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 levelatinception	:	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-2013to 31-Mar-2014**

	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	**Nil**	**Nil**	**Nil-**
Amount utilized during the year	**Nil**	**Rs. 30, 212/-**	**Rs.30, 212/-**
Date of first sanction (Current phase)	**No sanction received between 01-04-2013 to 31-03-2014**		
Total grants received since inception	**Rs. 30,00,000/-**	**Rs.7,50,000/-**	**Rs.37,50,000/-**

Coordinator's Name	:	Prof.J.S.Virdi
Dy. Coordinator’s Name:		Dr.RajeevKaul
Address	:	Department of Microbiology, University of Delhi South Campus
City	:	New Delhi
Pin	:	110021
State	:	Delhi
Tel.	:	011-24157240
Fax	:	011-24115270

1. (a) Thrust Area(s) :

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

Future Thrust Area proposed : NA

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

1.Dr.ShankarAlavandi, Senior Scientist, Microbiology, Central Institute of Brackish Aquaculture, R.A .Puram, Chennai-600028(Tamil Nadu).

2. To be nominated by the UGC for which request has already been sent (AfterProf.H.Devraj, University of Madras, Chennai (Tamil Nadu) joined as Vice- Chairman of the UGC)

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 was revised asper the semester system; significant changes in the syllabus have been made to accommodate newer and state-of –art topics ibn Microbiology.

c. **Examination reforms last made with special features** : Semester system adopted in 2009-10; Examinations are now held twice a year as per the semester system introduced.

d. **Teaching lab./equip./new facilities created** : Ultracentrifuge has been purchased and installed from the SAP grant and is being used by the faculty members regularly.

(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).

INDUSTRIAL ENZYMES

(*THRUST ARAE I AS SANCTIONED BY UGC*)

Prof.T.Satyanarayana

Thermo-alkali-stable endoxylanase encoding gene was retrieved from soil-compost metagenome, cloned and expressed in *Escherichia coli* and *Bacillus subtilis*. The recombinant xylanase is useful in generating prebiotic xylo-oligosaccharides and pre-bleaching of paper pulps. The endoxylanase encoding gene of *Bacillus halodurans* was cloned and expressed in *E. coli* and *Pichiapastoris*. The recombinant enzyme has been shown to be useful in generating xylo-oligosaccharides from agroresidues, pre-bleaching of paper pulps and deinking of printed-paper. Theβ-xylosidase of *Geobacillusthermodenitrificans* was cloned and expressed extracellularly in *P. pastoris*. The recombinant enzyme is useful in producing pentose sugars from agro residues, which could be fermented by the yeasts *Pichiastipitis* and *Pachysolentannophilus* to ethanol. The α-amylase and amylopullulanases of *G.thermoleovorans* have been cloned and expressed. The recombinant enzymes have been characterized and shown to be useful in the saccharification of starch into maltose and malto-oligosaccharides.

Prof.Rani Gupta

Cloning and Expression of Industrially Useful Enzymes (Extremophilic Lipase from *Bacillus halodurans*)

Lipases (E.C. 3.1.1.3) are triacylglycerol hydrolases, which are known for their immense potential as important biocatalyst in large number of industrial applications. They are known to catalyze a variety of enantioselective, regioselective and chemoselective reactions and by virtue of this specificity they are considered as indispensable enzyme in pharmaceutical and other important industries. Today, thermostable lipases are of great interest due to their potential to catalyze solvent free reactions. During our ongoing program in our laboratory, *Bacillus halodurans* genome (NC_002570.2) was analyzed for industrially important enzymes. A single annotated gene was found for lipase (Gene ID: 891880), coding for a 385 amino acid protein with a molecular mass of 42.3 Kda.

Sequence comparison and phylogenetic analysis of *lip*H gene showed that it shared 40-45 % homology with lipases/esterases from extremophilic microorganisms namely *Pyrobaculumcalidifontis, Sulfolobustokodaii, Alicyvlobacillusacidocaldarius, Archaeglobusv fulgidus***(Fig. 1)**

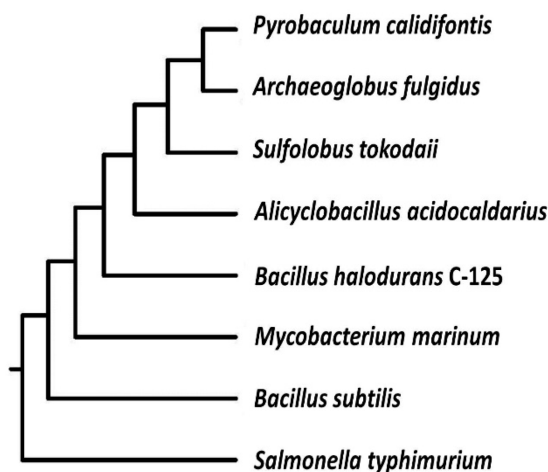


Fig.1 Phylogenetic analysis of lipases/esterases, the amino acid sequences of lipases/esterases were taken from NCBI database.

The multiple sequence alignment of LipH showed that the enzyme belongs to hormone sensitive lipase family with conserved characteristic signature motif G-D-S-X-G. Also, the catalytic triad

serine, histidine and aspartic acid were also conserved. **(Fig. 2**)

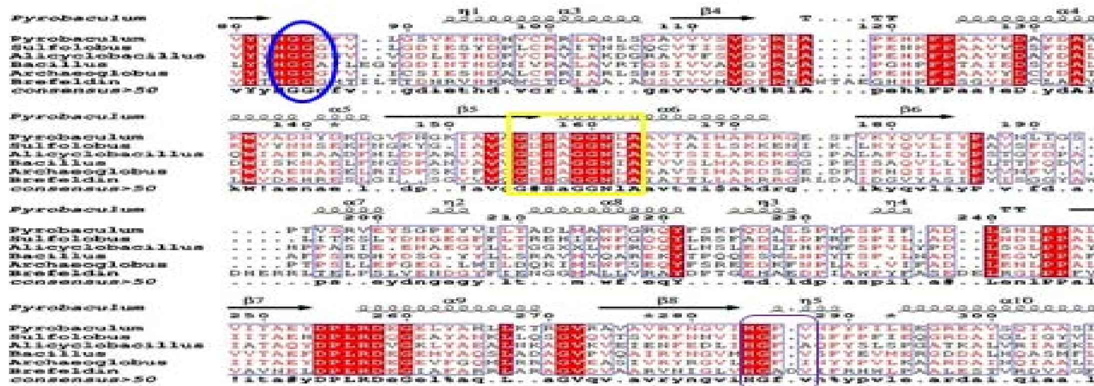


Fig 2. Multiple sequence alignment of LipH with its homologs.LipH was aligned with *Pyrobaculumcalidifontis, Sulfolobustokodaii, Alicyvlobacillusacidocaldarius, ArchaeglobusfulgidusandBacillus subtilis.* **The conserved motif is encircled.**

