ANNEXURE-VII

UNIVERSITY GRANTS COMMISSION
NEW DELHI

FORMAT FOR PROGRESS REPORT ANNUAL/ MID-TERM/FINAL REVIEW UNDER SAP (CAS/DSA/DRS)

Name of the University	:	University of Delhi
Name of the Department	:	Department of Microbiology
Date of first approval with levelat inception	:	31-Oct-2012 at level DRS-I
Date of implementation ofcurrent phase as noted by the UGC	:	01-Apr-2012
Status(CAS/DSA/DRS with phase)	:	DRS-I
Period of Report	:	01-Apr-2012 to 31-Mar-2013

	NR	**R**	**Total**
Amount allocated for 5 years	Rs.32,25,000	Rs.34,50,000	Rs.66,75,000
Amount sanctioned during the year	Rs.30,00,000	Rs.7,50,000	Rs.37,50,000
Amount utilized during the year	0*	Rs.5,72,303	Rs.5,72,303*
Date of first sanction (Current phase)	30-Oct-2012		
Total grants received since inception	30.00 lakh	07.50 lakh	37.50 lakh

***Purchase order have been places for Equipment on 18-Mar-2013 & 28-Mar-2013, and expected to receive soon.**

Coordinator's Name	:	Prof.J.S.Virdi
Dy. Coordinator's Name:		Dr.Rajeev Kaul
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1. (a) Thrust Area(s) :

Identified since inception	**Ongoing**	**Modified to, if any, and when UGC approval reference no and date**
Industrial Enzymes Microbial Pathogenesis	Industrial Enzymes Microbial Pathogenesis	No

Future Thrust Area proposed: NA

(b).UGC nominees with Address, City, Pin, State,Tel.,Fax, E- mail (as approved bythe UGC) :

1.Dr.Shankar Alavandi, Senior Scientist, Microbiology, CIBA, RA Puram, Chennai-600028, TN
2.Prof.H.Devraj, University of Madras, Chennai, TN

2. Major achievements (last two/five years depending on mid/final term review) as thecase may be:
(i) Teaching:

a. New courses introduced : None

b.	Curriculum last revised & significant changes	:	2009-10, curriculum revised as per semester system
c.	Examination reforms last made with special features	:	Semester system adopted in 2009-10
d.	Teaching lab./equip./new facilities created	:	Ultracentrifuge is being procured from SAP grant

(ii) **Research**

a. Research(highlight major objectives set-forth (as proposed) andachievements made with breakthrough, innovation brought in, technologytransferred, international collaboration which have created resources).

Prof.T.Satyanarayana

Xylanase encoding genes from compost-soil metagenome, *Geobacillus thermoleovorans* and *Geobacillus thermodenitrificans* have been cloned and expressed in *Eschericha coli* and/or *Bacillus subtilis*. The recombinant xylanases have been produced, purified and characterized. The acidic α-amylase and thermostable α-amylase and amylopullulanase encoding genes from *Bacillus acidicola*, *Geobacillus thermoleovorans* NP54 and *G. thermoleovorans* NP33 have been cloned and expressed in *E. coli*. The recombinant starch hydrolyzing enzymes have been produced, purified and characterized. Literature on microbial strains and their carbon monoxide dehydrogenases has been surveyed and initiated work on these aspects.

Dr.Swati Saha

The lab has laid the groundwork for characterizing histone acetylations in Leishmanai donovani. The next two years will be devoted to characterizing the role of these acetylation events in Leishmania.

Dr.Amita Gupta

We have developed methods for studying genome- wide expression profile of M. tuberculosis using microarrays. The same is now being used to elucidate the bacterial stress transcriptome.

Dr.Y.P.Khasa

The cloning of PIR1 gene from Pichia Pastoris GS115 strain has been done under GAP and AOX1 promoter.

Prof.Rani Gupta

Objective: Studies on peptide –subtilisin interaction

Structural analysis of peptide-subtilisin complex: Proposed novel mechanism of its disulphide reductase activity

<u>Peptide analysis:</u>

Novel $P_{19}$was retrieved from chymotrypsin digest of papain (R8-W26) protein [1]. PSI blast and secondary structure analysis against PDB database suggests respective fragment was well conserved as active sub domain of cysteine proteases from all living organisms.P_{19}has characteristics Trx motif CXXC (CGSC) which is well reported for DSR activity [2]. In papain C25 is catalytic triad residue of the enzyme whereas C22 form a disulphide bridge with C53. At secondary structure level it was found $P_{19}$to exist in random coil which was also observed in CD study but can acquire helix at its carboxy terminal if the size of the peptide is exceeded by five

amino acids. Carboxy terminal of the peptide ended with aromatic residue tryptophan whereas N-terminal is highly variable and hydrophobic.

Peptide-Subtilisin interactions model:

Three dimensional structure of subtilisin Carlsberg (1SCN) was retrieved from PDB where Asp32, His64 and Ser221 were observed as catalytic triad residues [3]. Further protein-protein interactions of P_{19} and subtilisin were observed by using ZDOCK software [4].P_{19} –Subtilisin interactions analysis showed peptide binds on the active site surface of the subtilisin by hydrogen bonds and nonbonding interactions. Further it was observed that P_{19} forms external loop region surrounding the active site of subtilisinwhich may act as lid loop for P_{19}-Subtilisin protein complex. Out of 19 residues only 10 were observed in interactions with subtilisin. Head of the peptide (K17-G20) makes a covering shadow on antiparallel β sheets $\beta_8\beta_9$ and parallel sheets $\beta_6\beta_7$ whereas peptide tail covers two more parallel sheets $\beta_4\beta_5$of subtilisin [Fig1]. Further detailed P_{19}-Subtilisin interaction analysis was done by Pymol [5] and it was observed carboxy terminal of the peptide interacted srongly with protein surface as compared to N terminal. There were nine amino acids of peptide (K17-W26) which interact with 20 amino acids of subtilisin on the interface of P_{19}-Subtilisin by 8 hydrogen bonds and 201 nonbonding interactions [Fig2a]. P_{19}-Subtilisin interaction analysis suggests Cys22 of P_{19} in interactions with His64 by distance of 3.5Å and may play a crucial role in reaction mechanism whereas Trp26 held Cys25 by aromatic sulphur interactions (4.45 Å). Further it was also observed Trp26 was highly interacting residue with P_{19} which was alone interacted with 11 amino acids of protein by forming one hydrogen with Tyr104 of subtilisin and more than 50 nonbonding interactions with other amino acids of subtilisin. Negative control ProteinaseK (3OSZ) interaction with P_{19} was analyzed it was observed that peptide dissociates into some small fragments and showed nonspecific binding complex [6]. Overall P_{19}-Subtilisin complex model suggests that peptide interactions alter original subtilisin folding and acquire a new scaffold over the binding pocket of subtilisin in close association with its catalytic residues to facilitate the novel DSR activity of the complex.

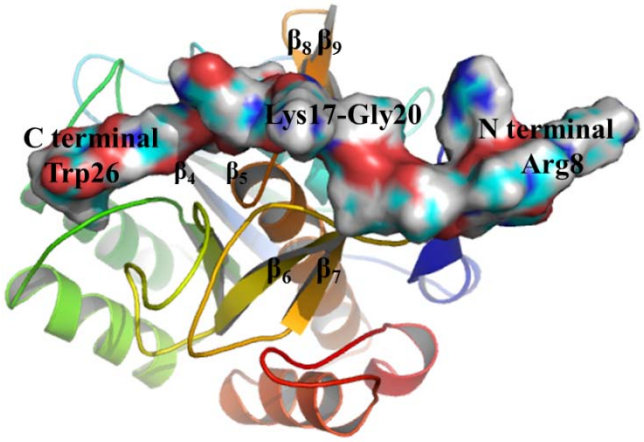


Fig.1: P_{19}-subtilisin complex model where peptide shadow form an external scaffold over the ligand sensing surface of subtilisin.

