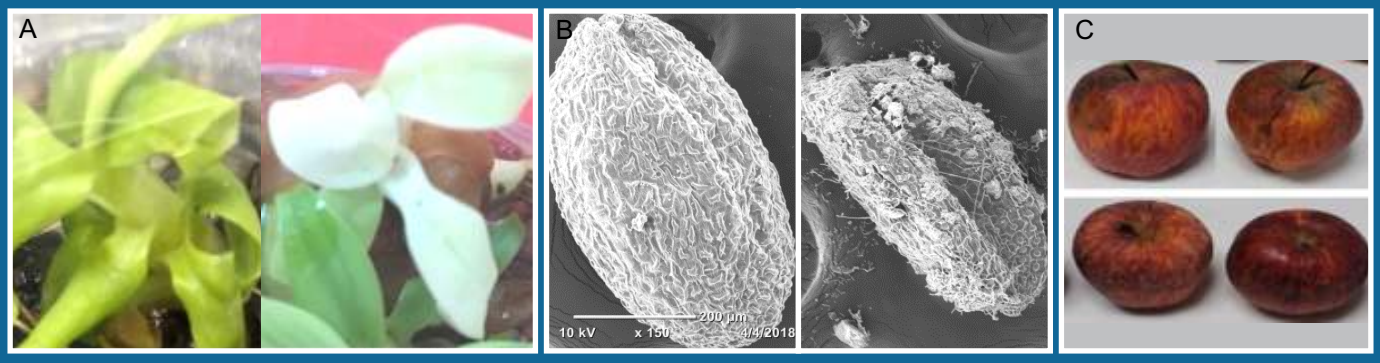
ANNUAL REPORT
2017-18

NATIONAL AGRI-FOOD BIOTECHNOLOGY INSTITUTE (NABI)



NATIONAL AGRI-FOOD BIOTECHNOLOGY INSTITUTE

(DEPT. OF BIOTECHNOLOGY, MINISTRY OF SCIENCE & TECHNOLOGY, GOVERNMENT OF INDIA)
SECTOR-81, KNOWLEDGE CITY, MOHALI, PUNJAB 140306 INDIA

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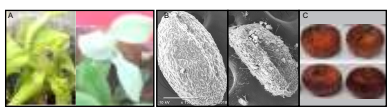

Cover page:- (A) Phenotype of genome-edited lines of Banana PDS gene. (B) SEM pictures of col 0 (left) and A-ZIP53 transgenic (right) seeds. (C) Images of un-coated apples (upper panel) and coated with 1% AX-SABG (lower panel)

Contents

FROM THE DESK OF EXECUTIVE DIRECTOR

National Agri-Food Biotechnology Institute (NABI) was established by the Department of Biotechnology, Govt. of India in 2010 with the objectives of working on four broad areas like Agricultural Biotechnology, Food and Nutritional Biotechnology, Human Resource Development and Technology Transfer and Outreach. The institute has started functioning from its new campus since March 2017, which was formally inaugurated by Dr Harsh Vardhan Ji, Union Minister for Science and Technology, Earth Sciences and Environment, Forests and Climate Change on August 6, 2017.

In the area of Agri-biotechnology, wheat and banana improvement have been the major focus at NABI. Various nutritional traits viz. increasing amylose content, improved processing quality for its product development, enhancing micronutrient content and Pro-vitamin A has been the central theme areas for the past few years. During the last one year, considerable progress has been made to characterize the wheat TILLING population at the candidate gene level. Improved varieties of anthocyanin rich coloured wheat have been taken to the commercial level and four MoU`s have been signed with different companies to extend the work for product development. On the similar lines, transgenic approach has been used to generate low phytate wheat and iron homeostasis related genes. Researchers at NABI have also demonstrated proof of concept in Banana for the feasibility of carrying out CRISPR based genome editing. These innovations could be applicable for plants like Banana, wheat and other fruit crops having immense potential for the Indian agricultural sector.

In the area of food and nutritional biotechnology significant achievements have been made during the past one year. Under the research program dealing with functional foods and nutraceuticals for better health, putative probiotic bacterial strains that could prevent low protein, moderate fat and high sucrose diet induced metabolic, inflammatory and behaviour abnormalities have been identified and now prioritized for further studies. A proof of concept has been developed for the usage of sweet prebiotics such as isomalto-oligosaccharides in combination with antioxidant/anti-inflammatory agents such as cinnamaldehyde and cranberry extract in protecting against high fat diet induced obesity and associated complications to develop novel class of functional foods as "Cobiotics". We have developed fabricated nanomaterials in food for enhancement of micronutrients bioavailability, a novel

liposomal drug delivery system (NH+) encapsulating GDP (NH+GDP). We are also developing multifunctional gold nanorod based colorimetric nanobiosensor for detecting food borne bacteria. A novel edible coating formulation has been developed at NABI from agricultural by-products that could enhance shelf life of perishable fruits such as apple and peaches while maintaining the nutritional quality.

With the developing landscape of the institute three Ramalingaswamy fellows and five DST-Inspire faculties have joined at NABI during the last one year. These new scientists will be working on challenging areas of Agri-Food and Nutritional sciences.

During the past one year, we have also organized an international conference and a brain storming session on developing a multi-institutional research programme on "Development of biofortified and protein rich wheat" under the Chairmanship of Dr. R.S. Paroda, Chairman, SAC. In this one-day deliberation many scientists from, NABI, NARS and International organization participated and discussed to develop a research programme in which partners from different organizations from India and aboard can be involved.

Our aim is to develop trained human resource in the form of Ph.Ds, postdoctoral fellows and visiting scientists in the above research areas. I am happy to inform that NABI has been recognized as a center for pursing Ph.D. degree in Biotechnology as well as NABI scientists are now recognized as adjunct faculty of The Regional Centre for Biotechnology, Faridabad.

I sincerely place on record my gratitude to Dr Harsh Vardhan ji, President, NABI Society and Honorable Minister of Science and Technology, Environment, Forests & Climate Change and Earth Sciences for his valuable input to improve various programmes of the institute.

I express my gratitude to Prof. K. VijayRaghavan, former Chairman, Governing Body (GB) of NABI and Secretary Department of Biotechnology (Govt. of India) and Dr. Renu Swarup, present Chairperson, GB and Secretary DBT as well as other members of the GB for their valuable suggestions in shaping various programmes of the institute. I am also grateful to Dr. R.S. Paroda, Chairman, Scientific Advisory Committee (SAC) and all the members of the SAC and PACs for their scientific advices and intellectual inputs which have helped in evolving and focusing the research plans and activities of the Institute. I place on record my sincere thanks to Dr. V. S. Chauhan, Chairman, Building Committee (BC) and all the members of BC as well as Dr. R. S. Khandpur Chairman, Consultant Management Committee (CMC) and all the members of CMC for their kind support as well as efforts for the development of new campus.

All time help, support and co-operation of Smt. Gargi Kaul, former Financial Advisor and Mr B. Anand, Additional Secretary & Financial Advisor and Shri. C. P. Goyal, Joint Secretary, Dr M. Aslam and Dr. A. Vamsi Krishna, Scientist (Food and Nutrition) Department of Biotechnology, Government of India is thankfully acknowledged.

I am happy to inform that this annual progress report is an outcome of the efforts of scientists, staff and students working at NABI. My special thanks are due to Dr. Ajay Pandey, Dr. Kanthi Kiran, Dr. Mahendra Bishnoi, Dr. Siddharth Tiwari and Mr. Arun Kumar for their help in compiling and editing of the annual report.

(Dr. T.R Sharma)
Executive Director

VISION, MISSION & GOAL OF NABI

Vision

Food and nutritional security for all through agri-food biotechnology research and innovation.

Mission

To be a centre of excellence and provide leadership in agri-food biotechnology research.

Goal

Improving nutritional quality and availability of affordable agri-food and food products through innovations

HUMAN RESOURCE & SCIENTIFIC ACHIEVEMENTS

Ph. D. Awarded : 07	Publications : 154
Patents : 11	Conferences attended/Lectures delivered : 130
Guest Lectures : 26	Conference & workshops organised : 03
Trainees : 124	Scientific / Administrative Staff : 33

(Till 31st March, 2018)

RESEARCH PROGRESS

(AGRICULTURAL BIOTECHNOLOGY- AB01)

DEVELOPMENT OF DESIGNER CROPS WITH HIGH NUTRITION, INCREASED SHELF LIFE AND PROCESSING QUALITY

1.1 Gene discovery for improvement of processing and nutrition quality in wheat

Principal Investigator
Joy K Roy

Research Fellows
Pankaj Kumar
Ankita Mishra
Saba Rahim
Afsana Parveen
Vinita Sharma

Objective 1: Improvement of Indian wheat varieties for high amylose or resistant starch (nutritional quality)

Introduction

Wheat (*Triticum aestivum* L.) flour is processed into several end-use food products, whose processing and nutrition quality are largely determined by storage protein (~12%) and starch (~70%). Starch affects processing, cooking, and organoleptic qualities as well as nutritional value of food products. The present wheat varieties require the improvement in nutrition and processing quality to meet the increasing demand of consumers and food industries. The availability of variation in starch quality in wheat germplasm and knowledge of genome-wide distribution of genes/chromosome regions controlling starch processing and nutrition quality are pre-requisite for starch quality improvement. In this project, variation in amylose content, which is otherwise narrow in wheat germplasm, is induced via non-transgenics approach by chemical mutagenesis using, ethyl methyl sulphonate (EMS). The mutant lines showing variation in amylose content and resistant starch are identified in the EMS-treated lines. Some of high amylose mutants are being used for introgression of high amylose into the present high yielding wheat varieties as well as for the studies of molecular and genetic basis of high amylose. Genomics approaches will be implemented to identify single nucleotide polymorphisms (SNPs) which can be used along with microsatellites on a diverse wheat germplasms, mutant population, and biparental mapping populations to identify markers for QTLs (quantitative trait loci). Candidate QTL regions will be further saturated using SNPs to identify causal genes. Validation of the associated genes will be done using functional genomics tools. In long term, pyramiding will be done by combing high amylose/resistant starch with other important biomolecules such as high grain protein content. In this context following activities were undertaken, a) Updating and maintaining repositories of wheat germplasms including mutation population, association, and biparental mapping populations and genomic resources including transcriptome and genome sequences for marker development and gene discovery; b) genetics and molecular basis of high amylose and processing quality variation using biparental, mutation, and association mapping populations and lastly, c) identification of candidate genes and their validation using functional genomics tools.