The gene was cloned into pGEMT-Easy vector system using standard protocol.(Fig. 3). A set of gene specific primers (oligonucleotide) were designed from the ORF BH2248 of lipase gene identified from the complete genome of *B. halodurans*C-125 available at NCBI database. The forward primer alongwith*EcoRI* site 5’GAATTCGACGGTCTCCAAAAGA3’ and the reverse primer with *BamHI* site 5’GGATCCGGTTAGAAGCTGCTGAA3’ were synthesized and the sequences recognized by restriction enzymes are underlined. The amplicon of 1.16 kb was ligated into pGEM-T Easy vector and was transformed into the cloning host, *E. coli* DH5*α.* The positive transformants were designated as pGEM-T-*lip.* The clone was sequenced at Central Instrumentation Facility (CIF), University of Delhi South Campus, and New Delhi.

Expression and Purification of recombinant lipase

The gene was subsequently sub cloned into pET22b expression vector and transformed into the expression host, *E. coli* BL21 (DE3). After transformation, the recombinant colonies were further screened by PCR using gene specific primers to confirm the positive transformants which were designated as *LipH*(Fig. 3)

The recombinant *LipH*was cultivated in TB (Terrific Broth) medium supplemented ampicillin (100 *µ*g/ mL) at 37°C/ 200 rpm until the OD_{600nm} reached 0.5 and then induced with 0.5 mM IPTG. After 48 h incubation, samples were harvested and the cells were separated by centrifugation at 7400 X g for 10 min. Harvested 1 g cell pellet was suspended in 10 mL ice cold 1X PBS and lysed on ice by sonication at 2 sec pulse on and 2 sec pulse off for 10 min and the lysate clarified by centrifugation and expression was checked in the clear lysate by lipase assay and SDS-PAGE analysis. *E. coli* BL21 (DE3) cells harboring only pET-22b(+) without insert was processed in a similar manner and taken as control. Thereafter, purification of *LIpH*was done using Ni^{2+} affinity chromatography and identified by western blotting. Initial characterization showed that the enzyme was active in extreme in alkaline condition (pH 9-13) and temperature(50-100C). Noteworthy was that the enzyme was autoclave stable.

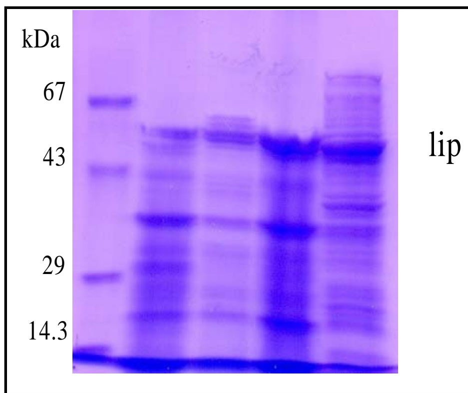


Fig. 3 Expression analysis of LipH by SDS-PAGE and Western Blot, Lane 1: Protein Marker, Lane 2: pET22b only vector in BL21, Lane 3: Supernatant LipH, Lane 4: Only Pellet, Lane 5: Total Broth

CONCLUSIONS

- *In-silico* studies showed its identity with archeal homologs from*Pyrobaculumcalidifontis, Archaeoglobusfulgidus, Sulfolobustokodaii, Alicyclobacillusacidocaldarius*and belonging to Hormone Sensitive Lipase (HSL) family. Its affinity with extremophilic organisms indicated its probable thermophilic nature.

- The lipase gene was cloned and expressed in different *E. coli* vector system and the production from the recombinants was optimized.

- Initial characterization showed protein is autoclave stable.

Prof. R.K.Saxena

Bacterial nanocellulose: a biopolymer of multifarious industrial applications

Importance of bacterial cellulose

Bacterial cellulose has emerged as an important biopolymer having multifarious applications in various fields. It has proven to be the most viable alternative to plant cellulose. Bacterial cellulose has many unique and better properties as compared to plant cellulose like higher purity (free from lignin and hemicelluloses), greater mechanical strength, extraordinary water holding capacity, *in-situ* moldability, higher biodegradability and biocompatibility. Due to these unique properties, it finds applications in various industrial sectors particularly in healthcare, food, textile, cosmetics, paper, audio products, environmental remediation etc. The products manufactured from bacterial cellulose will be of superior quality having more durability and efficiency as it has much better properties. Also, using bacterial cellulose will be more eco friendly, as the need for plant cellulose results in depletion of forest resources which in turn increases the danger of pollution. In this present world, where the pollution is increasing day by day, it is our duty to minimize each and every smallest factor that creates pollution.

Achievements and novelty of the present work

Realizing the importance of bacterial cellulose, we at our place started working on Bacterial Cellulose. It has been more than 5 years working on bacterial cellulose. We started from the very first point, *i.e.* searching a potential cellulose producer. After performing an exhaustive screening, we succeeded in isolating **a novel and potent cellulose producing micro-organism**. We then focused on producing bacterial cellulose in bulk amounts. We worked on developing efficient fermentation technology for producing high amounts of cellulose in an economical way. After doing a great deal of research, we achieved our aim and succeeded **high titers of bacterial cellulose(approx. 17 g/L**) using **an economic optimized process**. We further scaled up the cellulose production **in trays upto 5 L** of the production medium. We have also designed a fermentor, **Biological Contact Reactor**, for large scale production of bacterial cellulose. We successfully **scaled up the bacterial cellulose production in this reactor upto 20 L** of the production medium. In the present work, **a simple, efficient and scalable process for purification of bacterial cellulose** was developed which resulted in **approx. 98 % pure bacterial cellulose.** After purification, analysis of different properties of bacterial cellulose showed that it has **high purity, nanoporous structure, great mechanical strength, high water holding capacity, high thermal stability, good biodegradability and biocompatibility.** Further, we also developed **an efficient process for preparation of bacterial cellulose powder**. Finally, **different potential applications** of bacterial cellulose were evaluated. It was successfully used for **preparation of wound dressings, gloves (for wounded hand) and vessels (artificial vessel for bypass surgeries).** Bacterial cellulose membranes were also used **as paper (for printing and writing), ultra-filtration membrane and for model preparation of dress material, carry bag and footwear**. It was also used as **antimicrobial membrane (drug delivery agent)** after impregnation with antibiotics and other antibacterial compounds.