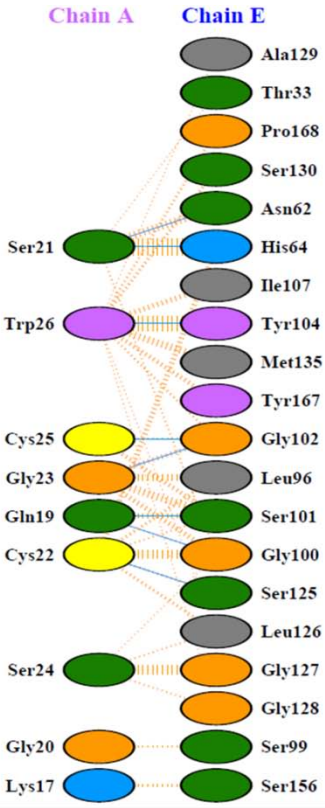


Fig. 2a

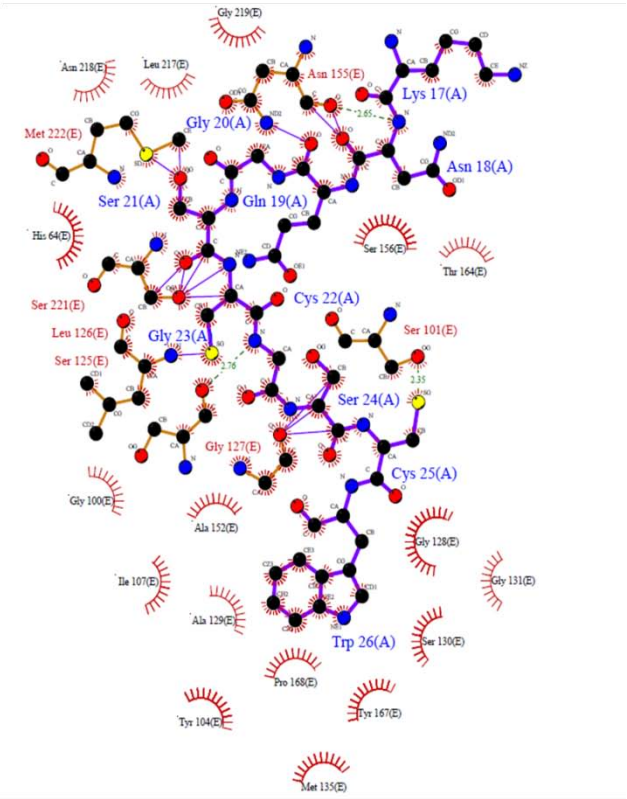


Fig2b

Fig2: **Fig2a** represent interactions overview between P_{19} and subtilisin where chainA representing residues of P_{19} and ChainE represents residues of subtilisin. Dark color blue lines showed possible hydrogen bonds (8) between P_{19}-sutilisin complex whereas dotted lines showing non-bonded interactions (201), width of dotted lines is directly proportional to interactions density. **Fig2b** representing interaction map of P_{10}-sutilisin complex where P_{10} shown in dark lines with dark solids and subtilisin residues shown in star half circles (red). Green color dotted lines show hydrogen bonds where non bonded interactions of peptide will be with surrounding residue of protein.

Truncation and mutation of carboxy terminal Trp26:

$P_{18}\Delta 26$ interactions revealed that single amino acid deletion at carboxy terminal tryptophan disturbed the peptide-subtilisin interacting interface and peptide binds nonspecifically away from the binding pocket of subtilisin. This could be reversed to original binding pattern by substituting other hydrophobic amino acid in place of tryptophan viz. F26/Y26/A26. However G26 substitution again disturbed the binding mode of peptide. Detailed interaction analysis revealed that aromatic carboxy terminal facilitated better interactions in comparison to non-aromatic i.e. alanine. Aromatic carboxy terminal of peptide showed interactions with 11, 12 and 13 residues of subtilisin in case of Trp, Tyr and Phe respectively where as in case of Alacarboxy terminal interact with only two residues of subtilisin. So the mutational and substitution study suggests carboxy terminal of peptide must be ended with aromatic group to facilitate tight binding of peptide tail by hydrogen bond, π-π, cationic-π and Vender wall interactions with subtilisin.

Peptide size optimization:

P_{19}-subtilisin interaction model suggest a part (K17-W26) of peptide is essential for interactions. Here computational approaches were used to optimize the crucial length of the peptide. Variable length (11,10,9,8,7 and motif) truncated peptides (residues from carboxy terminal) were used to carry out peptide-subtilisin interactions study and it was observed that from the all truncated peptide only 10 amino acids mer peptide showed better interactions as compare to other. Further this new truncated peptide P_{10}-subtilisin interactions were compared with P_{19}-subtilisin and maxima of interacting interface was observed in case of P_{10} where 42 interactions were observed where as in case of P_{19} lesser interactions (37) were observed [Tab 1]. So the peptide truncations study optimize the crucial length of peptide to be 10 amino acids from the carboxy terminal i.e. K17-W26 [Fig2b, Fig3].

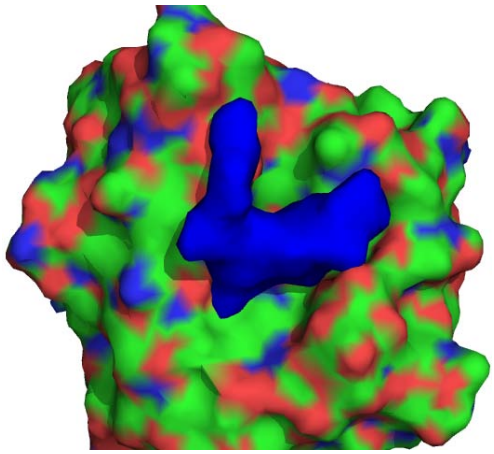


Fig.3: P_{10}-subtilisin interactions model where peptide showed in blue color provide an external cap over the subtilisin binding surface.

R_{P19}-R_{Sub}	R_{P19}-R_{Sub}
K17-S156	S24-L96
Q19-S101	S24-G102
Q19-G100	S24-G127
G20-S99	S24-G128
G20-G100	S24-L126
S21-H64	C25-S101
S21-N62	C25-G102
S21-T33	W26-Y104
C22-H64	W26-G128
C22-G100	W26-A129
C22-L96	W26-S130
C22-S101	W26-G102
C22-S125	W26-I107
C22-L126	W26-M135
G23-S101	W26-L126
G23-L96	W26-G127
G23-G100	W26-Y167
G23-G102	W26-P168

Tab 1a

R_{P10}-R_{Sub}	R_{P10}-R_{Sub}
K17-N155	G23-S125
K17-S156	G23-L126
K17-T157	G23-L96
N18-N155	G23-G100
N18-S156	G23-G127
Q19-N155	S24-L126
G20-N155	S24-G127
S21-N155	S24-G128
S21-N218	C25-G127
S21-G219	C25-S101
S21-S221	W26-G127
S21-H64	W26-G128
S21-M229	W26-A129
S21-L217	W26-Y104
C22-H64	W26-S130
C22-N155	W26-I107
C22-S221	W26-Y167
C22-S125	W26-L126
C22-L126	W26-M135
C22-A152	W26-P168
C22-G127	W26-G131

Tab 2b

Tab 1: Tab1a represent P_{19}-subtilisin complex interactions where all peptide residues forms 42 bonding and nonbonding interactions cluster with 20 residues of subtilisin. **Tab1b** represent P_{10}-subtilisin complex interactions where all peptide residues forms 42 bonding and nonbonding interactions cluster with 26 residues of subtilisin.

Computational support of the Peptide-subtilisin model:

As detailed peptide-subtilisin interaction study suggests that subtilisin undergoes lots of conformational changes on complexation with peptide. Fig. 4A shows 3D profile of subtilisin carlsberg (1SCN) where random and smooth protein profile was observed. Further drastic conformational changes in subtilisin were observed when in complex with P19 and affected region were 110-155 corresponding two beta sheets $\beta_4\beta_5$ and 270-293 a peptide stretch (Fig.4 B) this is well supported by CD spectral analysis where decrease in beta sheets and increased randomness was observed in peptide-subtilisin complex (Fig…). Similar analysis with P_{10} revealed that this truncated peptide also brought about conformational changes affecting more area of protein backbone than P_{19}. It affected two more additional stretches 206-208 and 213-230 corresponding two antiparallel beta sheets $\beta_8\beta_9$ (Fig.4 C). Further to estimate binding fitnesss of peptide-subtilisin complexes differences of accessible surface area (DASA) were analyzed by following formulation:

DASA = ASA (enzyme) - ASA (complex)

DASA (P_{19}-subtilisin) = 9805.9 $Å^2$-11058.4 $Å^2$ = -252.5 $Å^2$

DASA (P_{10}-subtilisin) = 9805.9 $Å^2$-9797.1 $Å^2$ = 8.8 $Å^2$

DASA analysis suggests how the buried accessible surface area of subtilisin side chain and main chain is affected by peptide binding. In case of P_{19}-subtilisin complex negative value of DASA show complex acquires more accessible surface area as compared to subtilisin this additional surface area coming from unbinding part of peptide where as positive value of DASA in case of P_{10}-subtilisin suggests that full stretch of peptide buried subsites accessible surface area of subtilisin [1, 7]. So protein conformational changes and positive value of DASA suggests P_{10}-subtilisin complex to be more stable as compared to P_{19}-subtilisin.