Research Progress

1. Germplasm and genomic resources: A collection of wheat germplasm comprising of about 500 indigenous and exotic wheat genotypes including landraces and Indian wheat varieties, 1,200 EMS treated advance (M7) population, ~250 anueploid stocks, and several biparental progenies have been multiplied in growing season 2017-18. Transcriptome sequence data of two mutant lines (high and low amylose lines) and the parent variety, 'C 306', a good chapatti variety are available for functional genomics analysis.
2. Amylose mutant population (AMLpop): A set of 101 mutant lines showing variation in amylose content (~ 3 to 76%) and resistant starch (0 to 45%) was advanced to M8 generation seeds at NABI research farm during rabi season 2017-18 through a single spike to row method. Each time, a single spike is harvested for next season multiplication. The amylose content is being validated on these lines.
3. Multiplication of high amylose mutation lines for product evaluation: The high amylose mutant lines along with parent variety ('C 306') and current high yielding variety ('WH 1105') was grown individually

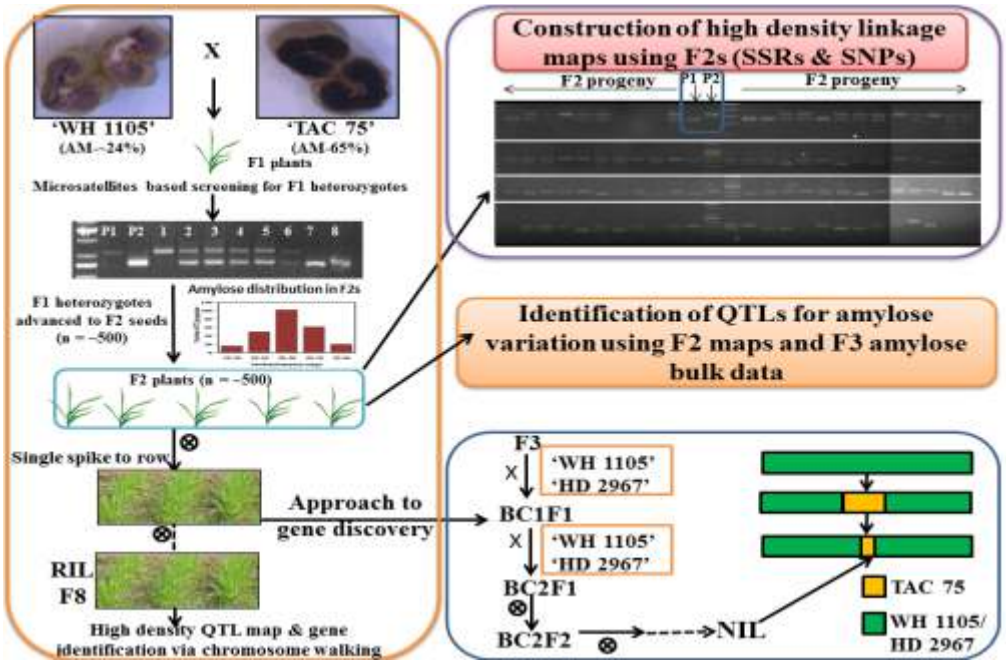

Figure 1: Strategies for development of mapping populations (F2, RILs, BCs, NILs), construction of linkage maps, QTL mappings and gene discovery for high amylose starch in wheat

in area of 100 square feet in 2017-18 season. The seeds will be evaluated for amylose and different end-use food products. High amylose starch wheat will be evaluated for glycemic index, mineral uptake, pre-and pro-biotics using mice model and/or cell lines. High amylose starch will be explored for pharmaceutical applications with the help of NIPER, Mohali. Profiling of gluten, vitamins, mineral, phenolics content, etc. will be done on high amylose mutant lines.

4. Construction of linkage maps and QTL mapping: The strategy for linkage map construction and high density QTL mapping is outlined in Figure 1. An individual seeds of about 500 F2 lines ('TAC-75' x 'WH 1105') were grown to F3 by single seed selection method. The mutant line 'TAC 75' is a high amylose mutant line in background of a good chapatti variety, 'C 306' and the Indian wheat variety, 'WH 1105' is current high yielding variety. A subset of 94 F2 progenies (randomly selected) and the two parents were genotyped using 70 SSRs (so far) and through genotyping by sequencing (SBS). The high throughput SNPs and SSRs genotyping data are being used for study of segregation distortion and construction of high linkage maps. Out of 210 SSRs, 70 SSRs (~30%) showed polymorphism between the parents. Chi-square test for marker fitted Mendelian segregation(1:2:1) in the population identified 15 SSRs showing linkage distortion at p = 0.05. SSR linkage data will be used as anchoring markers for SNPs-based linkage map construction. The amylose content is being quantified on the seeds of F3 lines for QTL mapping.
5. Identification of SNPs in promoter and coding regions of high amylose starch biosynthesis genes: Starch biosynthesis is controlled by a combination of key genes such as granule bound starch synthase (GBSSI), starch branching enzymes (SBE) and soluble starch synthases (SSI, SSII, SSIII, SSIV). The sequencing of the genes were done following cloning and transformation of their cDNAs and extracted recombinant DNAs were sequenced on ABI capillary sequencing system (3730XL). The sequencing of the amylose biosynthesis key gene, GBSS I identified point mutations that altered its amino acid sequences in low amylose ('TAC 6') and high amylose ('TAC 75') mutant lines in comparison to the parent wheat variety ('C 306') (Figure 2). The sequencing of promoter regions (~ 1 kb) of the genes identified 5 to 10 SNPs.
6. Identification of candidate bZIP TFs for high amylose variation. An important genomics approach is to

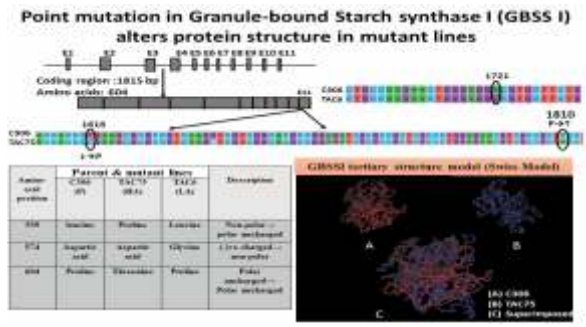

Figure 2: Point mutations (non-synonymous SNPs) induced by EMS mutagenesis in GBSS I gene causing alteration in its protein sequence and structure.

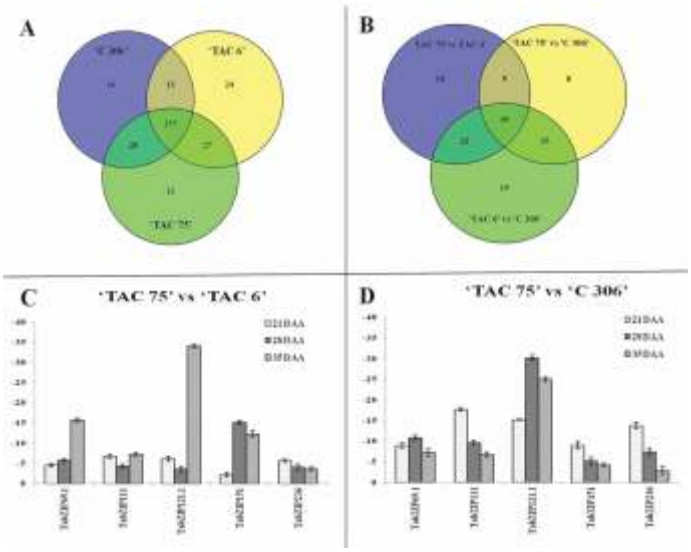

Figure 3: (A) Venn diagrams showing the number of bZIPs expressed (FPKM, fragment per kilo per million, > 0.02) in two mutant lines, 'TAC 75' (amylose content = 64%) and 'TAC 6' (amylose content = 7%) and the parent variety, 'C 306' (amylose content = 26%). (B): Comparative analysis of the differentially expressed bZIPs (>2-fold FPKM) in the three pairs, 'TAC 75' vs 'TAC 6', 'TAC 75' vs 'C 306' and 'TAC 6' vs 'C 306'. The overlapped regions show the common TabZIPs. The FPKM values were determined from nextgen sequencing data (two biological replicates). Comparative expression analysis (qRT-PCR) of candidate TabZIPs is represented in 'TAC 75' vs 'TAC 6' (C) and 'TAC 75 vs 'C 306' (D). The expression was analysed at three stages of seed development (21, 28 and 35 DAA). 'TAC 75', 'TAC 6' and 'C 306' represent high, low amylose mutant lines and parent respectively. All the data are represented as mean ± SD from three technical replicates.

identify regulatory factors controlling AM biosynthesis using mutant lines, which is not known in wheat. Genome survey identified 370 wheat bZIPs, (Tab ZIPs) showing variation in composition and physiochemical properties and about 50% of them were new. The functional genomic approaches identified positive and negative candidate bZIPs regulators using mutant lines deciphering bZIP's pivotal role in amylose biosynthesis, which is not known in wheat.

For example, the analysis of transcriptomic sequences (284 Gb) conducted on the two contrast mutants (65% AM or ~37% RS vs 7% AM or 1% RS) and their parent variety identified 12 TabZIPs that expressed only in high AM mutant. Additional two (bZIPs, TabZIP96.1 and TabZIP13.4) and four (TabZIP237.3, TabZIP237.1, TabZIP77.1, and TabZIP59.6) bZIPs identified with very high (>100-fold) up and down expression, respectively in the high amylose mutant line (Figure 3). qRT-PCR analysis during seed development identified additional five negative TabZIP regulators. Candidate TabZIPs can be manipulated for the improvement of high amylose starch in wheat grains and to understand molecular mechanism of TabZIP regulation.

Salient Achievements

1 The 101 mutant lines showing variation in amylose content was advanced to M8 generation. Out of the, the high amylose mutant lines were multiplied in large blocks for product evaluation. Introgression lines (F3) and back cross lines (BC1F3) were produced for amylose estimation and QTL mapping.

2 The 94 F2 progenies were genotyped using 70 SSRs and genotyping by sequencing (GBS) for SNPs.

3 The sequencing of GBSSI gene identified non-synonymous mutation in its Exon 11 that can change GBSSI structure effecting its activity.

4 The analysis of transcriptomic sequences (284 Gb) conducted on the two contrast mutants (65% AM or ~37% RS vs 7% AM or 1% RS) and their parent variety and qRT-PCR identified candidate 23 TabZIPs transcription factors that may regulate the biosynthesis of amylose in wheat.

1.2 Improvement of processing and nutritional quality in wheat

Principal Investigator
Monika Garg

Research Fellows
Aman Kumar
Amandeep Kaur

Introduction

Wheat is an important cereal crop being consumed as staple food by Indian population. It is source of starch, proteins and dietry fibers. But it is poor in essential micronutrients required for normal human growth and development like lysine, vitamin A, folic acid, iron, zinc, selenium, antioxidants etc. Wheat requirs improvement in terms of its nutritional quality. Its gluten causes celiac disease (CD); a T-cell mediated autoimmune enteropathy caused by permanent intolerance to gluten fraction of wheat in 1% of genetically predisposed persons. The only available treatment for this disease is the adherence to a strict life-long gluten free diet. There is need to improve wheat to make it safer for consumption for CD patients.

