "Evolutionary relationships among pyridoxal phosphate-dependent enzymes." In Enzymes Dependent on Pyridoxal Phosphate and other Carbonyl Compounds as Cofactors, (Eds. T. Fukui, H. Kagamiyama, K. Soda, and H. Wada), pp 35-42.

- Christen P, Jaussi R, Juretic N, **Mehta PK**, Hale TI, and Ziak M (1990). "Evolutionary and biosynthetic aspects of aspartate aminotransferase isoenzymes and other aminotransferases." Ann. N. Y. Acad. Sci. 585, (Ed. K. Dakshinamurti), pp 331-338.

REFERENCES
Provided upon request.