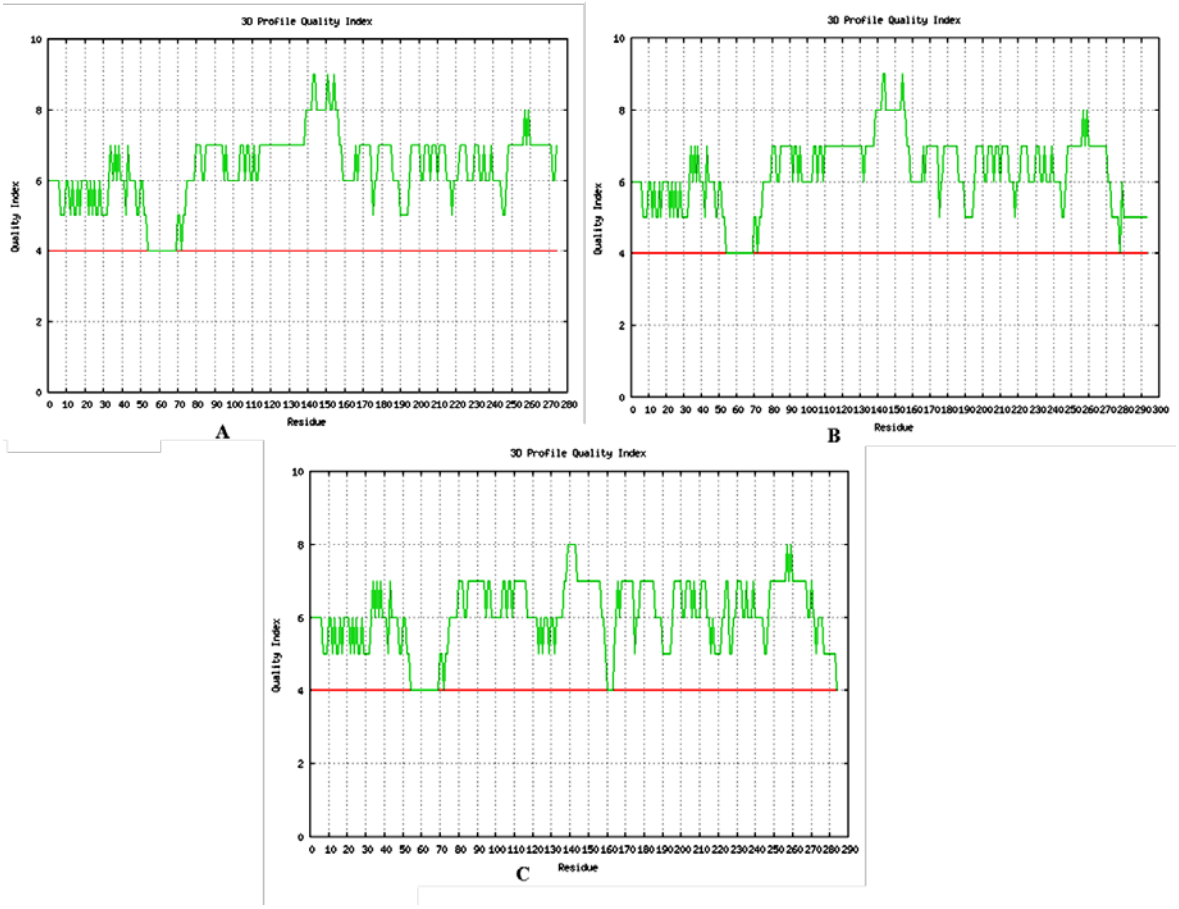


Fig. 4: Fig. 4 A, B and C showed 3D profile view of quality index vs. protein residues for subtilisin, P_{19}-subtilisin and P_{10}-sutilisin respectively.

Computational analysis of DSR activity:

P_{10}-subtilisin complex was used as receptor for docking study with oxidized glutathione (GSSG). GSSG was docked in novel binding pocket formed by P_{10}-subtilisin protein complex scaffold near by the ligand sensing core of subtilisin. As defined earlier peptide form an external loop surrounding the catalytic site this may have resulted to form a novel catalytic site for the complex which may play central role in GSSG catalysis and the DSR activity. C22 of external loop was observed to be at the distance of less than 4Å from the disulphide bond of GSSG [Fig4]. So this C22 of the complex may act as P_{10}-subtilisin complex nucleophile of complex and may attack on disulphide bond of GSSG for the initialization of catalysis and creating mixed disulphide. Further His64 may be functional base for electron transfer leading to completion of reaction. So the computational model of P_{10}-subtilisin complex with GSSG suggests initializing step for novel mechanism of P_{10}-subtilisin complex for DSR activity in absence of external reluctant.

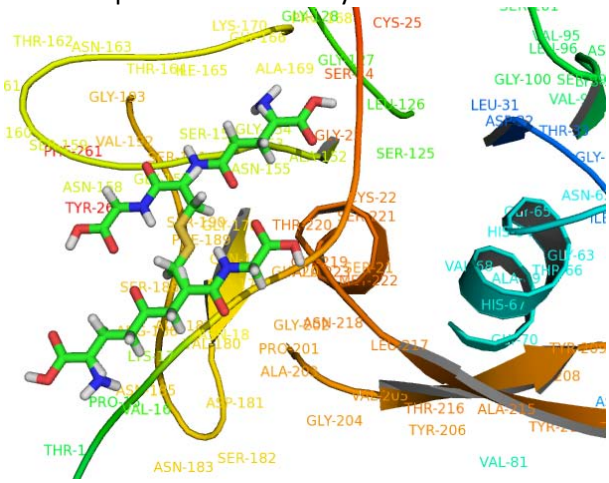


Fig. 4: Proposed mechanism for induced glutathione activity in protease and peptide complex:

1. Cys 22 and Cys 25 of peptide may behave as redox cysteine which can exist in both oxidized and reduced states**.**

2. Cys 22 may exist in transient bonding with His64 of subtilisin which pulls apart the two cysteines.

3. First nucleophilic attack on Oxidized glutathione by Cys22 will result in mixed disulphide bond.

4. Cys25 will interact with mixed disulphide bond and releases one GSH.

5. Cys22 and Cys25 will make disulphide in presence of water again His64 will pull Cys22 to bring the enzyme in original state.

References:

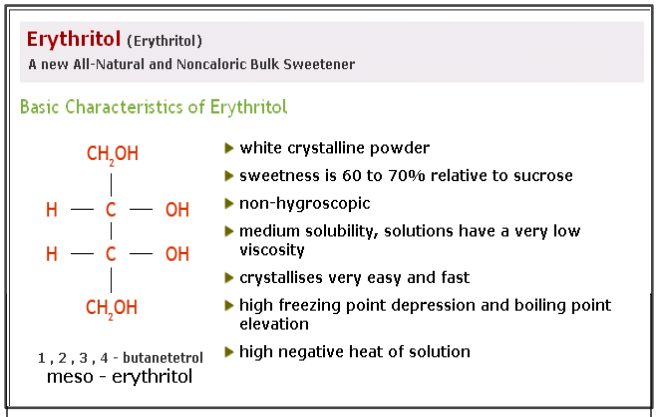
1. Moon-Jib KIM, Daisuke YAMAMOTO, Keita MATSUMOTO, Masatoshi INOUE, ToshimasaISHIDA,Hiroshi MIZUNO, Shigeyuki SUMIYA and Kunihiro KITAMURA. Crystal structure of papain-E64-c complex Binding diversity of E64c to papain S2 and S3 subsites. Biochem. J. (1992) 287, 797-803.