In the developed countries, grain market is driven by wheat quality. A wheat class/grade is awarded to a product based on its processing and end-use quality. But in India cultivars are released based on agro climatic zones, time of sowing and soil fertility. In India there is need of breeding cultivars based on processing quality (milling and baking characteristics). Processing quality of wheat depends on seeds harvested from field and its components like proteins, starch, non starch carbohydrates and lipids. Protein's contribution to processing quality is well known. The protein content and types determine the end product quality like bread, biscuit, cake, chapatti and noodles etc. It is important to understand structure, allelic variation and interaction pattern of different seed components and transfer them to high yielding, disease resistant and locally adapted cultivars.

Research Progress

1. For improvement of bread making quality, we are utilizing wild species *Agropyron elongatum, Aegilops longissima, Ae. searsii, Ae. geniculata* and *Ag. intermedium*. These genetic stocks were crossed with high yielding cultivars (PBW550, PBW621, HD2967). We intend to transfer HMW-GS genes related to high grain strength from wild species to chromosome 1A of wheat as later has least, rather negative effect on bread making quality in some backgrounds. Chromosome 1A specific translocation line of *Ag. elongatum* [1EL(1AS)] with potential of bread making quality improvement was generated in the background of wheat cultivars PBW621 (1EL(1AS)/5*PBW621-F8) (Figure 1). NILs of two grain textures Hard and Soft were created. Stability of grain texture was tested for several generations. Hard translocation line maintained hard texture and soft translocation line maintained soft grain texture (Table 1). These NILs retained HMW-GSs from *Ag. elongatum*. Yield, TKW and SDS sedimentation test indicated that although these had lower yield than check PBW621, dough strength of hard NIL was higher (Table 2). Other Agronomic parameters were similar to PBW621 (Table 3). Quality parameters including product making quality of these lines indicated that soft translocation line exhibited higher extensibility and hard translocation line higher mixing properties.

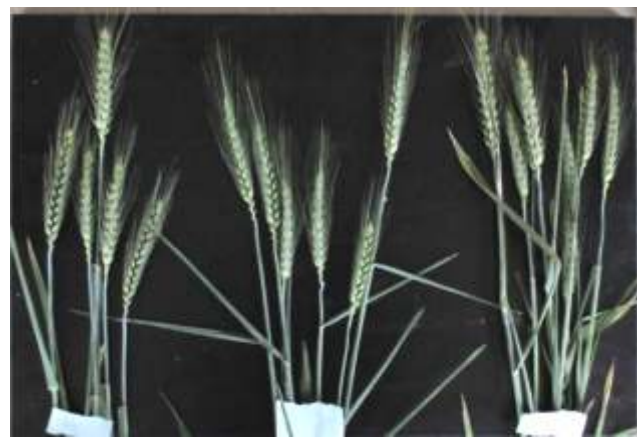

Figure 1: Spikes of hard and soft translocation lines in comparison to background cultivar.

Table 1. Stability of grain texture and HMW Gs observed in different years and locations

Name	Pedigree	2015-16		2016-17		2017-18	
		Grain texture	HMW GS by PAGE	Grain texture	HMW GS by PAGE	Grain texture	HMW GS
E532	PBW621/1EL(1AS)/5*PBW621/F_8	Hard	1Ex,1Ey present	Hard	1Ex,1Ey present	Hard	1Ex,1Ey present
PBW621	Recipient parent	Hard	1Ex,1Ey absent	Hard	1Ex,1Ey absent	Hard	1Ex,1Ey absent
1EL.1AS (Soft N61 background)	Donor parent	Soft	1Ex,1Ey present	Soft	1Ex,1Ey present	Soft	1Ex,1Ey present
E542	PBW621/1EL(1AS)/5*PBW621/F_8	Soft	1Ex,1Ey present	Soft	1Ex,1Ey present	Soft	1Ex,1Ey present

Table 2. SDS sedimentation, Yield and thousand kernel weight observed in different years and locations

Name	Pedigree	2015-16			2016-17			2017-18		
		Yield Q/Acr	SDSs	TKW(g)	Yield Q/Acr	SDSs	TKW(g)	Yield Q/Acr	SDSs	TKW(g)
E532	PBW621 /1EL(1 AS)/ 5*PBW621 /F_8	18.5	5.9	32.5	16.9	6.8	37.3	17.2	5.1	33.1
PBW621	Recipient parent	20	4. 8	37	21.5	5.2	35	22	4.2	36.6
1EL.1AS (Soft N61 background)	Donor parent	13.7	3	32.1	16.1	2.8	30.5	16.9	3.2	28
E54 2	PBW621/1EL(1 AS)/ 5*PBW621 /F_8	15.4	4	33.2	16.5	4.2	34.2	18.3	3.8	32.5

Table 3. Agronomic traits of E532 translocation line and high yield parent

Name	Plant height	Spike length	Spikelets per spike	Awn length
E532	93.8	11.0	21.6	5.9
PBW621 (Recipient)	97.7	11.2	21.8	5.1
1EL.1AS (Soft N61 background)	104.6	9.3	18.8	3.8
E542	115.2	12.1	21.9	5.9

2. To reduce the immunogenicity associated with alpha-gliadins encoded by chromosome 6AS of wheat, and to introduce soft grain trait in Indian wheat to improve its biscuit making quality, translocation of Hynaldia villosa in wheat (6VS.6AL) were selected. It carries resistance to both yellow rust (Yr26, chromosome 1B) and powdery mildew (Pm21, 6VS). It had soft grain texture. It was crossed with high yielding cultivar HD2967 and resultant line with yellow rust resistance and soft grain texture was developed. Three lines 1. Hexaploid wheat HD2967 background (6VS.6ALxHD2967xHD2967xHD2967-F6), 2. Tetraploid durum wheat PDW233 (6VS.6ALxPDW233XPDW233-F6), 3. Tetraploid durum wheat PDW291 (6VS.6ALxPDW291xHD2967xHD2967-F6), showed improved yield potential, reduced plant height, improved disease resistance with a new source of yellow rust resistance (Yr26) and above all lowered immunogenicity. It was further purified by single spike decent. One line NABIMG-3 gave best yield and field performance (Figure 2). Stability of grain texture was tested for several generations. NABIMG-3 showed stable soft grain trait (Table 4). Its yield and

thousand kernel weight (TKW) were significantly higher than donor wheat cultivar (Table. 5). Initial plant pathological screening nursery (IPPSN) data for stem rust, leaf rust, stripe rust and leaf blight indicated desired resistance for different rusts as well as blight in NABIMG-3 (Table 6). This line can be used directly for development of soft wheat products, alternately it can be used in future breeding programs.

1. Crosses were made to combine (1EL.1AS) and (6VS.6AL) translocation lines. Several lines with vigorous growth, better yield potential, disease

Figure 2: Field performance of NABIMG-3 in early and late stage of seed development

Table 4. Stablility of seed texture observed in different years and locations

Name	Pedigree	Grain Texture 2015-2016 (NABI)	Grain Texture 2016 (Kelong)	Grain Texture 2016-2017 (NABI)	Grain Texture 2017 (Kelong)	Grain Texture 2017-2018 (NABI)
NABIMG-3	EC753717/3* HD2967-F8	Soft	Soft	Soft	Soft	Soft
HD2967	Recipient parent	Hard	Hard	Hard	Hard	Hard
EC753717	Donor parent	Soft	Soft	Soft	Soft	Soft

Table 5. Yield and thousand kernel weight observed in different years and locations

Name	Yield 2017-18 (Late sown) T/Acre	TKW (g) 2017-18 (Late sown)	Yield 2017-2018(PSCST) T/Acre	TKW (g) 2017-2017 (PSCST)	Yield 2017-2018 (NABI) T/Acre	TKW (g) 2017-2018 (NABI)
NABIMG-3	4.2	38.2	5.2	40.5	6.1	42
HD2967	4.5	38	5.0	40.2	5.8	42
EC753717	3.2	36	4.5	38	4.8	40

Table 6. Two year initial plant pathological screening nursery (IPPSN) data of NABIMG-3 line for stem rust, leaf rust, stripe rust and leaf blight

IPPSN (2017-18)											
Sr. No.	Entry	Rust score								Leaf blight	
		Stem		Leaf				Stripe		(0-9) dd	
		South		South		North		North			
		HS	ACI	HS	ACI	HS	ACI	HS	ACI	HS	AV.
676	NABIMG-3	10MS	3.1	20S	6.3	TR	0.1	20S	6.5	68	46
680A	Infector	100S	70.0	100S	70.0	80S	60.0	100S	80.0	79	68
IPPSN (2016-17)											
1235	NABIMG-3	10MS	2.7	10S	2.5	0.0	0.0	20S	11.4	56.0	36.0
20A	Infector	100S	86.7	100S	82.0	80S	73.3	80S	80.0	89.0	79.0

resistance and possessing (6VS.6AL) translocation lines have been selected at F3 and F4 stage and sent to kelong for generation advancement/disease screening.

2. To characterise Yr26 gene, and its chromosome location and linkage with HMW-Glutenin Glu-B1 gene, endosperm half of around 2000 F2 seeds from above cross were screened for HMW-glutenin profile. Parental lines were screened for race specific rust resistance (IIWBR, flowerdale, Shimla) and was found to resistant to all the races. Emryo half of around 500 seeds was screened for most virulent race. Linkage was found between rust resistance and Glu-B1 locus.

Salient Achievements:

1. Translocation line of Ag. elongatum in soft and hard wheat background 1EL(1AS)/5*PBW621-F7 has been created, quality assessed and transferred to breeders.
2. Advanced material with potential to reduce immunogenicity and soft grain trait in hexaploid background and hard grain trait in durum background has been generated.

Objective 2: Transfer and characterization of anthocyanins from blue, purple and black grain colored germplasm to high yielding Indian wheat cultivars

Principal Investigator

Monika Garg

Research Fellows

Saloni Sharma

Payal Kapoor

Plant phytochemicals such as anthocyanins can act as antioxidants and show anti-inflammatory, anti-cancer, anti-aging activity and prevent cardiovascular diseases and type-2 diabetes. In the present proposal, we aim to develop colored wheat lines with high anthocyanin content that could be exploited for nutraceutical applications. It has advantage over anthocyanin rich fruits and vegetables, as later has very short shelf life and cannot be stored for long. Wheat is major farmer crop, with all required machinery in place. Colored wheat can be used as novel ingredient resource for the development of value added products and functional foods. The project revolves around generation of high yielding, localy adapted colored wheat commercial lines with non-GMO breeding technologies, chemical characterization of different anthocyanins, preclinical and clinical studies to enhance outreach and commercial abilities, development of value added and functional food products for better human health, generation of public awareness about the benefits, large scale multiplication with the involvment and additional income generation of farmers and technology transfer to different milling and baking industries.