Prof.R.C.Kuhad

The animal feed development process has been successfully scaled up to 50 Kg level in koji room facility and in a continuous attempt to produce sufficient feed required for *in vivo* animal feed trial. The feed developed has been tested *in vitro* and *in vivo* trials. The animals fed on biotech feed experienced higher weight gain. Moreover, It was also observed 50 %grain can be replaced from concentrate by Biotech feed without compromising its quality.
Xylanase and laccase has been employed for bleaching of paper pulp at Pilot scale in CPPRI, Saharanpur. It was observed that the xylanase helped in lowering down theClO_2 while laccase increased the brightness of the pulp. However, the combination of both the enzymes showed reduction of more than 30% chlorine dioxide usage.

Dr. Y. P. Khasa

Development of *Pichia* cell surface display system

We are working towards development of Pichia cell surface display technology, where native Pichia cell wall proteins are targeted for their heterogonous expression. In this regards, two Pichia PIR1 and PIR2 protein are cloned. Following is the highlight of work done during previous year.1. Cloning of PIR gene signal sequence was done under Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) and Alcohol oxidase (AOX1) we done to secrete targeted protein in Pichia culture supernatant.2. Addition Glu-Ala-Gla-Ala repeats was introduced for proper Kex2 cleavage of signal peptide from fusion protein.3. Gene coding for human Interleukin-3 was cloned under AOX1 and GAP Promoter. An addition His tag was introduced to ease the purification of secretedprotein.4. The clones

so developed were linearized using appropriate enzymes and transformed into competent Pichia cells for homologous recombinant into genome. The recombinant strains were screening using AOX1, GAP and gene-specific primer pairs. 5. For shake flask expression studies, cells were grown in BMGY media and later on transfer in BMMY media containing 0.5% methanol to induce gene expression.6. Protein expression was checked on SDS PAGE and purification of hIL-3 protein was done using affinity chromatography.

MICROBIAL PATHOGENESIS

(*THRUST ARAE II AS SANCTIONED BY UGC*)

Prof.J.S.Virdi

The interaction of two clonal groups of *Yersinia enterocolitica* with J774 macrophages *in vitro* and qualitative and quantitative release of selected pro-inflammatory and anti-inflammatory cytokines

Yersinia enterocolitica is an important food- and water-borne gastrointestinal pathogen. This organism is extremely heterogeneous in terms of biovars, serotypes and pathogenic potential. Currently, *Y. enterocolitica* is represented by six biovars (1A, 1B, 2, 3, 4 and 5) and more than 30 serotypes. Virulence of this organism is attributed to the presence of a 70 kbpYV (*p*lasmid for *Yersinia v*irulence) plasmid and many chromosomally-encoded virulence factors. *Y. enterocolitica*biovar 1A strains are known to lack pYV plasmid and are generally regarded as avirulent. However, several clinical, epidemiological and experimental evidences have indicated their potential pathogenicity (Tennant *et al.,* 2003). The distribution of certain virulence genes namely insecticidal toxins (*tccC*), mucoid*Yersinia* factor (*myfA*), subtilisin/kexin-like protease (*hreP*) and *Yersinia* stable toxin (*ystB*) in biovar 1A strains varied in the two clonal groups and showed higher prevalence in clonal group A strains (Bhagat&Virdi, 2007). As the underlying details of the host immune response towards such clonal differences among the strains is not known, the interaction of *Y. enterocolitica*biovar 1A strains with macrophage cell lines was studied in light of the two clonal groups identified previously. Response of the macrophages to these strains was also studied by quantifying the production of cytokines and activation of NF-κB.

Macrophage survival assay

To check the persistence of *Y. enterocolitica* inside macrophages post-phagocytosis, cultured macrophages were infected with *Y. enterocolitica*as described previously (McNally *et al*., 2007). Briefly, after 1 h of co-incubation at 37 °C,the cells were washed to remove any extracellular bacteria. Fresh supplemented DMEM containing 100 µg mL^{-1} gentamicin was added to each well and incubated further for 5 h. The cells were washed three times with PBS and lysed with 0.1% Triton X-100 solution. Dilutions of the lysate were plated onto TSA plates in duplicate and incubated overnight. Colonies were counted to obtain the total number of bacteria per milliliter that survived inside the macrophages (T =5). In a parallel series of wells, cells were lysed 15 min after the initial addition of gentamicin and plated in order to ascertain the number of bacteria internalized or phagocytosed by macrophages within 1 hour (T = 0).
In many biovar 1A strains, the number of bacteria recovered after 6 h was higher than those recovered after 1 h (**Figure 1**). The initial uptake of clonal group B strains as well as their survival inside macrophages was significantly higher than that of clonal group A strains (**Figure 1**).

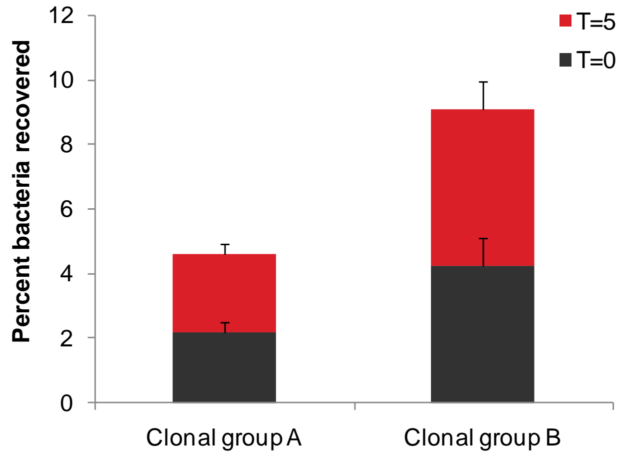


Fig. 1. Percent c.f.u. mL^{-1} recovered following interaction with macrophages *in vitro* after 6 h (T = 5) and 1 h (T = 0). Black and red portions of bar represent mean percent c.f.u. mL^{-1} at T = 0 and T = 5 respectively.

Cytokine production by macrophages

Cultured macrophages were challenged with *Y. enterocolitica* as in the survival assay. Culture supernatant was taken from each well after 5 h and centrifuged at 12,000 g for 5 min to remove bacteria and cell debris. Cytometric bead array (CBA) analysis (mouse inflammation arrays [BD Biosciences] specific for IL-6, IL-10, IL-12p70, TNF-α, IFN-γ and MCP-1) was performed for the culture supernatants according to the manufacturer's instructions. The assays were performed in duplicate on a FACS caliber flow cytometer (BD Biosciences) and the results were analyzed using FCAP 1.0 software (BD Biosciences). The culture supernatants from non-infected macrophages were used as cell controls.