2. ELIZABETH A. KERSTEEN and RONALD T. RAINES.Catalysis of Protein Folding by Protein Disulfide IsomeraseandSmall-Molecule Mimics. *Antioxid Redox Signal*. 2003 August ; 5(4): 413. doi:10.1089/152308603768295159.3. Anke C. U. Steinmetz, Hans-Ulrich Demuth,o and Dagmar Ringe. Inactivation of Subtilisin Carlsberg by*N-((*tertButoxycarbonyl) alanylprolylphenylalanyl)-

benzoylhydroxylamine:Formation of a covalent enzyme-inhibitor linkage in the form of a carbamate derivative. *Biochemistry* 1994, 33, 10535-10544.
4**.** Pierce B.G., Hourai Y., Weng Z. (2011) Accelerating protein docking in ZDOCK using an advanced 3D convolution library. PLoS One, 6(9): e2465.
5. D. Seeliger, B.L. de Groot, Ligand docking and binding site analysis with PyMOLand Autodock/Vina. J. Comput Aided Mol. Des. 24 (2010) 417–422.
6.NatasjaBrooijmans and Irwin D. Kuntz.MOLECULAR RECOGNITION AND DOCKING ALGORITHMS, Annu. Rev. Biophys. Biomol.Struct. 2003. 32:335–73.
7. Lee, B. & Richard, F. M. (1971) J. Mol. Biol. 55, 379-400.

Prof.R.K.Saxena

Project Summary: Erythritol occurs naturally in some fruits and fermented foods. At the industrial level, it is produced from glucose by fermentation with a yeast, *Moniliellapollinis*. It is 60–70% as sweet as table sugar yet it is almost non-caloric, does not affect blood sugar, does not cause tooth decay, and is partially absorbed by the body, excreted in urine and feces. It is produced from glucose which is fermented by safe and suitable food-grade osmophilic yeasts. Once erythritol is separated from the fermentation broth, it is purified by processes typical for carbohydrate sweeteners and sugar alcohols. The final crystalline product is more than 99% pure. It is less likely to cause gastric side effects than other sugar alcohols due to its unique digestion pathway. Under U.S. Food and Drug Administration (FDA) labeling requirements, it has a caloric value of 0.2 kilocalories per gram.



throughout the world.It was discovered in 1848 by British chemist John Stenhouse.

Results: In present study we have isolated sixty four yeast from different fruit samples, out of which only three isolate have capability to produce erythritol. Among these three only isolate no. E1C repeatedly produces erythritol when grown in the presence of glucose as the carbon source. The production medium composed of30% glucose, 0.5% peptone, 0.3% yeast extract and 0.5% malt extract in shake flask. Production of erythritolwas checked after every 24h and maximum production of erythritol was obtained at 72h. The detection of erythritol was carried out by HPLC on **Aminex HPX-87H** column. After optimizing different parameters like temperature, pH, inoculum density and carbon source the yield is increased to 3.5 g/l after 72h of incubation with the initial 0.6g/L.

Prof.J.S.Virdi

Title: Suppression subtractive hybridization (SSH) between clinical and non-clinical strains of *Yersinia enterocolitica* biovar 1A isolated from India

Yersinia enterocolitica is an important food- and water-borne enteric pathogen that causes a variety of gastrointestinal diseases such as acute diarrhea, terminal ileitis and mesenteric lymphadenitis. Long-term sequelae following infection due to this organism include reactive arthritis and erythema nodosum. *Y. enterocolitica* is extremely heterogeneous species and well characterized biochemically as well as serologically. Biochemically, it has been classified into six biovars namely1A, 1B, 2, 3, 4 and 5. All these biovars are represented by more than 30 serotypes. On the basis of clinical evidences, *Y. enterocolitica* have been divided into three groups*viz.* strains belonging to pathogenic group (biovar 1B), strains with moderate pathogenicity (biovars 2–5) and the so called non-pathogenic (biovar 1A) strains. Pathogenicity of biovars 1B and 2-5 is due to the presence of virulence genes which are present on both the pYV (plasmid for *Yersinia*virulence) plasmid and the chromosomal DNA.

Biovar 1A strains of *Y. enterocolitica*, on the other hand, have been reported to lack both pYV plasmid and chromosomal virulence genes such as *ail*, *myfA*, *ystA*, *ysa* TTSS and HPI. Such observations along with their inability to cause infection in mouse model have made the pathogenicity of biovar 1A controversial. Nevertheless, many epidemiological and clinical studies suggest their association with disease such as their isolation from diarrheic patients in various countries around the world. Also, some biovar 1A strains have been reported to produce symptoms indistinguishable from that produced by isolates belonging to known pathogenic biovars. Biovar 1A strains have also been implicated in nosocomial and food-borne outbreaks and were isolated from extra-intestinal infections. It has also been reported that biovar 1A strains have the capability to invade HEp-2 and Chinese hamster ovary (CHO) cells, and also survived within macrophages.

In our laboratory, *Y. enterocolitica* has been isolated from a variety of sources. These include wastewaters, pigs, pork and stools of diarrheic human patients. These strains belong to biovar 1A and are represented by a number of serotypes namely O:6,30-6,31; O:6,31; O:6,30; O:7,8-8-8,19; O:10-34; O:15; O:41,42; O:41,43 and NAG. While characterizing the Indian strains in our laboratory, two important observations were made. Firstly, all the strains clustered into two clonal groups when analyzed by different DNA fingerprinting techniques such as rep [repetitive extragenic palindrome (REP)- and enterobacterial repetitive intergenic consensus (ERIC)]-PCR, *rrn* locus genotyping (ribotyping and 16S-23S intergenic spacer (IGS) region polymorphism) and *gyrB* loci RFLP. These studies also revealed that clinical serotype O:6,30-6,31 strains formed a discrete cluster and the aquatic serotype O:6,30-6,31 strains formed yet another tight cluster, even though these belonged to same serotype. Other studies carried out in the past have also shown some differences in the virulence-related characteristics of clinical and non-clinical (strains isolated from wastewater or swine) biovar 1A strains isolated from India. This included a greater number of clinical biovar 1A strains being associated with enterotoxin production, invasion of epithelial cells, and survival inside macrophages than non-clinical strains.

These findings clearly suggested that the clinical isolates possessed some additional (virulence related) genes as compared to the non-clinical strains, which enabled them to colonize the human gut and cause a variety of syndromes. Thus to further unravel the genomic heterogeneity of clinical strains, this work was intended to understand the genomic differences between clinical (isolated from diarrheic humans, serotype O:6,30-6,31) and non-clinical (isolated from wastewater, serotype O:6,30-6,31) strains of *Y. enterocolitica* recovered from India. The major objective of this study was to detect the genomic fragments which were specific to clinical strains (related to virulence) of *Y. enterocolitica* using suppression subtractive hybridization (SSH).

SSH was carried out between a clinical (IP 27366, serotype O: 6,30-6,31, tester strain) and non-clinical (IP26315, serotype O: 6,30-6,31, driver strain) strain of *Y. enterocolitica* using

the PCR-select genome subtraction kit (Clontech). Genome subtraction yielded one hundred and fifty clones after one round of subtraction. These clones were confirmed using colony PCR and restriction digestion which also revealed the presence of inserts ranging from 200 - 1500 bp. Of these, 24 clones were found to carry no insert. Thus one hundred and twenty five clones were confirmed as positive. Further, the clones carrying tester-specific genomic fragments were identified by southern hybridization and dot blot hybridization with genomic DNA from both tester and driver strains as shown in Fig. 1a and 1b. After dotblot hybridization, thirty eight clones were selected and sequenced. Using these sequences primers were designed and the tester-specific sequences were confirmed by PCR with tester and driver genomic DNA. Nine tester-specific (clinical) sequences were confirmed, which were not found in driver (non-clinical) strain of *Y. enterocolitica* biovar 1A (serotype O: 6,30-6,31). The results are shown in Fig. 2.