Research progress

1. Colored wheat was non-existent in Indian germplasm. There is no publication on colored wheat from India. NABI initiated research on colored wheat lines eight years back and came out with commercial product. Three advanced colored wheat (Black, blue and purple) were registered with NBPGR and MOUs were signed with Fram producer company, Ambala and Borlaug farm association of south Asia, Ludhiana. Colored wheat was sown by several farmers (Figure 3). The farmers field trials were conducted in Punjab, Haryana, UP, MP, Gujrat and Chattisgarh. Around 80 farmers have grown it, with 56% followed the normal agricultural pratices and 44% grew it in organic method of cultivation.

Yield assessment in comparison to white wheat

Figure 3: Farmer field location of purple wheat. Red, green and yellow arrows represent normal, organic and partly organic cultivation practice used.

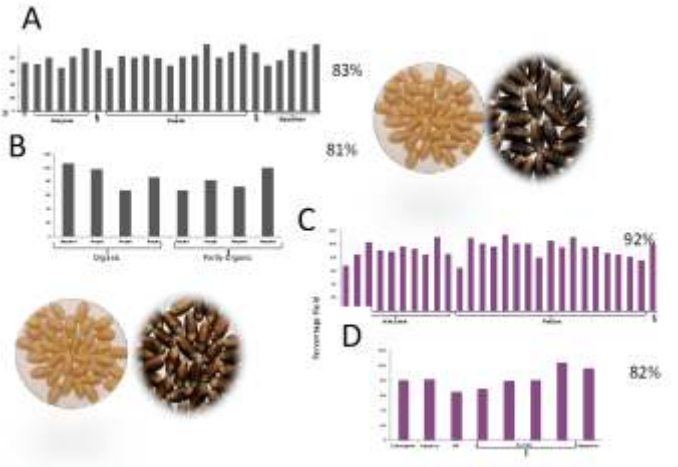

Figure 4: Yield performance of black and purple wheat grown under normal and organic cultivation at farmers field. A- Black normal, B- Black organic, C-Purple normal, D-Purple organic

check at NABI and at farmers' field indicated 80-90% yield for purple wheat and around 70% in black and blue wheat. Comparison was also made in organic and normal method of cultivation (Fig. 4). For black wheat under normal and organic cultivation, yield was 83%, 81% respectively. For purple wheat it was 92% and 82% respectively.

2. In order to further improve the yield and rust resistance of colored wheat lines, several new crosses and further backcrossing were performed. One line (NABIMG-15) prepared by three back crosses with high yielding Indian cultivar PBW621 and was followed for production of the stable purple colored line (F7 generation). Developed colored wheat line had satisfactory yield potential and regional adaptation. Stability of grain color was monitored for several generations. NABIMG-15 showed stable purple color in the seeds (Table 7). Its yield and thousand kernel weight (TKW) were significantly higher than donor wheat cultivar (Table 8). Other agronomic traits like plant height, spike length and splikelets per spike were similar to PBW621, but its anthocyanin content was much higher than white wheat (Table 9). This line can be used directly for development of colored wheat products, alternately it can be used in future breeding programs.
3. Colored wheat lines showed anti-obesity effect on high fat diet (HFD) treated mice. In vivo studies using high fat diet induced obesity models suggested that black and purple wheat lines could effectively prevent fat deposition, improve glucose homeostasis, insulin tolerance and lower the serum cholesterol and free fatty acids levels. Transriptome analysis of liver and adipose tissue indicated pathway enrichment for Adipogenesis, Insulin Sensitivity, Antioxidative/Anti-inflammatory effect, Carbohydrate Metabolism, Extra Cellular Matrix (ECM) in case of adipose tissue. Adipogenesis, Insulin Sensitivity, Antioxidative/Anti-inflammatory, Xenobiosis, ECM and Transportation pathways were enriched in case of liver tissue in black wheat (HFD) and purple wheat (HFD) in comparison to white wheat diet (HFD) and normal pellet diet. After pathway enrichment common differentially expressed genes in all treatments, which were significantly different in tukey's post-hoc test were shortlisted and functionally evaluated from various literatures. They were grouped according to their functions as shown in Fig 5.

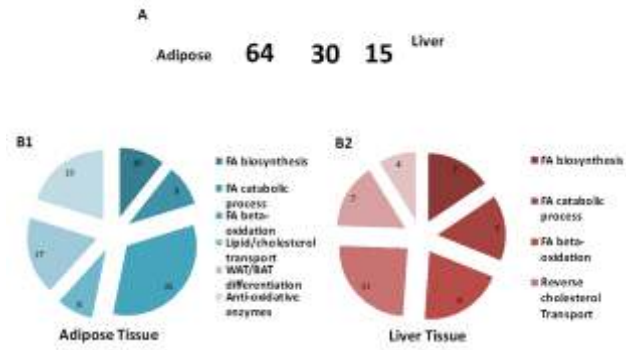

Figure 5: Transcriptome analysis of adipose and liver tissue : (A) Ven-diagram representing differential expresses genes, 94 in adipose and 45 in liver tissue, respectively. (B1) and (B2) Number of genes of different pathways in adipose and liver tissue.

Table 7. Stablility of purple color observed in different years and locations

Name	Pedigree	Grain color 2015-2016 (NABI)	Grain color 2016 (Kelong)	Grain color 2016-2017 (NABI)	Grain color 2017 (Kelong)	Grain color 2017-2018 (NABI)
NABIMG-15	28H129/ 4*PBW621	Purple	Purple	Purple	Purple	Purple
PBW621	Recipient parent	Amber	Amber	Amber	Amber	Amber
BW EC866732)	Donor parent	Purple	Purple	Purple	Purple	Purple

Table 8. Yield and thousand kernel weight observed in different years and locations

Name	Yield 2017-18 (Late sown) Q/Acre	TKW (g) 2017-18 (Late sown) Q/Acre	Yield 2017-2018(PSCST) Q/Acre	TKW (g) 2017-2017 (PSCST) Q/Acre	Yield 2017-2018 (NABI) Q/Acre	TKW (g) 2017-2018 (NABI) Q/Acre
NABIMG-15	18	38.2	21	40.5	22	42
PBW621	17	38	21.5	39.5	22	40
BWEC866732)	6	23	10.68	27.23	10.14	27.0

Table 9. Agronomic traits of colored wheat line and high yielding parent

Name	Plant height	Spike length	Splikelets per spike	Anthocyanin content (mg/kg)
NABIMG-15	93.0	12	20	65.6
PBW621	100.0	12	21	2.3

Salient Achievements

1. We have signed MOU with two companies and farmers have cultivated colored wheat with good yield.

1.3 Functional genomics strategies for improving micronutrient transport and its bioavailability in wheat

Principal Investigator
Ajay Kumar Pandey
Research Fellows
Anil Kumar
Parul Goel
Mandeep Kaur
Gazaldeep kaur
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Objective 1: Metabolic engineering of phytic acid pathway to enhance iron bioavailability in wheat grains

Introduction

Micronutrient deficiency is a nutritional disorder that affects human health globally. In particular iron and zinc deficiency is of serious concern for both poor and developed nations. Hexaploid wheat (Triticum aestivum L.) is one of the important food crops consumed widely in large amounts and thus can be a potential candidate for micronutrient biofortification. The breeding efforts to enhance iron and zinc content or its bioavailability in wheat face challenges because of the low genetic diversity. In addition to that, the presence of certain anti-nutrients like phytic acid (PA) and polyphenols in wheat grains renders low bioavailability of these micronutrients. Therefore, achieving lowered PA content in cereal grains is a desired trait to address the problem. However, strategies directly targeting the PA biosynthesis genes in wheat have not been explored. In an effort to generate low phytic acid wheat, we have studied the genes involved in PA biosynthesis pathway or its putative transporter. RNAi based silencing was performed for, *TaIPK1*(inositol pentakisphosphate kinase) and *TaABCC13* (an ABC type transporter)..

Research Progress

1) Earlier, silencing of *TaABCC13* showed major pleotropic effects that includes, grain development, PA reduction and lateral root formation. Silencing of *TaIPK1* also resulted in lowering of grain PA (upto ~55%) with enhanced accumulation of Fe and Zn.
2) The above work concluded that *IPK1* in wheat is preferable candidate to enhance iron content or its bioavailability. Overall, this work suggests that *IPK1* is a promising candidate for enhancing the micronutrient bioavailability in wheat. Currently, we are performing CRISPR tool for editing of *TaIPK1* and a negative regulator of iron uptake referred as iron homestasis as-*IRO3*.

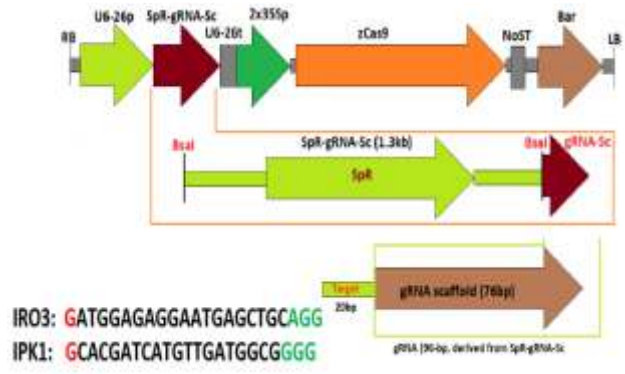

Figure 1: Schematic representation of CRISPR construct for editing of genes i.e. *IPK1* and *IRO3* in wheat.

Salient Achievements

1) *TaIPK1* is a suitable candidate to achieve low phytic acid in wheat.
2) Lowering of wheat IPK1 resulted in enhanced Fe:PA and Zn:PA molar ratio at T_3 stage.

Objective 2: Characterization of wheat major facilitator super family transporter genes to enhance micronutrient content in developing grains

Introduction

Wheat is one of the most important cereal crop, consumed by a large population in many parts of the world, yet it contains a suboptimal concentration of an essential micronutrient like Fe. Although limited progress has been made to understand iron homeostasis in cereal grains the contribution of these metal transporter remains obscure. Few other studies in wheat have provided a proof of concept for improving the grain Fe content by employing transgenic approaches mostly targeting micronutrient bioavailability. These findings have encouraged researchers to identify novel candidate genes in hexaploid wheat genome those could be potentially used for transport of an specific micronutrients like iron or zinc. Very limited studies have been done to characterize wheat Yellow Stripe Like (YSL) protein and therefore comprehensive genome wide study is lacking in hexaploid wheat. The YSLs are the member of oligopeptide transporter (OPT) family. The members of YSL subfamily are specialized in long distance transport of metal-chelates thus playing a significant role in metal (Fe, Zn, Cu, Mn, Ni) homeostasis. Previous studies in Arabidopsis, rice and barley have signified the involvement of YSLs in Fe acquisition and its distribution in various plant tissues. Therefore, in order to work in the direction of crop biofortification it is very important to first identify plant YSL transporters and subsequently understand its specific role during the micronutrient homeostasis. Additionally, limited knowledge is available regarding the genes involved during the iron homeostasis in wheat. The current work is an attempt to identify specific metal transporters that could serve as an important resource to address micronutrient enhancement in grains.