The mean levels of IL-6, MCP-I and TNF-α secreted by macrophages following interaction with different strains of *Y. enterocolitica* are represented in **Figure 2**. No significant (P>0.05) difference was observed in the production of different cytokines *viz*. IL-6, MCP-1 and TNF-α by the macrophages in response to infection by *Y. enterocolitica*biovar 1A strains belonging to two clonal groups (**Figure 2**). There were no variations in the production of three cytokines namely, IFN-γ, IL-10 and IL-12 in response to different strains.

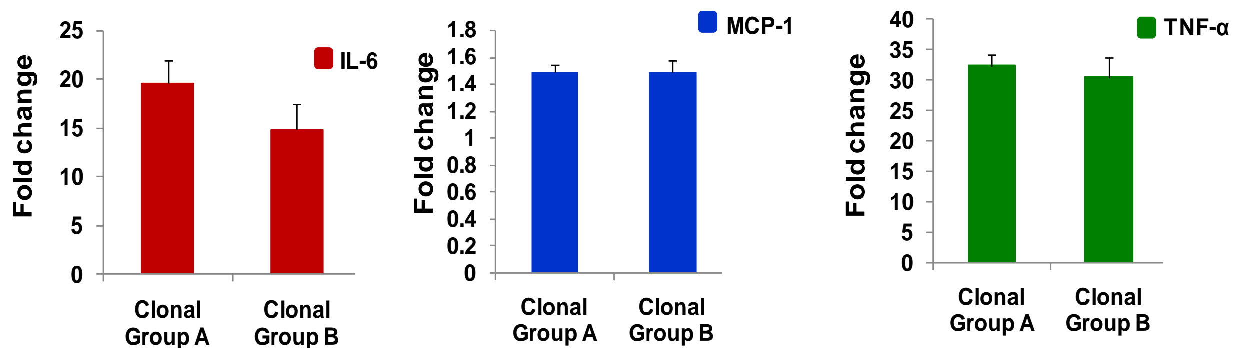


Fig. 2. Comparison of cytokine levels IL-6, MCP-1 and TNF-α in response to strains belonging to the two clonal groups (biovar 1A). The results are expressed as means±SEM and are presented as fold difference relative to the cell control.

NF-κB activation

Macrophages were challenged, in duplicate, with *Y. enterocolitica* for 5 h. Nuclear proteins were extracted from the macrophages using NE-PER nuclear and cytoplasmic extraction reagents (Pierce, Thermo scientific), according to manufacturer's instructions. Quantification of active NF-κB was performed by NF-κB p65 transcription factor assay kit (Pierce, Thermo scientific). Luminescence was recorded at 425 nm on a microplate reader (Spectramax M2). Nuclear proteins extracted from uninfected macrophages were used as cell control.

The levels of activated NF-kB from macrophages infected with different strains of *Y. enterocolitica* were compared to that of the uninfected macrophages (**Figure 3**). Macrophages infected with *Y. enterocolitica*biovar 1A strains showed a substantial increase in the activation of NF-kB. No significant (P>0.05) difference was observed in the activation of NF-kB by the strains belonging to the two clonal groups.

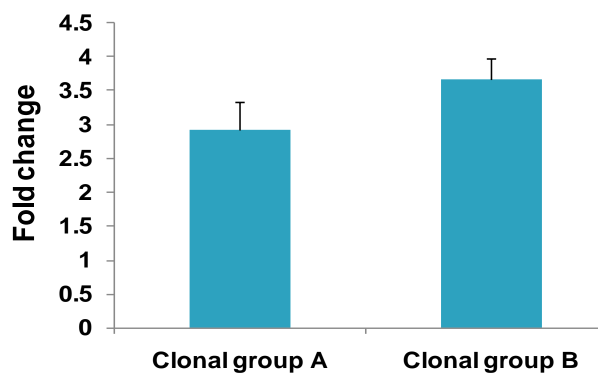


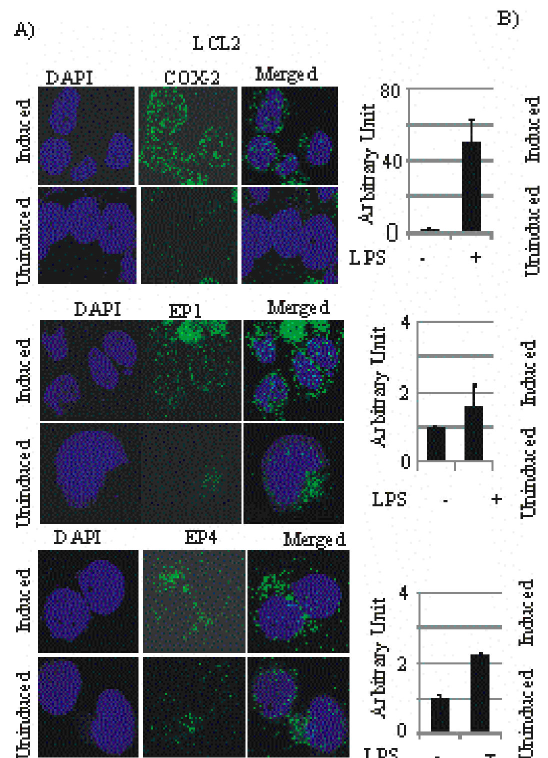
Fig. 3. Comparison of activated NF-κB level in response to strains belonging to two clonal groups (biovar 1A strains). The results are expressed as means±SEM of three experiments performed in duplicate.

Dr.RajeevKaul

Investigate the role of COX-2 downstream effector molecules PGE2 and EP cell surface receptors in EBV lytic reactivation

Epstein Barr Virus (EBV) is a gamma herpesvirus ubiquitous to humans, widely known for its oncogenic properties. One of the predisposing factors known to be associated with EBV mediated tumorigenesis is inflammation. However it is not well understood whether inflammation in itself plays a role in regulating the life cycle of this infectious agent. COX-2, a key mediator of the inflammatory process, is frequently over-expressed in EBV positive cancer cells. In various tumours, PGE2 is the principle COX-2 regulated downstream product which exerts its cellular effect through the EP1-4 receptors. In our study, we further elucidated how inflammation characterized by upregulated COX-2 levels can modulate the events in EBV life cycle related to latency-lytic reactivation. Our data suggest a direct role of upregulated COX-2 on modulation of EBV latency through its downstream effector PGE2 which acts via the EP1 and EP4 receptors to induce lytic reactivation of EBV. The progeny virion released as a result of COX-2 modulated lytic reactivation is biologically active which can successfully infect naïve B-cells leading to their transformation. Our study demonstrates a direct role for increased COX-2 levels in modulation of EBV latency. This is important for understanding the pathogenesis of EBV-associated cancers in people with chronic inflammatory conditions. Our study now adds another dimension to our understanding of the role of inflammation in the progression of cancers mediated by the oncovirus EBV.