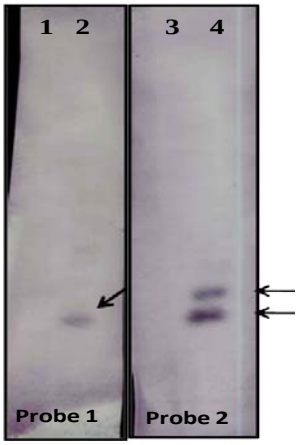


Fig. 1a. Southern hybridisation for the identification of tester-specific clones: D- *Rsa*1 digested genomic DNA of driver strain (Non-clinical); **T-** *Rsa*1 digested genomic DNA of tester strain (Clinical)

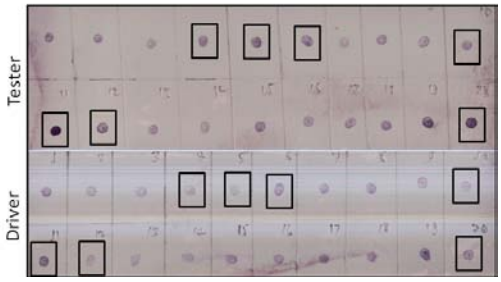


Fig. 1b. Dot-blot hybridization to identify tester-specific clones: The DNA (PCR-product) from the subtractive clones was spotted on nylon membrane and hybridized with DNA probes prepared from driver and tester strain genomic DNA. Spots in the boxes represent the clones harbouring tester-specific genomic fragments.

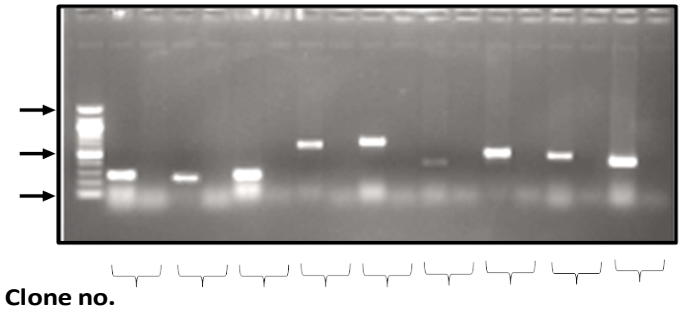


Fig. 2. Confirmation of tester-specific sequences by PCR using genomic DNA of tester (T) and driver (D) strains: Lane M- 100 bp DNA ladder; Lane 1- PCR amplified product of clone no. 8 using tester strain; Lane 3- clone no. 10; Lane 5- clone no. 18; Lane 7- clone no. 51; Lane 9- clone no. 57; Lane 11- clone no. 66; Lane 13- clone no. 70; Lane 15- clone no. 87; Lane 17- clone no. 124; Lane-2, 4, 6, 8, 10, 12, 14, 16, 18 – the corresponding amplicons were not detected when genomic DNA of driver strain (D) was used for PCR-amplification.

These sequences were analyzed at both nucleotide and protein level using BLAST homology search. The results showed their homology to proteins involved in iron acquisition, haemin storage, outer membrane protein PgaA, flagellar hook proteins, secretion system, transport systems and others of unknown function. These are summarized in Table 1.

Table 1. Homologies of the tester-specific sequences of *Y. enterocolitica* biovar 1A identified by SSH

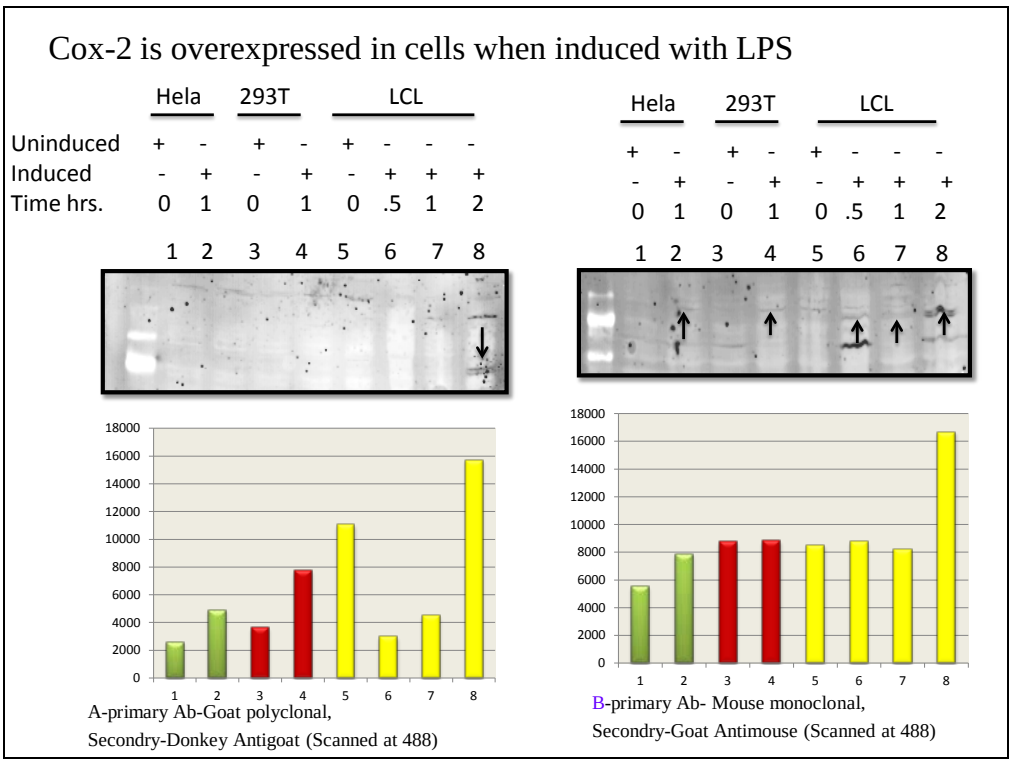
S. No.	Clone no.	Insert size	Predicted encoded protein	E-value	Similarity (% amino acid)	Genbank Accession No.
1.	**Clone no. 8**	276	Conserved hypothetical protein	2e-39	81/84 (96%)	GU253386
2.	**Clone no. 10**	236	Hemophore A (HasA)	2e-14	42/52 (80%)	GU253387
3.	**Clone no. 18**	265	Type 1 secretion protein	2e-48	110/123 (89%)	GU253388
4.	**Clone no. 51**	643	Outer membrane protein (PgaA)/haemin storage system (hms) protein	8e-104	212/218 (97%)	GU253389
5.	**Clone no. 57**	688	Flagellar hook protein	1e-71	206/216 (95%)	GU253390
6.	**Clone no. 66**	402	Putative 5′nucleotidase	5e-94	110/113 (97%)	--
7.	**Clone no. 70**	521	Restriction modification system	7e-90	127/140 (96%)	GU253391
8.	**Clone no. 87**	492	Putative exported protein	2e-34	133/166 (80%)	GU253392
9.	**Clone no. 124**	430	ABC type multidrug transport system	2e-68	122/139 (87%)	GU253393

All these sequences showed high homology to sequences with *Yersinia enterocolitica* 8081 biovar 1B, *Y. pseudotuebculosis*, *Salmonella enterica*, *Aeromonas* spp., and *Serratia* spp. Detection of these genes only in clinical strain indicated that clinical strain possessed additional virulence related genes in comparison to non-clinical strain and some of these might play role in the pathogenicity of clinical strains *Y. enterocolitica* biovar 1A.

Dr.Rajeev Kaul

Role of inflammation in life cycle of EBV and how these interaction lead to propagation of its infection and ultimately to the development of an environment of transformation was studied.EBV is an oncogenic virus, closely associated with several human malignancies like Burkitt's lymphoma, Hodgkin disease, PTLD, nasopharyngeal carcinoma etc. Also, highly inflamed condition as in rheumatoid arthritis is associated with EBV reactivation.EBV cleverly evades host immune system, regulates various cellular signaling pathways and successfully establishes a life–long persistence. EBV posses a unique ability to transform B lymphocytes, this system provides an excellent model to study the interaction of EBV with B lymphocytes. Studies have shown over-expression of Cox-2/ PGE2 in several human malignancies. Studies have also shown direct involvement of Cox-2 over-expression in several EBV associated cancers like NPC.

Lps is a biologically active compound found in the outer membrane of gram negative bacteria. In our study, by protein extraction and western blot analysis we have shown that Lps (1ug/ml) induction of cell lines including Hela,293t and Lcl-2 causes over-expression of critical enzyme Cox-2 ,which is highly associated with several human malignancies. Lps induction of EBV positive cells (Lcl-2 and B95a) not only causes up-regulation of Cox-2 but also leads to lytic cycle reactivation of Epstein Barr Virus in latently infected cells, thus suggesting a possible link between Cox-2 over-expression in response to induction with extracellular stimuli Lps and reactivation of EBV lytic cycle in otherwise latently infected cells.