Research Progress

Till date multiple YSL transporter genes have been identified from Arabidopsis thaliana, Oryza sativa, Brachypodium distachyon and Zea maize. Although limited progress has been made to understand iron homeostasis in cereal grains the contribution of these metal transporter remains obscure in wheat. Therefore, in order to work in the direction of crop biofortification it is very important to first identify plant YSL transporters and subsequently understand its specific role during the micronutrient homeostasis.

1) In this study, sixty seven putative wheat YSL proteins were identified. These proteins were then subsequently subjected to phylogenetic analysis resulting in their distribution into four discrete YSL clades. Comparative synteny mapping of wheat YSL proteins with *O. sativa* and *Brachypodium* was also performed that enabled us to understand the evolution of the YSL orthologs within the grass species.

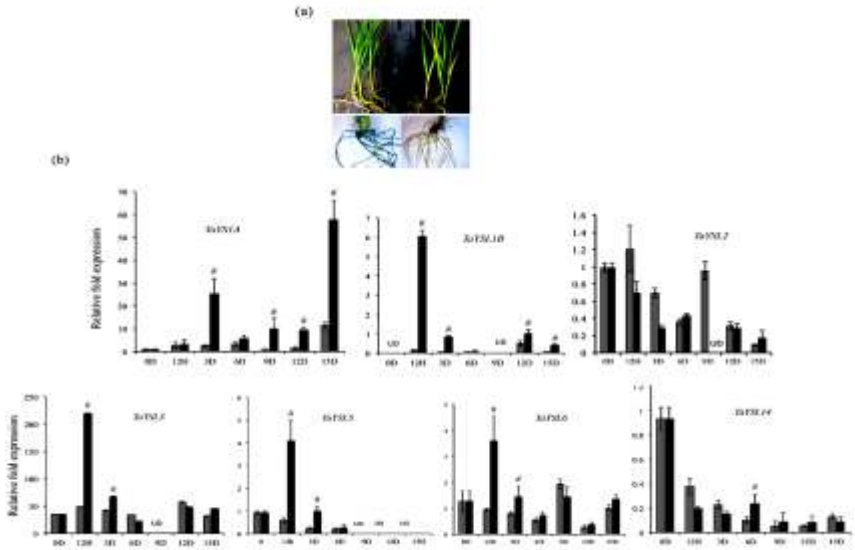

Figure 1: Analysis of wheat seedling under control (+Fe) and iron limiting (-Fe) conditions. (A) Perl's Staining showing iron accumulation in roots of control and Fe starved plants. (B) Expression analysis of selected wheat YSL genes was performed in wheat seedling roots subjected to Fe-starvation and control for 0D (days), 12Hr, 3D, 6D, 12D and 15D using quantitative real time PCR (qRT-PCR). DNA free RNA was extracted from all the time point studied. Data represents mean of three biological replicates. Vertical bars represent the standard deviation. # on the bar indicates that the mean is significantly different at $p < 0.05$ with respect to their respective control. (UD- no expression of the genes for the given cDNA).

2) Expression pattern in tissue and organs suggested their importance in plant development. Under Fe-limiting conditions, differential expression pattern of wheat YSL genes showed early transcript abundance in roots whereas, in shoots most of the genes were induced at the late phase of starvation. Transcript accumulation of *TaYS1A, TaYS1B, TaYSL3, TaYSL5* and *TaYSL6* showed an early induction in the iron-starved root samples (Figure 1).
3) Their expression during various developmental stages, biotic and abiotic response also emphasized on their alternative functions. Overall, this work provides a much neededcomprehensive inventory and characterization of wheat YSL transporter genes.
4) Furthermore, we have cloned full length of few selected wheat YSLs to check their functional activity in yeast mutants and will be evaluating their candidacy for grain iron enrichment.
5) To identify more candidate micronutrient transporter in wheat, we performed RNASeq analysis of roots subjected to the iron starvation conditons. A total of 3678 genes were highly expressed in –Fe condition whereas, 2530 were down-regulated were Fe limiting experiment. In general we also observed the predominance of strategy-II based pathway activation for Fe acquisition. Most of these genes belongs to the facilitator super family transporter category. Genes encoding for nicotinamine synthase, metallo-thionein, probable metal transporter and an ABC transporter were highly induced under Fe starvation in the roots.
6) We also observed up-regulation of genes encoding for s-adenosyl methionine, a precursor of mugenic acid biosynthesis. All the genes encoding this pathway were highly induced in roots under Fe starved condition.

Salient Achievements

1) Largest number of YSL genes were identified in hexaploid wheat. The gene expression suggested roots and seed specific expression.
2) Full length cloning of four wheat YSL genes including *TaYSL1A, TaYSL2, TaYSL19* and *TaYSL6* was done to assess their functionality for iron uptake.

1.4 Genetic Transformation of Banana for Quality Improvement

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Project SRFs
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Navneet Kaur

Project Assistant
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Objective 1: Transfer and Evaluation of Indian Banana with Pro-Vitamin A (PVA) Constructs

Introduction

In continuation with previous year work, transgenic lines of cultivars Grand Naine and Rasthali have been generated by using four Generation 2 (Gen 2) and one Generation 3 (Gen 3) constructs received from QUT, Australia. Plants generated by Gen 2 constructs have been analyzed for carotenoid estimation in leaf samples. All transgenic plants are being grown for fruit development in the net-house as per DBT biosafety guidelines.

Research Progress

1. Phenotypic analysis of the transgenic plants: Most of the transgenic plants showed normal phenotype and growth in the net house. However, some of the plants developed with construct DC-32: *(ACO>APsy2a)*, where fruit-specific promoter regulated the expression of *APsy2a* gene has shown orange and pink color phenotype in leaf petiole/midrib (Figure 1).
2. Carotenoid estimation in leaf samples of events developed by Gen 2 constructs: Randomly 10-15 transgenic lines of both the cultivars were selected from Gen 2 constructs for carotenoid estimation of leaf samples. Most of the transgenic lines were found to contain an enhanced level of β-carotene, α-carotene, and lutein in comparison to non-transgenic (control) plants. In Grand Naine, DC-34 *(Ubi>APsy2a)* transgenic lines showed highest β-carotene in leaf samples, while in Rasthali DC-12 *(Exp1>APsy2a)* showed highest β-carotene content as compared to control. The β-carotene equivalents (µ/g fresh weight) calculated in leaves of transgenic lines with different QUT constructs are summarized in Tables 1 and 2.
3. Development of transgenic plants with Gen 3 gene construct: Desirable number (20) of events with Gen 3 gene construct *(MT2a>DXS + MT_2a>APsy2a)* have been developed and transferred to the green house and subsequently in net-house for further growth and development.

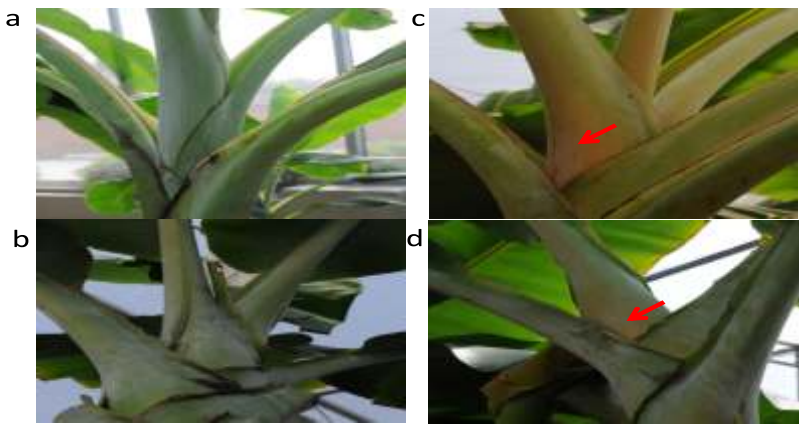

Figure 1: Phenotypic observation of transgenic plants in net house: a) Rasthali control (non-transgenic), b) Rasthali transgenic, c) Grand Naine control (non-transgenic), d) Grand Naine transgenic plant.

Table 1: β-carotene equivalents range and fold change in leaves of transgenic events (Grand Naine) comparison to non-transgenic control.

Construct	Name of the transgenic lines (GRAND NAINE)	β-Carotene equivalents range (µg/g FW)	Fold change in comparison to average β-Carotene equivalents of control
pBMGF-DC-12 (Exp1>APsy2a)	GN302 - GN316 (14 Independent lines)	67 – 145	1.2 – 2.5
pBMGF-DC-32 (ACO>APsy2a)	GN320 - GN348 (15 Independent lines)	64 – 95	1.1 - 1.6
pBMGF-DC-34 (Ubi>APsy2a)	GN420 - GN450 (15 Independent lines)	47 – 167	0 - 2.9
pBMGF-DC-35 (BT4a>APsy2a)	GN516 - GN530 (10 Independent lines)	49 - 87	0 - 1.5
Control (Non-transgenic plants)	GN301, GN317, and GN543 (3 Independent lines)	48– 68 (Average 58)	-

Table 2: β-carotene equivalents range and fold change in leaves of transgenic events (Rasthali) in comparison to non-transgenic control.

Construct	Name of the transgenic lines (RASTHALI)	β-Carotene equivalents range (µg/g FW)	Fold change in comparison to average β-Carotene equivalents of control
pBMGF-DC-12 (Exp1>APsy2a)	R2 – R16 (15 Independent lines)	58 – 201	1 - 3.6
pBMGF-DC-32 (ACO>APsy2a)	R21 – R103 (15 Independent lines)	42 – 113	0 - 2
pBMGF-DC-34 (Ubi>APsy2a)	R126 – R209 (15 Independent lines) + (8 new Independent lines)	55 – 94 + 99.6 – 177	0 - 1.7 + 1.7 – 3.1
pBMGF-DC-35 (BT4a>APsy2a)	R227 – R242 (15 Independent lines)	69 – 157	1.2 – 2.8
Control (Non-transgenic plants)	R17, R140, and R202 (3 Independent lines)	52 - 59 (Average 56)	-

Objective 2: Metabolic engineering for enhanced biosynthesis of pro-vitamin A in Indian banana fruit

Introduction

In exploratory work, to understand the regulatory mechanism of carotenoid biosynthesis pathway, we selected rate-limiting genes such as 1-deoxyxylulose 5-*phosphate synthase (DXS)* and *phytoene synthase (PSY)* for over expression study. Genome editing technique i.e. CRISPR/Cas9 has been established in banana and demonstrated by editing of *Phytoene desaturase (PDS)* gene. Further to understand *Lycopene epsilon-cyclase (LCYε)* and *carotenoid cleavage dioxygenases (CCD)* genes function, CRISPR/Cas9 is targeted with respective guide RNA in banana.