Fig.LCL2 were induced with LPS (1ug/ml) for 24 hours and harvested for immunofluorescence assays using anti-COX-2, anti-EP1 and anti EP4 antibodies. The COX-2 expression, EP1 expression, & EP4 expression were up-regulated in induced cells as compared to un-induced cells. The images were analyzed using Image J software for quantification of immunofluorescence signals. The mean values and standard error of three independent experiments are presented as bar graph in right panel.



Dr.SwatiSaha

The laboratory has focused on the study of histone acetylationevents in *Leishmaniadonovani*. Histone acetylases HAT2, HAT3 and HAT4 have beenbiochemically characterized to determine their substrate specificity. We find that all three HATs target the N-terminal tail of histone H4 for acetylation. While HAT2 acetylates the lysine at the 10th position, HAT3 acetylates the lysine at the 4thposition and HAT4 acetylates the lysine at the 14th position. There isno functional redundancy among these HATs, unlike what is seen inyeast and higher eukaryotes where each HAT acetylates multipleresidues. The expression and subcellular localization of allthreeproteins have been analyzed. We find that all three proteins areexpressed at all stages of Leishmania life cycle and cell cycle. WhileHAT2 and HAT3 are constitutively nuclear, HAT4 is cytosolic at allstages though it is present in the nucleus at mitosis.

Dr.Amita Gupta

Despite the introduction of directly observed therapy, short course (DOTS), in 1995, tuberculosis continues to be a serious problem worldwide. *Mycobacterium tuberculosis*(Mtb), the causative agent of tuberculosis (TB), responds to changes in its environment by altering the expression level of critical genes to effect metabolic changes favoring continued survival. Whole genome expression monitoring using microarray hybridization permits the identification of such differentially expressed genes.

For studying gene expression, robust methods for mRNA extraction are paramount. As part of this work, a reproducible method for the preparation of gDNA-free, pure and intact RNA from mycobacteria was optimized. A new updated oligonucleotide microarray for *M. tuberculosis* $H_{37}Rv$ was designed and used for expression profiling of *M. tuberculosis* under different *in vitro* stress conditions mimicking host

environments. A wide range of gene sets have been identified to be differentially regulated and are being further analyzed.

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** :

			UG-	PG-
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 Equipment(>Rs.3 lacs):Ultra Centrifugewas procured from the non-recurring grant received under SAP,installed and is being used.

   Besides this the department has the following major equipment: Fast Protein Liquid Chromatography (FPLC),Biolog automated system, VITEK-2 automated system for identification of bacteria,Fermentor, Fluorescence Microscope, Inverted Light Microscope, Sorvall centrifuge, Gel Documentation system, Thermal Cycler, Spectrophotometers', Shakers, Online RO System, State of art M.Sc. Laboratories, Lyophilizer, Electroporator, Gel Electrophoresis equipment, Rota Evaporator, Speed Vac, -80 Deep Freezer and Well equipped Research Laboratories.

b. Central Schemes/facilities for PG, Research and Extension Activities (Pleasetick the one applicable to your Department :

   (i) STEP : NA
   (ii) IIPC : NA
   (iii) USIC / RSIC : Central Instrumentation Facility Available
   (iv) Patent Promotion Cell : Available
   (v) Guesthouse with capacity : Available, 6-Rooms Facility
   (vi) Seminar /Conference Room with capacity: Departmental Seminar Room (seating capacity 50 persons); Biotechnology Building Seminar Room (seating capacity 200 persons)and the Management Department Seminar Hall (seating capacity 300 persons) are available on the campus and may be reserved for any function with prior permission of the Head of the Institution.
   (vii) Regional/Mainframe computing facilities : Available
   (viii) Central Library with documentation facilities: Available
   (ix) Continuing EducationCentre : Available at the North Campus
   (x) Women Development Cell : Available at the North Campus

c. Networking(Please tick the right one):

   (i) Library : Available
   (ii) Laboratory : Available
   (iii) UniversityDepartment : Available

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

i. Other teaching institution (Name, No. of faculty involved) : All faculty members of the Department have been delivering invited lectures in several institutions and conferences inareas of their expertise which mainlyfall into two thrust areas namely Microbial Enzymes and Microbial Pathogenicity

ii. The faculty members have also been Involved in teaching of other Departments *viz*. Biochemistry, Plant Molecular Biology and Genetics; Four faculty namely Prof. J.S.Virdi, Dr. Swati Saha, Dr. Rajeev Kaul, Dr. Amita Gupta members have been involved in this.

iii. Industry (Name with amount received if any) : None

iv. Rural/Tribal/Govt./NGOs(Provide No. with amount) : None

v. International (name organization) : None

vi. Others : None

vii. Innovation/excellencebrought in (Please specify in the identified thrust areas only):
Production of industrial enzymes
Production of Recombinant enzymes
Molecular epidemiology of enteric pathogens

5. Breakthrough (already recognized) : None

6. Emerging/Hi-tech/Priority area generated : Microbial whole genome sequencing of indigenous strains, and Recombinant enzymes of industrial importance.

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

Items	**Amount**	**Items**	**Amount**
Consultancy:	None	Sponsored(agency) R&D Projects: From DBT, DST, ICMR, DRDO, CSIR, MoFPI and UGC	Rs. 183 Lacs
Transfer of technology: In progress (With NRDC) Detection of adulterated milk using a simple kit)	None	Product & Prototype development: None	None
Patent utilization: In progress (With Aditya Birla Group) Use of Microbial Cellulose	None	Exploitation of internal facilities by user departments : The department uses various instruments available at Central Instrumentation Facility (CIF), DNA sequencing Facility, Liquid nitrogen facility, DBT Sub Distribution facility	None

National / International Collaboration: a) Neighboring institutions: ICGEB, TERI, JNU,IITD, NBRC b) Industries: Tata, Reliance, ABC Paper Mills, Dabur Research Foundation c) National organizations: BHU, Osmania University d) International Organizations: HZI, Inst Mol Enzyme Tech, Kayushu Univ e) Any other collaborative Program: None	None
Human Resource Training: a) International Students:One student admitted to M.Sc. Microbiology every year under the foreign student quota through the Foreign Student Registry (FSR) of the University of Delhi. b) Industrial: None c) Extension activities: None d) Other courses:The faculty members of the Department of Microbiology have been, time to time,involved in the teaching of interdisciplinary courses*viz*. Immunology, Pathogenic Microbes, Microbial Genetics, to students of other departments namely Departments of Biochemistry, Genetics and Plant Molecular Biology and Biotechnology (PMBB) of the University. The faculty members include -**Prof. J.S.Virdi, Dr. Swati Saha, Dr. Rajeev Kaul, Dr. AmitaGupta**	None

Sponsored and R and D Projects:

Prof. T. Satyanarayana

1. Cloning and expression of phytase of *Sporotrichum thermophile*
   (Department of Biotechnology* =Rs. 23.25 Lacs*)
1. Carbon monoxide dehydrogenase of Actinobacteria
   (*Department of Biotechnology* = Rs. 30.65 Lacs)

Prof. J.S. Virdi

1. Role of probiotic lactic acid bacteria in modulating antibiotic susceptibilities of enteric pathogens
   (Sanctioned by Indian Council of Medical Research= Rs. 40lac).