Prof.R.C.Kuhad

Lignocellulosic biotechnology laboratory has developed a process for concentrating the sugars in the hydrolysates and have filed the process for patenting. Also success has been achieved in cloning pectatelyase and laccase. The production of biotech feed (nutritive and digestible animal feed via SSF of wheat straw with lignin degrading fungus) has been scaled to pilot scale and has been developed and evaulated. The patent for the process has also been filed for patenting. The enzymes, xylanase and laccase have been evaluated for pulp bleaching.

b. If the objectives set-forth could not be achieved, the specific reasons thereof. Not applicable

c. Utilization of findings in policy formulation, development and modification ofstrategies (for Social Science departments mainly) Not applicable

(iii) **Human Resource Training** :

a.	Persons trained (Nos.)	:	UG-	PG-
b.	Rural/Tribal	:	Nil	Nil
c.	Industrial	:	Nil	Nil

d. International : Nil Nil
e. From other agencies : Nil Nil

3. Infrastructure Developed:

a. Name major Equipments(>Rs.3 lacs)- Ultra Centrifuge is being procured and order has been placed

b. Central Schemes/facilities for PG, Research and Extension Activities (Pleasetick the one applicable to your Department :
   (i) STEP
   (ii) IIPC
   (iii) USIC / RSIC
   (iv) Patent Promotion Cell
   (v) Guesthouse with capacity
   (vi) Seminar /Conference Room with capacity
   (vii) Regional/Mainframe computing facilities
   (viii) Central Library with documentation facilities
   (ix) Continuing EducationCentre
   (x) Women Development Cell.
   ✓**Not applicable/ None**

c. Networking(Please tick the right one):
   (i) Library
   (ii) Laboratory
   (iii) UniversityDepartment.
   ✓ **Not applicable/ None**

4. Knowledge disseminated to (in the thrust area identified):

i. Other teaching institution (Name, No. of faculty involved) : 1
Prof.T.Satyanarayana has delivered lectures on metagenomics, xylanases and amylases in workshops at BijuPatnaik University of Technology (Bhubaneswar, Orissa) and University of Sagar, Sagar (M.P.), and MHRD-sponsored lecture series at Vidyasagar University (Midnapur, West Bengal) and Rajasthan Central University (Jaipur, Rajasthan).

ii. Industry (Name with amount received if any) : None
iii. Rural/Tribal/Govt./NGOs(Provide No. with amount) : None
iv. International (name organization) : None
v. Others : None
vi. Innovation/excellencebrought in (Please specify in the identified thrust areas only)

5. Breakthrough (already recognized): Prof.T.Satyanarayana work has been recognized for the Possibility of obtaining xylanase gene from environmental DNA, its cloning and expression. Also for recombinant amylopullulanase generated by truncating 300 amino acids from C-terminal end exhibits higher rate of hydrolysis with enhanced thermostability and affinity for the substrate.

6. Emerging/Hi-tech/Priority area generated: Metagenomic approach for the retrieval of genes encoding useful enzymes by Prof.T.Satyanarayana

7. Resource generation (specify amount, Rs. in lakh):

Items	**Amount**	**Items**	**Amount**
Consultancy:		Sponsored(agency) R&D Projects:	Rs.3,13,92,876=00*
Transfer of technology:		Product & Prototype development:	
Patent utilization:		Exploitation of internal facilities by user departments	
International Collaboration: a. Neighboring institutions: Two** b. Industries: c. National organizations: d. International Organizations: e. Any other collaborative Program:			
Human Resource Training: a. International Students: b. Industrial: c. Extension activities: d. Other courses:			

***Sponsored projects**

Prof.T.satyanarayana

- UGC project on cloning and expression of the phytase of Pichia anomala in Pichia pastoris (2012 -2015): Rs.13,26,800
- DST project on acidic amylase of Bacillus acidicola (2012 – 2015): Rs.33,31,000
- DBT project on carboxydotrophic bacteria (2013 -2016): Rs.30,65,000
- DBT Project on 'Production of recombinant phytase of Sporotrichum thermophile (2013-2016): Rs. 23,25,276.
- DU-DST-PURSE project on 'Cloning amylopullulanase of Geobacillus thermoleovorans' (2011-2013):Rs. 30,30,000

Dr.Swatisaha

- Two projects worth Rs.80 lakh

Prof.R.K.Saxena

- Joint Indo-Finland RFBR "Butanol from sustainable sources" (DST) for Rs. 9.03 lakhs (2012-13)
- TwoJoint Indo-Russian Enzymatic Transformation of Fucodians as a base for Drug Design, structural and functional investigations from Indian and Russian seaweeds (DST) for Rs.10.11 lakhs (2012-13)

Dr.Rajeev Kaul

- One UGC major research project for Rs.14,00,800 (2012-15)

Prof.R.C.Kuhad

- One MNRE funded project for Rs.70 lakhs

****Collaboration with national organizations:**

Prof.T.satyanarayana

- With the Dr. Bijender Singh of the Department of Microbiology, M.D. University (Rohtak) on 'Thermophilic fungal phytase cloning'.
- With Dr. Debananda S. Ningthoiujam of the Department of Biochemistry, Manipur University (Imphal) on 'Actinobacterial carbon monoxide dehydrogenase'.

a. Total amount of resource generated from all sources above

b. Also mention development grant received from University in other areas of the Department.

8. Use of output of research, teaching in (tick and fill up the right one)

Item	**No.**	**Item**	**No.**
a. Industries	Three (Prof.R.C.Kuhad) • Jay Biozyme Technologies, Pune • Varuna Biocell Pvt. Ltd., Varanasi • CPPRI, Saharanpur	b. Other user deptts	None
c. National orgns	None	d. Other Organizations	None

9. a. Other activities:

Items	**Numbers**	**Time Duration**
Seminar	1 (SAP Symposium)***	1 Day
Summer Institute	None	None
Conference	None	None
Refresher Course	None	None

***One day seminar was organized in our department on **18-March-2013** as part of DRS-I under UGC special assistance program (SAP) awarded to our department. The title of seminar was "Developing Strategies for understanding and exploiting microorganisms" with focus on theme area 'Industrial Microbiology' for this seminar. The seminar was organized in Biotech auditorium in our campus. Each speaker was allotted a 40 minute slot for presentation. The audience consisted of our department faculty, doctoral and masters students, and project fellows. Following distinguished speakers delivered lectures in the seminar: Dr.A.K.Panda from NII Delhi, Dr.Sunil K Khare from IIT Delhi, Dr.D.K.Sahoo from IMTECH Chandigarh &Dr.D.K.Tuli from IOC Delhi.Dr.Tuli talked about challenges in the field of Cellulosic ethanol, Dr.Amulya Panda presented on E.coli fermentation for recombinant protein production. Prof.SunilK.Khare gave a talk on novel biocatalysts from extremophiles. Dr. Debendra K. Sahoo talked on Strategizing for Success in Microbial Process Development. The one day symposium was attended by around 130-150 participants and was well received.

b. Autonomous Character: Yes/No.

Financial	Yes
Administrative	Yes
Academic	Yes

Others	Yes

c. Advisory Committee Meeting (No. with Dates)

One meeting on 18-Mar-2013

Major Recommendations

1. Head of Department, Prof.Virdi, gave an elaborate presentation on the activities of the program for the year 2012-13 and the proposed activities for the year 2013-14.
2. The committee endorsed the purchase of ultracentrifuge from the sanctioned funds and also recommended the purchase of accessory rotors for the ultracentrifuge from allotted funds
3. UGC nominee, Prof.Alavandi expressed satisfaction over the progress of program and congratulated the Department for the achievements.

10. Faculty Involved

a.