Research Progress

1. Over expression study in banana

i) **Phytoene synthase (PSY)**

- In continuation to the last year work, out of six *PSY* genes from both Nendran (high β-carotene) and Rasthali (low β-carotene), *NEN-PSY1* was selected for over expression due to its high activity in a bacterial complementation assay.
- *NEN-PSY1* was cloned into a binary vector under ubiquitin promoter and transformed into banana embryogenic cell suspension (ECS).
- *NEN-PSY1* over expression banana lines are growing in the net-house as per DBT biosafety guidelines.
- Leaf tissue carotenoid estimation of some randomly selected lines have been performed by HPLC and variation (high contents) of different carotenoid was observed in comparison to the control plants leaf tissue (Figure 1). Plants are growing in the Net-house for fruit development and analysis.

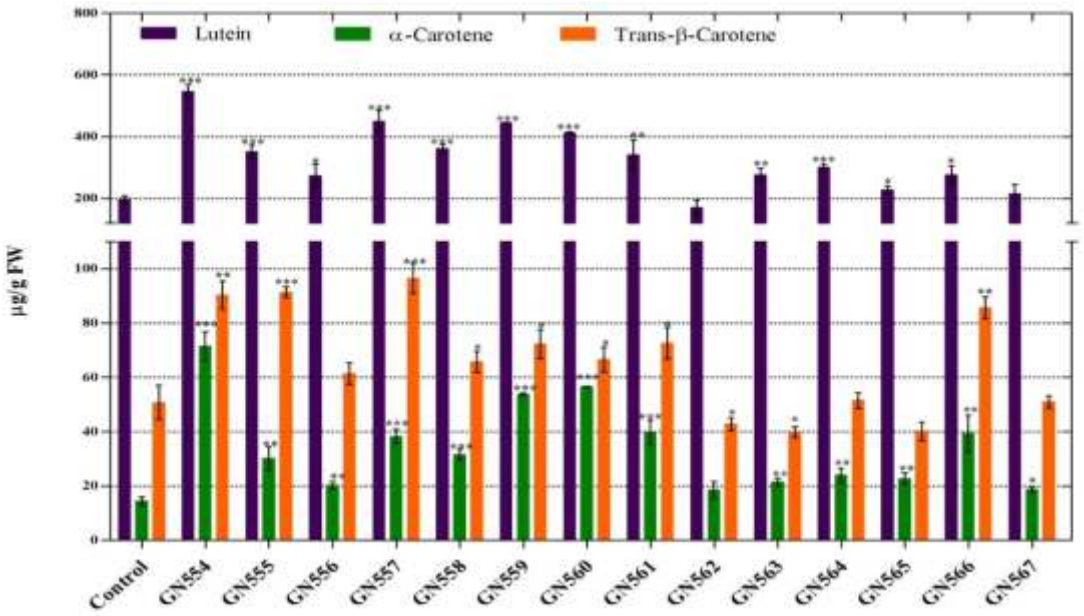

Figure 1: Carotenoid content in leaves of *PSY* over expressing Grand Naine plants. Lines designated GN554 to GN567 are generated by using *NEN-PSY1* gene.

ii) 1-Deoxyxylulose 5-phosphate synthase (DXS)

- Three *DXS* genes were identified in banana genome and their expression analysis was performed in different tissues of Rasthali and Nendran cultivars. In comparison to *RAS-DXS, NEN-DXS* expression was higher at both unripe and ripened fruit stage. *NEN-DXS2* gene was observed to be highly expressed at ripened stage (Figure 2).
- *NEN-DXS2* was cloned into a binary vector under ubiquitin promoter and transformed into banana ECS.
- *NEN-DXS2* over expression banana lines are growing in the net-house as per DBT biosafety guidelines.
- Leaf tissue carotenoid estimation of some randomly selected lines have been performed by HPLC and variation (high contents) of different carotenoids was observed in comparison to the control plant leaf tissue (Figure 3). Plants are growing in the Net-house for fruit development and analysis.

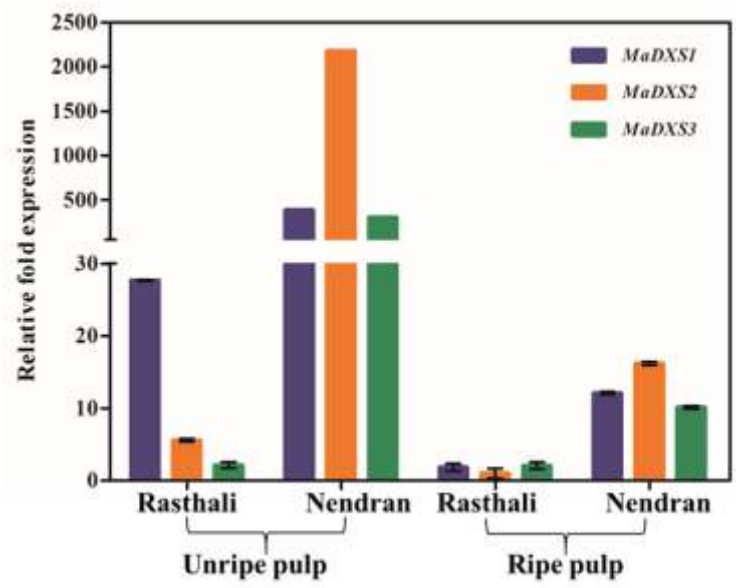

Figure 2: *MaDXS* expression in two developmental stages of pulp (Unripe and Ripe) of Rasthali and Nendran banana cultivars.

2. Genome editing study in banana

CRISPR/Cas9 has been used as genome editing tool in banana.

i) Demonstration of CRISPR/Cas9 in banana by editing PDS gene

- We have demonstrated a successful mutation in *phytoene desaturase (RAS-PDS)* of banana cv. Rasthali using the CRISPR/Cas9 system.
- Complete albino and variegated phenotypes were observed among regenerated plantlets (Figure 4). DNA sequencing of plants confirmed 59% mutation frequency in *RAS-PDS*, suggesting activation of the non-homologous end-joining (NHEJ) pathway.
- The mutations were either insertion (1–5) or deletion (1–4) of nucleotides near to protospacer adjacent motif (PAM) (Figure 4).
- These mutations have created stop codons in *RAS-PDS* sequences which suggest premature termination of RAS-PDS protein synthesis. The decreased chlorophyll and total carotenoid contents were detected in mutant lines that revealed the functional disruption of *RAS-PDS* gene (Figure 4).
- This work has been published in "Functional & Integrative Genomics (Jan. 2018)" as "CRISPR/Cas9-mediated efficient editing in *phytoene desaturase (PDS)* demonstrates precise manipulation in banana cv. Rasthali genome".

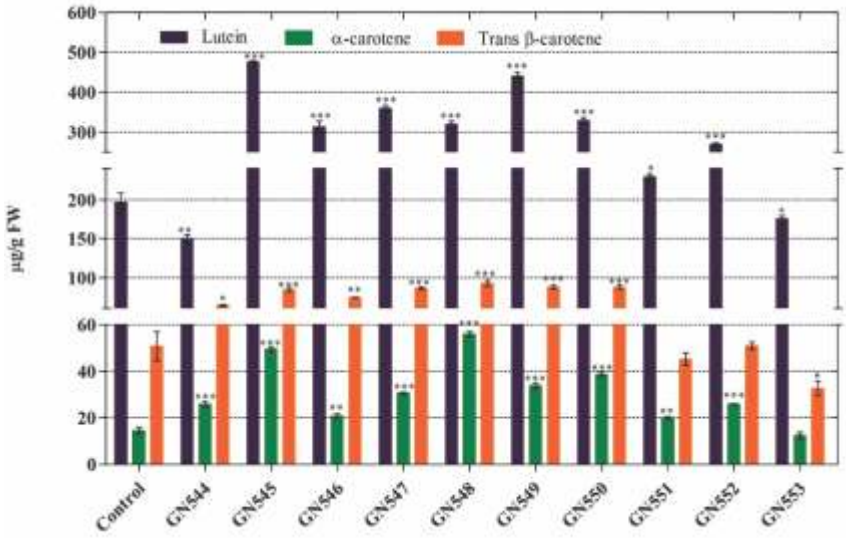

Figure 3 : Carotenoid content in leaves of *NEN-DXS2* over expressing Grand Naine plants.

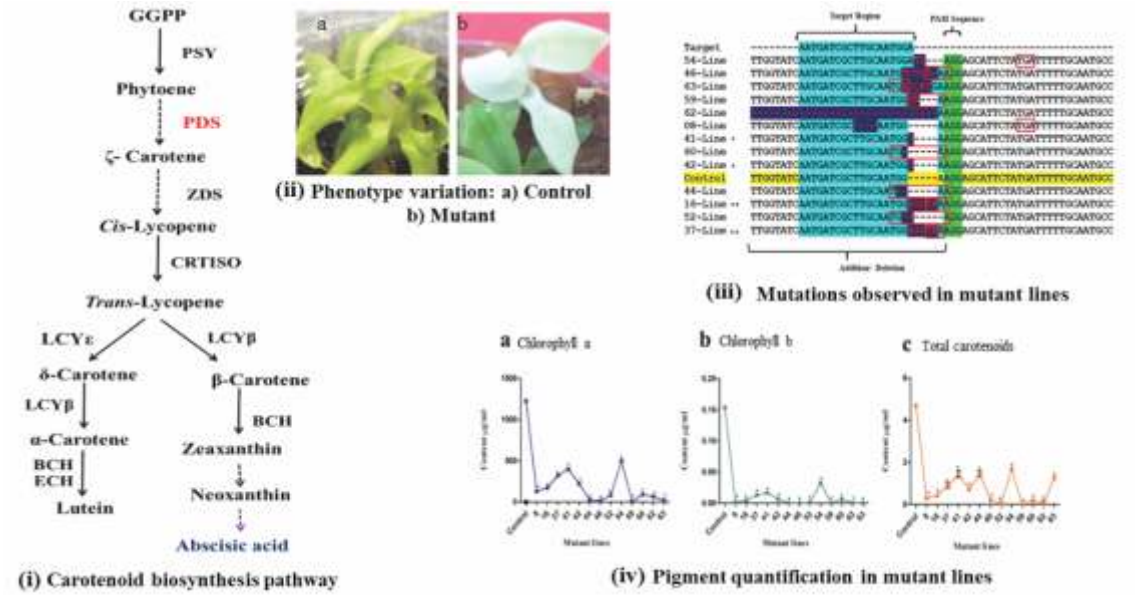

Figure 4: *Phytoene desaturase* editing using CRISPR/Cas9 (i) Carotenoid biosynthetic pathway (ii) Phenotypic variation among control and mutant. (iii) Indels observed in *RAS-PDS* targeted region. (iv) Quantification of chlorophyll (a, b) and total carotenoid content in mutant lines.

ii) **CRISPR/Cas9 towards banana biofortification by editing *LCYε*.**

- To apply CRISPR/Cas9 towards biofortification, we targeted the *LCYε* editing, which works at a branching point diverting the flux towards lutein formation.
- The construct with defined target site of *LCYε* has been designed and transformed into banana ECS.
- The plants have been shifted into soil pots for further analysis.