Dr. Rajeev Kaul

1. Generation and characterization of a panel of Epstein Barr virus transformed lymphoblastoid cell lines of diverse origin
   (Funded by UGC=Rs. 14 lac)

Collaboration with national organizations:

Prof. T.Satyanarayana

1. M.D. University, Rohtak (In DBT funded project)
2. Manipur University, Imphal (in DBT funded project)

Prof. J.S. Virdi

1. Department of Biophysics, University of Delhi South Campus (In an ICMR funded project)

a. **Total amount of resource generated from all sources above** : Rs. 183 lacs

b. **Also mention development grant received from University in other areas of the Department**:
The Department has received grant from Department of Science and Technology under the DU-DST-PURSE programme.
Funds received under DU-DST-PURSE Grant (Phase I) :Rs. 2.50 Crore
Funds received under DU-DST PURSE Grant (Phase II)
: Rs. 2.00 Crore

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

Item	No.	Item	No.
a. Industries	**Yes**	b. Other user Deptts	Ministry of Food Processing Industries
c. National organizations	**Yes**	d. Other Organizations	None

9. a. Other activities:

Items	Numbers	Time Duration
Seminar	Two seminars were delivered to the Departmental Faculty and students by eminent scientists from India and abroad	1 hour each
Summer Institute	None	N.A
Conference	National :None International : None	N.A N.A
Refresher Course	None	N.A

b. Autonomous Character : Yes

Financial	Yes
Administrative	Yes
Academic	Yes
Others	Yes

c. Advisory Committee Meeting (No. with Dates):

1. One meeting of the Advisory Committee was held on 21-Feb-2014. The following members attended the meeting:

    i. Vice Chancellor (represented by Dean FIAS, Prof. Madan Mohan), Chairperson Advisory Committee
    ii. Prof. J. S. Virdi, Head, Member Secretary Advisory Committee & Coordinator SAP
    iii. Dr. S. Alavandi, UGC Nominee
    iv. Prof. R. K. Saxena, Member Advisory Committee
    v. Prof. T. Satyanarayana, Member Advisory Committee
    vi. Prof. Rani Gupta, Member Advisory Committee
    vii. Dr. Swati Saha, Member Advisory Committee
    viii. Dr. Amita Gupta, Member Advisory Committee
    ix. Dr. Yogender Pal Khasa, Member Advisory Committee

2. At the outset, the Chairman welcomed all the members and the UGC Nominee present at the meeting, and invited Prof. J. S. Virdi, Coordinator of the Program, to present the progress report of the SAP program for the year 2013-14.
3. Prof. J. S. Virdi gave an elaborate presentation on the activities of the program for the year 2013-2014 and the proposed activities and research planned for the year 2014-15.
4. The UGC expert, Prof. Alavandi expressed satisfaction over the progress of program and congratulated the Department for the achievements.
5. It was decided that the next Annual Meeting of the Advisory Committee will be held in March

Proceedings of the advisory committee attached: SEE NEXT PAGE

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	BRSI FAMI, BRSI - FAMI, BRSI -	Microbial Enzymes Microbial Enzymes Microbial Pathogenenesis Microbial Enzymes Microbial Enzymes
Associate Prof.	1. Swati Saha	-	Microbial Pathogenesis
Assistant Prof.	1. Amita Gupta 2. YogenderKhasa 3. Rajeev Kaul	- - -	Microbial Pathogenesis Recombinant Proteins Microbial Pathogenesis
Emeritus/ Visiting Prof.	None	-	N.A.

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

INDUSTRIAL ENZYMES

Prof. R.K. Saxena

Mahajan, R V., Rajendran, V. J., Kumar, V., Saran, S., Ghosh, P. C. andSaxena R. K.Purification and Characterization of a novel and robust L-asparaginase having low- glutaminase activity from *Bacillus licheniformis*: in-vitro evaluation of anti- cancerous properties. (2014). ***PloS One, 10.1371/journal.pone.0099037***

Kumar, V., Jahan, F., Kameswaran, K., Mahajan, R. and Saxena, R.K. (2014). Eco-friendly methodology for efficient synthesis and scale up of 2-ethylhexyl-p-methoxycinnmate using *Rhizopusoryzae* lipase and its biological evaluation**. *J Industrial Microbiology Biotechnology, DOI 10.1007/s10295-014-1429-0***

Kumar, V., Yadav, S., Jahan, F., Raghuwanshi, S. and Saxena R.K. (2013). Organic synthesis of maize starch based polymer using *Rhizopusoryzae* lipase, scale up and its characterization. ***Preparative Biochemistry and Biotechnology, 44:321-31***

Rawat, G., Tripathi, P. and Saxena, R.K. (2013) Expanding horizons of shikimic acid. Recent progresses in production and its endless frontiers in application and market trends. ***ApplMicrobiolBiotechnol. 97:4277-87***

Saran, S., Mahajan, R.V., Kaushik, R., Isar, J., and Saxena R.K. (2013) Enzyme mediated beam house operations of leather industry: a needed step towards greener technology. ***J. Cleaner Production 54:315–322***

Rawat, G., Tripathi, P., and Yadav, S. and Saxena R.K. (2013) An interactive study of influential parameters for shikimic acid production using statistical approach, scale up and its inhibitory action on different lipases*. **Bioresource Technology,144 : 675–679***

Yadav, S., Rawat G., Tripathi, P. andSaxena R.K. (2013) Dual substrate strategy to enhance butanol production using high cell inoculum and its efficient recovery by pervaporation***Bioresource Technology, pp- 377-383.***

Kumar, V., Jahan, F., Raghuwanshi, S., Mahajan,R.V., and SaxenaR.K. (2013) Immobilization of *Rhizopusoryzae* lipase on magnetic Fe3O4-chitosan seeds and its potential in phenolic acid ester synthesis. ***Biotech. Bioprocess Engg. 18: 787-795***