Faculty Strength Created	**Positions Available**	**Working**	**Vacant**
(Put Numbers) In thrust Area(1) Other Areas(2) (1) (2) (1) (2)under SAP/ ASIST			
Professor	2	2 + 3*	0
Reader	3**	1	1
Lecturer	6***	3	1
Other	0	0	0

* Three positions are upgraded (one Associate and two Assistant Professor)

** One position has been upgraded to Professor and one is vacant

*** Two have been upgraded to Professor and one is vacant

b. In the identified thrust area(s):

Faculty	**Name**	**Membership (INSA/ BHATNAGAR/ BIRLA)**	**Specialization/ Specific Areas of Expertise**
Professor	1. R.K.Saxena 2. T.Satyanarayana 3. J.S.Virdi 4. R.C.Kuhad 5. Rani Gupta	 AMI, BRSI	Microbial Enzymes Microbial Enzymes Microbial Pathogenicity Microbial Enzymes Microbial Enzymes
Reader	1. Swati Saha		Microbial Pathogenicity
Lecturer	1. Amita Gupta 2. Yogender Khasa 3. Rajeev Kaul		Microbial Pathogenicity Microbial Enzymes Microbial Pathogenicity
Emeritus/ Visiting Prof	None		

• Provide a list of publication records in referred journals (group area wise,faculty member wise, year-wise).

Microbial Enzymes

1. Sharma, A. and Satyanarayana, T. 2013. Microbial acid-stable α-amylases: Characteristics, genetic engineering and applications. Process Biochem. 48: 201-211.

2. Verma, D. and Satyanarayana, T. 2013. Cloning, expression and characteristics of a novel alkalistable and thermostable xylanase encoding gene (Mxyl) retrieved from compost-soil metagenome. PLoS One 8(1): e52459.

3. Mehta, D. and Satyanarayana, T. 2013. Biochemical and molecular characteristics of recombinant acidic and thermostable raw starch hydrolyzing α-amylase from an extreme thermophile Geobacillus thermoleovorans. J. Mol. Catalysis. B. Enzymatic 85-86: 229-238.

4. Anand, A., Kumar, V. and Satyanarayana, T. Characteristics of thermostable endoxylanase and β-xylosidase of the extremely thermophilic bacterium Geobacillus thermodenitrificans TSAA1 and its applicability in generating xylooligosaccharides and xylose from agro-residues. Extremophiles (Published online: DOI 10.1007/s00792-013-0524-x).

5. Verma, D., Anand, A. and Satyanarayana, T. 2013. Thermostable and alkalistable endoxylanase of the extremely thermophilic bacterium Geobacillus thermodenitrificans TSAA1: Cloning, expression, characteristics and its applicability in generating xylooligosaccharides and fermentable sugars. Appl.Biochem. Biotechnol. (Published online: doi:10.1007/ s12010-013-0174-6.

6. Kumar, V., Poonam and Satyanarayana, T. Highly thermo-halo-alkali-stable β-1,4-endoxylanase from a novel polyextremophilic strain of Bacillus halodurans. Bioproc. Biosyst. Engg. (Published online: DOI: 10.1007/s00449-012-0811-4).

7. Kumar, V. and Satyanarayana, T. 2012. Thermo-alkali-stable xylanase of a novel polyextremophilic Bacillus halodurans TSEV1 and its application in biobleaching. Intern. Biodeter. Biodegr. 75: 138-145.

8. Verma, D. and Satyanarayana, T. 2012. Phytase production by the unconventional yeast Pichia anomala in fed batch and cyclic fed batch fermentations. Afr. J. Biotechnol. 11: 13705 – 13709.

9. Singh, B. and Satyanarayana, T. 2012. Production of phytate-hydrolyzing enzymes by thermophilic moulds. African J. Biotechnol. 11: 12314-12324.

10. Sharma, A. and Satyanarayana, T. 2012. Production of acidstable and high maltose-forming α-amylase of Bacillus acidicola by solid state fermentation and immobilized cells and its applicability in baking. Appl. Biochem. Biotechnol. 168: 1025 – 1034.

11. Anand, A. and Satyanarayana, T. 2012. Applicability of carboxydotrophic bacterial carbon monoxide dehydrogenase in carbon sequestration and bioenergy generation. J. Sci. Indust. Res. 71: 381-384.

12. Sharma, A. and Satyanarayana, T. 2012. Cloning and expression of acidstable, high maltose-forming, Ca2+-independent α-amylase from an acidophile Bacillus acidicola and its applicability in starch hydrolysis. Extremophiles 16: 515-522.

13. Verma, D. and Satyanarayana, T. 2012. Molecular approaches for ameliorating microbial xylanases. Bioresource Technology 117: 360-367.

14. Verma, D. and Satyanarayana, T. 2012. Cloning, expression and applicability thermo-alkali-stable xylanase of Geobacillus thermoleovorans in generating xylooligosaccharides from agro-residues. Bioresource Technol. 107: 333-338.

15. Sharma, A., Kawarabayasi, Y. and Satyanarayana, T. 2012. Acidophilic bacteria and archaea: Acidstable biocatalysts and their potential applications. Extremophiles 16: 1-19.

16. Nandal P, Ravella SR, Kuhad RC. Laccase production by Coriolopsiscaperata RCK2011: Optimization under solid state fermentation by Taguchi DOE methodology.Sci Rep. 2013 Mar 6;3:1386.

17. Sharma KK, Shrivastava B, Sastry VRB, Sehgal N and Kuhad RC (2013). Middle redox potential laccase from Ganodermasp: its application in imrovement of feed from monogastric animals. Scientific Reports. 3:1299

18. Kumar S., Gupta R., Kumar G., Sahoo D. and Kuhad R.C. (2012). Bioethanol production from Gracilariaverrucosa, a red alga, in a biorefinery approach. Bioresource Technology (Accepted).

19. Chandna P., Mallik S. and Kuhad R. C. (2012). Assessment of bacterial diversity in agricultural by-product compost by sequencing of cultivated isolates and amplified rDNA restriction analysis. Applied Microbiology and Biotechnology. (Accepted).

20. Gupta R., Mehta G and Kuhad R.C. (2012). Fermentation of pentose and hexose sugars from corncob, a low cost feedstock into ethanol. Biomass and Bioenergy. 47:334-341.

21. Deswal D., Gupta R., and Kuhad R.C. (2012). Enhanced exoglucanase production by brown rot fungus Fomitopsis sp. RCK2010 and its application for cellulose saccharification. Applied Biochemistry and Biotechnology. 168:2004-2016.

22. Kidwai, M., Jain, A., Sharma, A. and Kuhad, R.C. (2012) Ecofriendly approach for detection of phenols in water u sing laccase from different fungi. Water Science and Technology 66:385-393.

23. Sharma KK, Sharma S, Karp M and Kuhad RC (2012). Ligninolytic enzymes improve soil DNA purity: Solution to methodological challenges of soil metagenomics. Journal of Molecular Catalysis B: Enzymatic. 83: 73-79

24. Gupta R, Kumar S., Gomes J. and Kuhad R.C. (2012). Kinetic study of batch and fed-batch enzymatic saccharification of pretreated substrate and their subsequent fermentation to ethanol. Biotechnology for Biofuels 5:16

25. Singh S, Kumar P, Gopalan N, Shrivastava B., Kuhad RC and Chaudhary HS (2012). Isolation and partial characterization of actinomycetes with antimicrobial activity against multidrug resistant bacteria. Asian Pacific Journal of Tropical Biomedicine.2:1147-1150

26. Pundir C.S., Rawal R., Chawla S., Renuka, Kuhad R.C. (2012). Development of an amperometric polyphenol biosensor based on fungal laccase immobilized on nitrocellulose membrane. Artificial Cells, Blood Substitutes, and Biotechnology.40:163-70.

27. Kumar A., Gupta R., Shrivastava B., Khasa Y.P. and Kuhad R.C. (2012). Xylanase production from an alkalophilic actinomycete isolate Streptomyces sp. RCK-2010, its characterization and applicationin saccharification of second generation biomass. Journal of Molecular Catalysis B.: Enzymatic. 74:170-177.

28. Das T.K., Banerjee D., Chakarborty D., Pakhira M.C., Shrivastava B. and Kuhad R.C. (2012). Saponin: role in Animal System. Veterinary World 5:248-254.

29. Shrivastava B., Nandal P., Sharma A., Jain K.K., Khasa Y.P., Das T.K., Mani V., Kewalramani N.J., Kundu S.S. and Kuhad R.C. (2012) Solid state bioconversion of wheat straw into digestible and nutritive ruminant feed by Ganoderma sp. rckk02. Bioresource Technology. 107:347-351.