Salient Achievements

1) Transformed main plant crops of banana with different constructs are being grown in the net-house for fruit development and analysis.
2) Leaf tissue of over expression lines are showing increase in pro-vitamin A carotenoid.
3) Genome editing CRISPR/Cas9 tool has been successfully demonstrated in banana and work has been published in Functional & Integrative Genomics (2018) 18:89–99. Two PDS sequences from Rasthali have been deposited in the Gene Bank data libraries under accession numbers: *RAS-PDS1 (MF574096)* and *RASPDS2* (MF574097).
4) New project entitled "CRISPR/Cas mediated genome editing of genes for high pro-vitamin A accumulation and its stability in banana" has been sanctioned for financial support for four years by DBT on 26th March 2018 under the call for proposals in the area of "Genome Engineering Technologies and Their Applications".
5) CRISPR/Cas9 construct for *LCYε* editing has been prepared and transformed it into banana ECS cells.

1.5 Application of genomics approaches for reducing ODAP content in *Lathyrus* spp.

Principal Investigator
Pramod Kandoth

Research Fellows
Akanksha Bharadwaj
Nidhi

Introduction

Lathyrus is an important legume crop cultivated mainly in India, Bangladesh, Ethiopia, and some parts of Europe. This is one of the early domesticated food crops. Though this leguminous plant seeds are rich source of protein, second only to soybean in terms of protein content, is not promoted widely for cultivation owing to the presence of neurotoxin β-L-oxalyl-2,3-diamin-opropionic acid (β-ODAP). The seeds, if consumed in large quantities lead to a condition called neurolathyrism characterized by the irreversible paralysis of lower limbs in humans. At the same time, this crop has important agronomical attributes such as drought tolerance, pathogen resistance and also can survive and give reasonably good yield in water logged situations. This crop is also valuable for health promoting compounds such as homoarginine. Global warming and climate change is leading to reduction in area of cultivable land worldwide, this crop need promotion as it can be a hardy crop with guaranteed yield in such soils. The major impediment for the promotion and wide acceptability of this crop is the presence of neuro toxin. Our efforts are focused on understanding the pathways leading to the production and accumulation of ODAP in seeds, its relationship with stress tolerance, and thereby use genome editing approaches to produce a lathyrus cultivar with low or no ODAP production. The activities undertaken during this work deals with the a) Identificaiton of genes and pathways influencing ODAP content in seeds by genomic approaches; b) Isolation of genes involved in the ODAP pathway and; c) silencing of genes that leads to development of cultivars with no/reduced ODAP in seeds

Research Progress

1. Procurement of germplasm: We procured Lathyrus sativus germ plasm accessions from Indian Institute of Pulse Research, Kanpur and cultivars from Indira Gandhi Agricultural University, Raipur and IARI, New Delhi. We have a total of 68 lines consisting of 60 accessions and 8 cultivars. Efforts are on to obtain international germplasm from ICARDA.
2. Multiplication of seeds, selfing and crossing of Lathyrus cultivars: Last winter, we grew 30 accessions and 4 cultivars in our field at NABI. We performed reciprocal hybridizations between low and high ODAP cultivars in order to develop a segregating F2 population. Selfed seeds were also collected to maintain purity of these lines.
3. DAP estimation protocol. We standardized and established an ODAP estimation protocol for seeds, seedlings, and plant tissues based on the spectrophotometric method developed by Rao et.

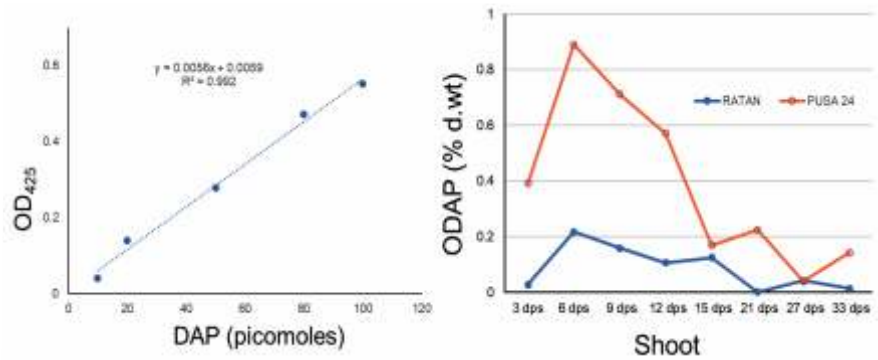

Figure 1: Estimation of ODAP in plant tissues of Lathyrus. ODAP levels in shoots were determined at different plant growth stages in high and low ODAP lines.

al, 1978. We are also working on establishing an HPLC protocol for ODAP estimation which might be more accurate and suitable for high throughput analysis.

4. RNAseq experiment: ODAP profiles were determined for two cultivars with high or low ODAP content at different growth stages. Based on ODAP profile (figure 1), tissues at 4 and 7 days post germination were chosen for RNAseq experiment to obtain differential gene expression profiles of the two cultivars.
5. RNAseq analysis: De novo transcriptome assembly was performed using software Trinity. To ensure proper sequencing depth approximately 15 GB data were generated per sample. A total of 12 samples representing two genotypes, two time points, and three biological replicates were sequenced. Summary statistics of assembly are given in figure 2.
6. Differential gene expression analysis: Differential gene expression analysis was performed to develop insights into the gene expression patterns in low and high ODAP cultivars. The summary of analysis and heat map of top 100 unigenes is in Figure 3. A finer analysis of these datasets, will enable us to identify genes important to ODAP biosynthetic pathway.

Description	Total Trinity unigenes	Total Trinity transcript (isoforms)	Percent GC
Counts of genes/transcripts	97,330	216,299	40.29

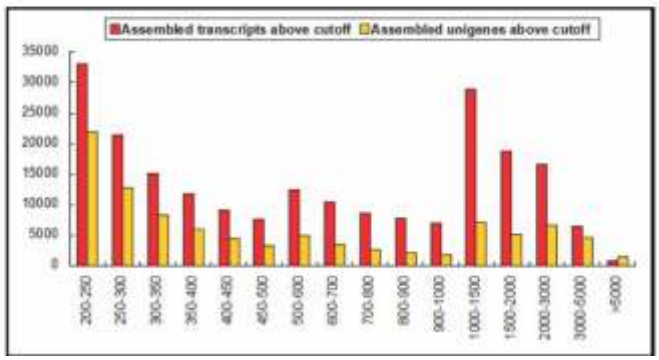

Figure 2: Details of RNAseq study including pipeline and length distribution of gene transcripts.

Control Vs Treated	Up Regulated	Down Regulated
LsP24-4d vs LsRAT-4d	428	912
LsP24-7d vs LsRAT-7d	635	641
LsP24-4d vs LsP24-7d	403	388
LsRAT-4d vs LsRAT-7d	736	251
LsP24 vs LsRAT	544	817

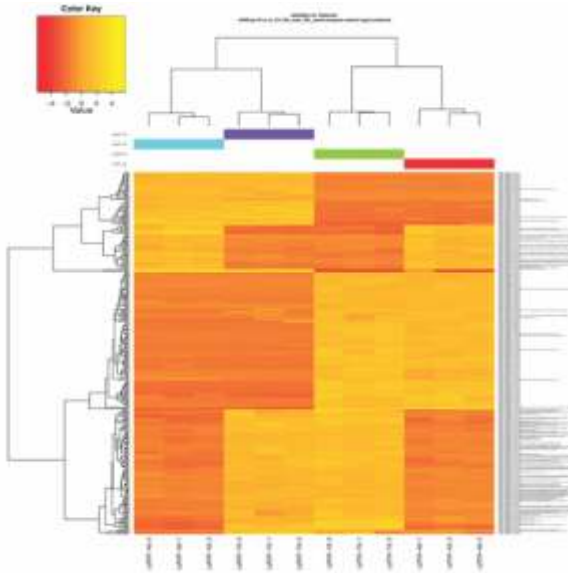

Figure 3: Summary of differential expression analysis of RNAseq data. Heat map showing the expression pattern of top 100 unigenes with hierarchical clustering is shown on the right.

Salient Achievements

1) Established resources, manpower, basic lab setup, and procedures to work on genetic improvement of Lathyrus
2) Developed RNAseq expression profiles for low and high ODAP cultivars at seedling stage.

(AGRICULTURAL BIOTECHNOLOGY - AB02)

GENOMICS AND COMPUTATIONAL BIOLOGY FOR MARKER AND GENE DISCOVERY

2.1 Development of advanced algorithms, databases, tools and pipelines for data mining and comparative analysis of food crop genomes

Principal Investigator
Shrikant Subhash Mantri

Research Fellow
Abhilasha Indoria

HPC Application Support Engineer
Abhijeet Singh Panwar

Objective1: A universal biomolecular entity and relationship database- CONNECTIONS

Introduction

Biological literature house immense information on relationships but the relationship data available at hand is very limited. Large amount of information about different biomolecular relationships/ interaction is available in the form of published literature. Most of the databases that house relationship information are focused primarily on proteins. But if information about the interactions is needed at other levels then it becomes a tough task. Many biological entities other than proteins also play vital role in the biological system.

There are ~70K genes, ~3.8 million proteins and ~ 2 million nucleotide Sequences, DNA & RNA for Arabidopsis thaliana. These numbers are too high that too for a single species. For around 8 million species these numbers will be huge. There are many encyclopedic repositories on biomolecules but when inter-molecular relationships are needed there is limited amount of readily accessible resources.

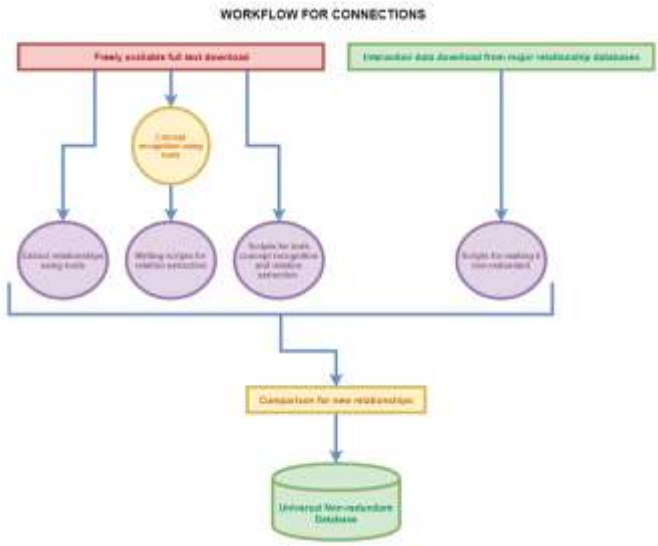

Figure1: Workflow of Connection

A utility that houses interaction information between different biomolecules will boost system level studies and thus provided clearer picture of biological systems. It will house interactions obtained from major relationship databases, from scripts written for Named Entity Recognition (NER) and Relation extraction and from combination of NER tools and in-house scripts for relation extraction (Figure 1).