Tripathi, P., Rawat, G., Yadav, S. and Saxena R.K. (2013). Fermentative production of shikimic acid: a paradigm shift of production concept from plant route to microbial route. ***Bioprocess and Biosystems Engineering. DOI 10.1007/s00449-013-0940-4***

Rawat, G. Tripathi, P., Jahan, F. and Saxena, R.K. (2013). A natural isolate producing shikimic acid: isolation, identification and culture condition optimization. ***Applied Biochem. & Biotech. DOI:10.1007/s12010-013-0150-1***

Mahajan, R.V., Saran, S.,Saxena, R.K(2013) A rapid, efficient and sensitive plate assay for detection of L-asparaginase producing microorganism. ***FEMS Microbiol Letters, 341: 122-126***

Prof. T.Satyanarayana

Joshi, S. and Satyanarayana, T. 2014. Optimization of heterologous expression of the phytase (PPHY) of*Pichiaanomala* in *P. pastoris* and its applicability in fractionating allergenic glycinin from soy protein*.* ***J. Indust. Microbiol. Biotechnol. DOI 10.1007/s10295-014-1407-6***

Mehta, D. and Satyanarayana, T. 2014. Domain C of thermostable α-amylase of *Geobacillusthermoleovorans* mediates raw starch adsorption. ***Appl. Microbiol. Biotechnol. DOI 10.1007/s00253-013-5459-8***

Kumar, V. and Satyanarayana, T. 2014. Production of endoxylanase with enhanced thermo-stability by a novel polyextremophilic*Bacillus halodurans* TSEV1 and its applicability in waste paper deinking. ***Proc. Biochem. 49 (2014)386–394***

Verma, D. and Satyanarayana, T. 2013. Production of cellulase-free xylanase by the recombinant *Bacillus subtilis* and its applicability in paper pulp bleaching.***Biotechnol. Progress. 29:1441-1447***

Verma, D. and Satyanarayana, T. 2013. Improvement in thermostability of metagenomic GH11 endoxylanase (Mxyl) by site-directed mutagenesis and itsapplicability in paper pulp bleaching process. ***J. Indust. Microbiol. Biotechnol. 40: 1373-1381***

Kumar, V. and Satyanarayana, T. 2013. Biochemical and thermodynamic characteristics of thermo-alkali-stable xylanase from a novel polyextremophilic*Bacillus halodurans* TSEV1. ***Extremophiles 17: 797-808***

Kumar, V. and Satyanarayana, T. 2014. Production of thermo-alkali-stable xylanase by a novel polyextremophilic*Bacillushalodurans*TSEV1 in cane molasses medium and its applicability in makingwhole - wheat bread. ***Biopr. Biosyst. Engin. 37: 1043-1053***

Joshi, S. and Satyanarayana, T. 2013. Characteristics and applications of a recombinant alkaline serine protease from a novel bacterium *Bacillus lehensis*.***Biores. Technol. 131: 76-85***

Sharma, A. and Satyanarayana, T. Characteristics of a high maltose-forming, acidstable and Ca^{2+}-independent α-amylase of the acidophilic *Bacillus acidicola*.2013. ***ApplBiochem Biotechnol. 171: 2053-2064***

Sharma, A. and Satyanarayana, T. 2013. Structural and biochemical features of acidic α-amylase of *Bacillus acidicola*. ***Intl. J. Biol. Macromol. 61: 416-423***

Mehta, D. and Satyanarayana, T. 2013. Dimerization mediates thermo-adaptation, substrate affinity and transglycosylation in a highly thermostablemaltogenic amylase of *Geobacillusthermoleovorans.* ***PLoS One e73612: 1 – 13***

Kumar, V. and Satyanarayana, T. 2013. Biochemical and thermodynamic characteristics of thermoalkali-stable xylanase from a novel polyextremophilic*Bacillus halodurans* TSEV1. ***Extremophiles 17: 797-808***

Verma, D., Anand, A. and Satyanarayana, T. 2013. Thermostable and alkali stable endoxylanaseof the extremely thermophilic bacterium *Geobacillusthermodenitrificans* TSAA1: Cloning, expression, characteristics and its applicability in generating xylo-oligosaccharides and fermentable sugars*.* ***Appl. Biochem. Biotechnol. 170: 119-130***

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

Anand, A., Kumar, V. and Satyanarayana, T. 2013. Characteristics of thermostableendoxylanase and β-xylosidase of the extremely thermophilic bacterium*Geobacillus thermo-denitrificans* TSAA1 and its applicability in generatingxylooligosaccharides and xylose from agro-residues***Extremophiles 17: 357-366***

Verma, D. andSatyanarayana, T.2013.Cloning, expression and characteristics of a novel alkalistable and thermostablexylanase encoding gene (Mxyl) retrieved fromcompost-soil metagenome. ***PLoS One 8: e52459: 1- 8***

Prof. R.C. Kuhad

Raghuwanshi, S., Deswal, D., Karp, M.,Kuhad, R.C**.** (2014)Bioprocessing of enhanced cellulase production from a mutant of *Trichodermaasperellum* RCK2011 and its application in hydrolysis of cellulose. ***Fuel 124: 183–189***

Deswal, D., Gupta, R., Nandal, P., Kuhad RC(2014) Fungal pretreatment improves amenability of lignocellulosic material for its scarification to sugars. ***Carbohydrate Polymers*****99:264-269**

Upadhyay, M., Srivastava, B., Jain, A., Kidwai, M., Kumar, S., Gomes, J., Goswami, DG., Panda, A.K.,Kuhad, RC**.,** (2014)Production of ganoderic acid by *Ganodermalucidum* RCKB-2010 and its therapeutic potential.***Annals of Microbiology. DOI 10.1007/s13213-013-0723-9***

Sharma S, Sharma KK and Kuhad RC (2013). An efficient and economical method for extraction of DNA amenable to biotechnological manipulations, from diverse soils and sediments. ***Journal of Applied Microbiology*. *116:923-933***

Kumar S, Srivastava N, Gupta BS, Kuhad RC and Gomes J. (2013). Lovastatin production by *Aspergillusterreus* using lignocellulose biomass in large scale packed bed reactor. ***Food and Bioproducts Processing. Doi.org/10.1016/j.fbp.2013.10.007***

Kidwai M, Jain A, Sharma A andKuhad RC. (2013).Laccase catalyzed reaction between Meldrum's acid and catechols/hydroquinones- An investigation**. *ComptesRendusChimie*16*:728-735***

Kumar, L., Kumar, D., Nagar, S., Gupta, R., Garg, R., Kuhad, RC., Gupta, VK. (2013). Modulation of xylanase production from alkaliphilic*Bacillus pumilus*VLK-1 through process optimization and temperature shift operation*.* ***Biotech.DOI 10.1007/s13205-013-0160-2***