30. Kidwai M., Jain A., Sharma A. and Kuhad R.C. (2012). First time reported enzymatic synthesis of new series of quinoxalines-A green approach. Journal of Molecular Catalysis B: Enzymatic. 74:236-240.

31. Deswal D., Sharma A., Gupta R. and Kuhad R.C. (2012). Application of lignocellulytic enzymes produced under solid state cultivation conditions. Bioresource Technology. 115:249-254

32. Rajput R, Verma VV, Chaudhary V, Gupta R. A hydrolytic γ-glutamyl transpeptidase from thermo-acidophilic archaeon Picrophilus torridus: binding pocket mutagenesis and transpeptidation.Extremophiles. 2013 Jan;17(1):29-41

33. Rajput R, Gupta R.Thermostablekeratinase from Bacillus pumilus KS12: Production, chitin crosslinking and degradation of Sup35NM aggregates. Bioresour Technol. 2013 Jan 28;133C:118-126.

34. Murty NA, Tiwary E, Sharma R, Nair N, Gupta R. γ-Glutamyl transpeptidase from Bacillus pumilus KS 12: decoupling autoprocessing from catalysis and molecular characterization of N-terminal region. Enzyme Microb Technol. 2012 Mar 10;50(3):159-64

35. Kumari A, Gupta R. Extracellular expression and characterization of thermostable lipases, LIP8, LIP14 and LIP18, from Yarrowia lipolytica. Biotechnol Lett. 2012 Sep;34(9):1733-9.

36. Gupta R, Sharma R, Beg QK. Revisiting microbial keratinases: next generation proteases for sustainable biotechnology.Crit Rev Biotechnol. 2012 May 30.

37. Rajput R, Tiwary E, Sharma R, Gupta R. Swapping of pro-sequences between keratinases of Bacillus licheniformis and Bacillus pumilus: altered substrate specificity and thermostability. Enzyme Microb Technol. 2012 Aug 10;51(3):131-8

38. Sharma R, Gupta R. Coupled action of γ-glutamyl transpeptidase-glutathione and keratinase effectively degrades feather keratin and surrogate prion protein, Sup 35NM.

39. Anand P, Saxena RK. A comparative study of solvent-assisted pretreatment of biodiesel derived crude glycerol on growth and 1,3-propanediol production from Citrobacter freundii.N Biotechnol. 2012 Jan 15;29(2):199-205

40. Rawat G, Tripathi P, Jahan F, Saxena RK. A Natural Isolate Producing Shikimic Acid: Isolation, Identification, and Culture Condition Optimization. Appl Biochem Biotechnol. 2013 Feb 27

41. Misra S, Raghuwanshi S, Saxena RK. Evaluation of corncob hemicellulosic hydrolysate for xylitol production by adapted strain of Candida tropicalis. CarbohydrPolym. 2013 Feb 15;92(2):1596-601

42. Mahajan RV, Saran S, Saxena RK, Srivastava AK. A rapid, efficient and sensitive plate assay for detection and screening of l-asparaginase-producing microorganisms. FEMS Microbiol Lett. 2013 Feb 11.

43. Mahajan RV, Saran S, Kameswaran K, Kumar V, Saxena RK. Efficient production of L-asparaginase from Bacillus licheniformis with low-glutaminase activity: optimization, scale up and acrylamide degradation studies. Bioresour Technol. 2012 Dec;125:11-6

44. Misra S, Raghuwanshi S, Saxena RK. Fermentation behavior of an osmotolerant yeast D. hansenii for Xylitol production.Biotechnol Prog. 2012 Nov-Dec;28(6):1457-65

45. Saxena RK, Tripathi P, Rawat G. Pandemism of swine flu and its prospective drug therapy. Eur J Clin Microbiol Infect Dis. 2012 Dec;31(12):3265-79

46. Anand P, Saxena RK. A novel thin-layer chromatography method to screen 1,3-propanediol producers. J Ind Microbiol Biotechnol. 2012 Nov;39(11):1713-8.

47. Misra S, Raghuwanshi S, Gupta P, Saxena RK. Examine growth inhibition pattern and lactic acid production in Streptococcus mutans using different concentrations of xylitol produced from Candida tropicalis by fermentation. Anaerobe. 2012 Jun;18(3):273-9.

48. Jahan F, Kumar V, Rawat G, Saxena RK. Production of microbial cellulose by a bacterium isolated from fruit. Appl Biochem Biotechnol. 2012 Jul;167(5):1157-71.

49. Misra S, Raghuwanshi S, Gupta P, Dutt K, Saxena RK. Fermentation behavior of osmophilic yeast Candida tropicalis isolated from the nectar of Hibiscus rosasinensis flowers for xylitol production. Antonie Van Leeuwenhoek. 2012 Feb;101(2):393-402

Microbial Pathogenesis

50. Kumar D, Kumar D, Saha S. A highly basic sequence at the N-terminal region is essential for targeting the DNA replication protein ORC1 to the nucleus in Leishmania donovani. Microbiology. 2012 Jul;158(Pt 7):1775-82.

51. Kumar D, Rajanala K, Minocha N, Saha S. Histone H4 lysine 14 acetylation in Leishmania donovani is mediated by the MYST-family protein HAT4. Microbiology. 2012 Feb;158(Pt 2):328-37.

52. Mallik S, Virdi JS, Johri AK. Proteomic analysis of arsenite - mediated multiple antibiotic resistance in Yersinia enterocolitica biovar 1A. J Basic Microbiol. 2012 Jun;52(3):306-13.

53. Kumar P, Virdi JS. Identification and distribution of putative virulence genes in clinical strains of Yersinia enterocolitica biovar 1A by suppression subtractive hybridization. J Appl Microbiol. 2012 Nov;113(5):1263-72

54. Khasa YP, Khushoo A and Mukherjee KJ. "Enhancing toxic protein expression in E. coli Fed batch culture using kinetic parameters: hGM-CSF as a model system" Journal of Bioscience and Bioengineering. 2013. 115 (3):291–297.

c. Intake(Please put numbers)

	Identified Thrust Areas	**Other Than Thrust Areas**
PhD	10	0
PG	12	0
Fellows	1	0
NET Scholar	8	0
GATE Scholar	1	0
Research Associate	3	0
Project Associate	0	0
Others	1 MPhil	0

11. National/Nodal Character of the Department National/Nodal/All India Centre

a. Resource Persons Invited (Numbers)-

International	**National**
Prof. Matti Karp, TUT, Finland Dr. Ville Santala, TUT, Finland Dr. Tommy Aho, TUT, Finland Ms. Annina Kevisto, TUT, Finland	4

b. Serving for outside user departments in

	Numbers & Hours
i. Hands-on OR technical training	None
ii. Collaborative(international) to university/college teachers	None
iii. Teaching to neighboring institutions	None
iv. Visiting Teachers to foreign university	None
v. Equipment facilities	Serving for outside user department- Microarray facility for all users in country- facility processes samples and provides relevant data to outside campus users as well. Lyopholizer – regular users Spectrophotometer – regular users

	HPLC – regular users Deep Freezer (-80°C) – regular users
vi. Other major infrastructure facilities	Koji Room

12. Most critical and essential requirements that may be required to continue the programme if the UGC agrees to continue or extend support based on theevaluation and final review by expert committee.

Non-recurring	**Recurring**	**Total (Rs.in lakh)** **(As per items given in the guidelines)** **{Please add Annexure)**
Not applicable	Not applicable	Not applicable

13.

a. Whether the State Government will take up the liability of the faculties andthe staff approved under SAP after cessation of the tenure of theprogramme i.e. five years: Not applicable

b. Whether the State Government has already agreed or has taken up theliability after five years of completion of the tenure of the programme aswas communicated along with the approval letter? Not applicable

c. How the Department is going to maintain infrastructure and the status ifUGC disagrees to continue the support further. Whether the Department/University will agree for up gradation of the status on no cost basis, if it sohappens as per the recommendation of the Committee. Not applicable

14. Utilization Certificates may be provided as per the UGC format. Theaccounts of the earlier phase be completed, finalized, audited and dulyauthenticated by the competent authority (Registrar and Finance Officerboth) (item-wise and year-wise) for all the allocations and sanctions givento the Department for ongoing/current phase are to be submitted by theDepartment so that UGC, if provides support again, may immediatelyrelease the funds for the phase to be approved as per the above activities.

Signature of Program Coordinator: **Signature of Registrar of the University**