Chandna, P., Mayil R. Kuhad, RC. (2013). *Bacillus paraflexus* sp. nov., isolated from compost**. *Int J SystEvolMicrobiol. 63:4735-4743***

Varma A.J., Kuhad RC, Singh R, Gupta R, Adsul M, Gokhale D. (2013). Biodegradation of Styrene-Butadiene-Styrene Coploymer *via* sugars attached to the polymer chain. ***Advances in Materials Physics and Chemistry. 3:112-118***

Nandal P, Ravella SR. Kuhad RC (2013). Laccaseproduction by Coriolopsis caperata RCK2011: Optimization under solid ststefermentation by Taguchi DOE methodology. ***ScientificReports. 3:1386***

Sharma KK, Shrivastava B, Sastry VRB, Sehgal N and Kuhad RC (2013). Middle redox potential laccase from Ganoderma sp: itsapplication in imrovementoffeed from monogastric animals. ***ScientificReports. 3:1299***

Kumar S., Gupta R., Kumar G., Sahoo D. and Kuhad R.C. (2013). Bioethanol production from *Gracilariaverrucosa*, a red alga, in a biorefinery approach. ***Bioresource Technology*. 135:150-156**

Prof. Rani Gupta

Gupta R, Rajput R, Sharma R and Gupta N (2013), Biotechnological applications and prospective market of microbial keratinases, ***ApplMicrobiolBiotechnol*, 97(23), 9931-9940**

Rajput R and Gupta R (2013), Expression of *Bacillus pumilus*keratinase rK_{27} in *Bacillus subtilis*: enzyme application on developing renewable flocculants from bone meal**, *Ann Microbiol*, DOI 10.1007/s13213-013-0770-2**

Rajput R and Gupta R (2013), Thermostablekeratinase from *Bacillus pumilus* KS12: Production, chitin crosslinking and degradation of Sup35NM aggregates, ***Bioresource Technol*, 133, 118-126.**

Kumari A and Gupta R (2013), Heterologous expression, purification and characterization of thermostable lip11 from *Yarrowialipolytica* in *Pichiapastoris X33,* ***J Prot Proteomics,* 4, 5-10.**
Rajput R, Verma VV, Chaudhary V and Gupta R (2013), A hydrolytic *γ*-glutamyltranspeptidase from thermo-acidophilic archaeon*Picrophilustorridus*: binding pocket mutagenesis and transpeptidation, ***Extremophiles*, 17, 29-41**

Gupta R, Sharma R and Beg Q (2013), Revisiting microbial keratinases: Next generation proteases for sustainable biotechnology, ***Crit Rev Biotechnol*, 33(2) 216-228**
Sharma R, Verma VV and Gupta R (2013), Functional characterization of an extracellular keratinolytic protease, Ker AP from Pseudomonas aeruginosa KS-1: A putative aminopeptidase with PA domain, ***J. Mol. Catal.*, 91, 8-16**

MICROBIAL PATHOGENESIS

Prof. J.S. Virdi

Dhar MS, Gupta V, Virdi JS (2013) Detection, distribution and characterization of novel superoxide dismutases from *Yersinia enterocolitica* biovar 1A*.* ***PLoS One 8 (5) e63919***

Bhaduri A, Misra R, Bhetaria P, Mishra S, Maji A, Arora G, Virdi JS, Singh Y (2013) *Mycobacterium tuberculosis*cyclophilin A uses novel signal sequence for secretion and mimics eukaryotic cyclophilins for interaction with host protein repertoire***PLoS One 9 (3) e88090***

Rastogi N, Nagpal N, Alam H, Pandey S, Gautam L, Sinha M, Shin K, Manzoor N, Virdi JS, Kaur P, Sharma S, Singh TP. (2014) Preparation and antimicrobial action of three tryptic digested functional molecules of bovine lactoferrin.***PLoS One 9 (3) e90011***

Dhar MS, Virdi JS (2013) Interaction of *Yersinia enterocolitica*biovar 1A with cultured cells *in vitro* does not correlate with the two clonal groups. ***Journal of Medical Microbiology 62:1807-1804.***

Dhar MS, Kumar P, Virdi JS (2013) Exogenous phage recombinase-independent inactivation of Chromosomal genes in *Yersinia enterocolitica*. ***Journal Microbiological Methods, 95: 102-106***

Dhar MS, Virdi JS (2013) Strategies used by *Yersinia enterocolitica* to evade killing by the host: thinking beyond YOPS. ***Microbes and Infection, 16:87-95***

Srivastava A, Singhal N, Goel M, Virdi JS, Kumar M.(2014) Identification of family specific fingerprints in β-lactamase families.***ScientificWorldJournal doi 10.1155/2014/980572***

Dr. Swati Saha

Arora, J, Goswami, K, &Saha, S. (2014). Characterization of the replication initiator Orc1/Cdc6 from the archaeon*Picrophilustorridus*.***JBacteriol.*** **196: 276-286**

Dr. Amita Gupta

Venkataraman, B., M. Vasudevan, and A. Gupta, *A new microarray platform for whole-genome expression profiling of Mycobacterium tuberculosis.***J Microbiol Methods***, **2014. 97: 34-43***

Kumar, K., S. Rajasekharan, S. Gulati, J. Rana, R. Gabrani, C.K. Jain, A. Gupta, V.K. Chaudhary, and S. Gupta, *Elucidating the interacting domains of chandipura virus nucleocapsid protein.***Adv Virol, 2013. 2013: 594319***

Gupta, A., N. Shrivastava, P. Grover, A. Singh, K. Mathur, V. Verma, C. Kaur, and V.K. Chaudhary, *A Novel Helper Phage Enabling Construction of Genome-Scale ORF-Enriched Phage Display Libraries.***PLoS One, 2013. 8(9): e75212***

Venkataraman, B., N. Gupta, and A. Gupta, *A robust and efficient method for the isolation of DNA-free, pure and intact RNA from Mycobacterium tuberculosis.***J Microbiol Methods, 2013. 93(3): 198-202***

c. Intake(Please put numbers)

	Identified Thrust Areas	Other Than Thrust Areas
PhD	2 1 1 2	0
PG	2	0
Fellows	1	0
NET Scholar	1	0
GATE Scholar		0
Research Associate	1 1 1	0
Project Associate	1	0
Others	0	0

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

a. Resource Persons Invited (Numbers):

International	National
None	None

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. Lyophilizes – regular users, Spectrophotometer – regular users, Microscope- regular users from other departments.
vi. Other major infrastructure facilities	Koji Room Facilities

12. Most critical and essential requirements that may be required to continue theprogramme 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 programmeaswas 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 / Director of the University