Research Progress

Interaction Data from existing databases: A pilot of Connections is being made for *Arabidopsis thaliana.* Data from four major relationship databases- IntAct, BioGrid, MINT, and APID. Python scripts were written to extract data for *A. thaliana* and to make the data non-redundant. Similarly, python scripts were written to make whole dataset from the four major databases non-redundant.

Concept Annotation: Two tools- NEJI and BECAS were configured on cluster for concept recognition. Abstracts for *Arabidopsis thaliana* were downloaded from PubMed. Scripts were written to obtain a desired input format. NEJI uses machine learning models as well as inbuilt dictionaries for concept recognition. Output from NEJIi is obtained in the form of a JSON file. Python script was written to obtain a proper tabular structure in the form of a csv file (Figure 2).

Relation Extraction: Python script was made that uses BeCas REST API and Regex to extract biomolecular relationship data. Script takes PMIDs and Dictionary of trigger words. Output of the script is a csv file that contains UNIPROT IDs of the interactors, PMIDs, Sentences in which the relationship is found and the type of relationship, Direct/indirect based on the appearance of trigger word. Another script was written

to store each abstract as a JSON object for further processing.

Comparison with existing relationships

1. Interactor IDs from the output files have been extracted and compared using Pandas in Python.
2. PMIDs were also extracted and compared.

Gene Citation Count

1. Extraction of PMIDs according to date from the date of release of PubMed using python script.
2. Collapsed per day list of file into a single file.
3. Obtained the list of citations maintained by NCBI for each gene.
4. Filter for A.thaliana using taxonomic ID.
5. Gene information file which give description and name of each gene of NCBI
6. Filter for A.thaliana using taxonomic ID.
7. A python script that uses SCALA and Apache spark was written for the calculation of gene citation count per gene and per gene per year. (Figure 3)
8. All the above steps were repeated for Wheat, Rice and Maize.

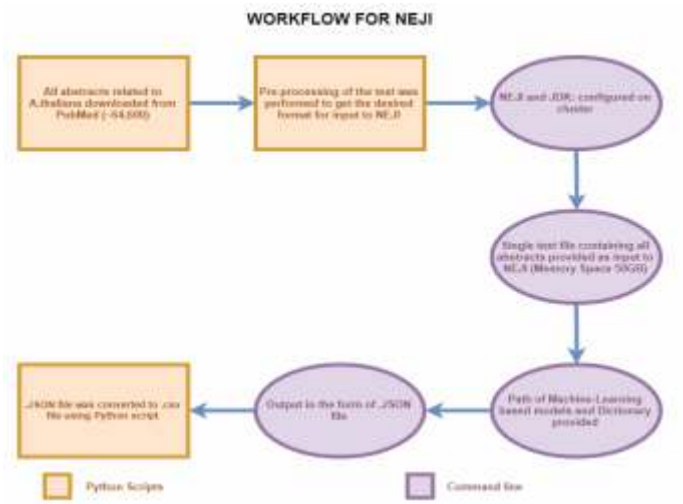

Figure 2: Workflow of NEJI

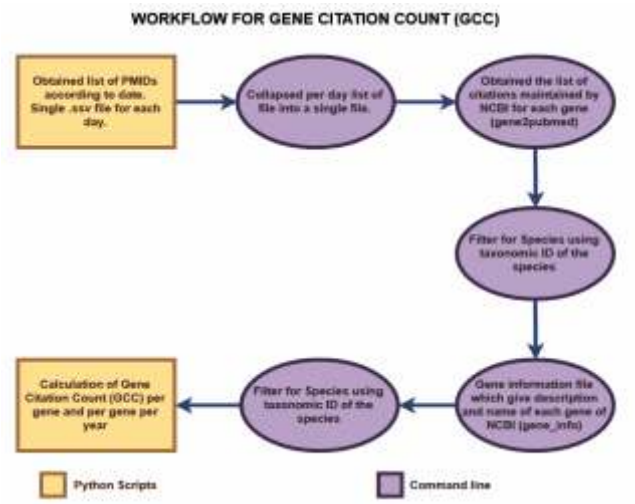

Figure 3: Workflow for Gene Citation Count

Objective2: Development of a utility to use Blast+ parallelly on compute nodes

Introduction

BLAST is one of the most widely used bioinformatics programs for sequence searching. While BLAST is fast and uses multithreading for utilizing cores, it is not able to use multiple nodes for computation. There are many parallel implementations for the BLAST e.g. mpiBLAST, ScalaBlast but they are not being updated for years and are not updated with latest BLAST+ versions. With Blast+ wrapper, we have tried to overcome this limitation of BLAST+ in Blast+ wrapper by implementing data parallelism.

BLAST+ wrapper is an abstraction created around Blast+, which submits Blast+ jobs on a parallel computing environment (HPC) and can be easily configured with latest Blast+ releases. Utility analyses computing resources such as CPU, load averages, I/O, network utilization for computation nodes, and accordingly, submits tasks on compute nodes. In our in-house cluster setup of 27 nodes and 432 cores, Blast Wrapper scales well and performs as good as mpiBLAST installation on the cluster.

To make it easier for bioinformaticians to take advantage of Blast+ wrapper, we have also developed a web portal for using Blast+ wrapper.

Research progress

Improvements in Blast+ wrapper utility

Blast+ wrapper started as a small project for utilizing our home HPC cluster setup and it has been evolving as a utility since then. We have been working on Blast+ wrapper utility to make it easier to use and more efficient. Following are the main improvements in Blast+ wrapper utility:

1. Allows users to declare the required number of fragments with --fragments flag, which provides fine-grained control over Blast+ wrapper. Allows users to test Blast+ wrapper with a different number of fragments on the cluster for maximum utilization of resources.

2. As the code base has been increasing for the utility, some part of the code has been modified from functional to an object-oriented approach.
3. Use of virtual environment for automatically installing required python modules.
4. Implementation of multithreading for submitting jobs on compute nodes, which has decreased the time for submitting jobs on compute nodes.
5. Implementation of the module for generating a log file for runs.
6. Bug with file names containing digits has been fixed.
7. Implementation of web utility for using Blast+ wrapper.
8. Can be used as a system-wide utility on the cluster.
9. Use of property files for runtime variables and configurations.

Development of Web Portal for Blast+ utility

We intend to make an efficient and easy to use utility for utilizing compute nodes for Blast+ wrapper. So have developed a web portal for abstracting complications of using the command line for Blast+ wrapper

1. User-friendly web interface for using BLAST on multiple compute nodes.
2. Blast Wrapper Utility is written in Python using Django web framework with Bootstrap front-end framework and follows MVT architecture pattern (Figure 4).
3. Uses MySQL in the backend for maintaining all the related information.
4. Easily configurable with Blast+ wrapper utility.
5. Prevents major Owasp attacks as SQL injection, XRS attacks.
6. Hosted on a different server than the main server for security. It uses "Celery" and RabbitMQ message broker for remote job submission.

Salient Achievements

1. Non-redundant list of interactors' IDs was obtained by processing the complete interaction dataset downloaded from four major existing relationship databases (MINT, BIOGRID, APID and IntAct). Interaction table containing the biomolecular interaction details was generated for these IDs. Interactions for *A.thaliana* were extracted out from the complete data set.
2. Recognized concepts/ Biomolecules from publicly available abstracts for *A.thaliana* using NEJI and BECAS.
3. Non redundant relationships extracted from publicly available abstracts for *A.thaliana* using a python script which utilizes NER and relation extraction.
4. Gene citation count script completion reflecting the most studied genes in the genome of *A.thaliana, Triticum aestivum, Oryza sativa* and *Zea mays* also providing complete gene descriptions.
5. More efficient, faster and more fault tolerant utility- Blast+ wrapper was developed.

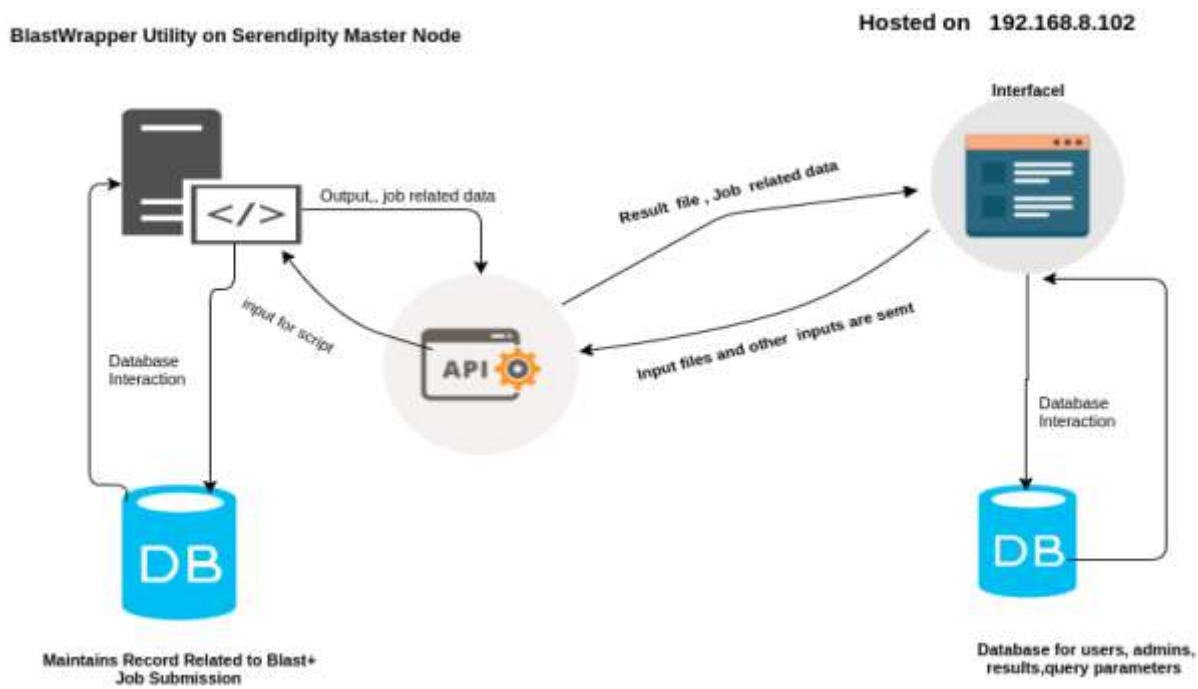

Figure 4: Architectural design for Blast+ wrapper

(AGRICULTURAL BIOTECHNOLOGY-AB03)

BASIC BIOLOGY FOR CROP IMPROVEMENT

3.1 Transcriptional regulation of seed development and maturation in plants

Principal Investigator
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Objective 1: Exploring B-ZIP-mediated transcriptional regulation in seed development and maturation phase by A-ZIP53, a designed dominant negative protein

Introduction

Environmental colonization by spermatophytes is due to their ability to bear and disperse seeds. Seeds of various plant species are major food source for majority of the human population. Not only they provide calories but also are rich source of minerals and vitamins required for the overall health and well-being. Therefore a complete knowledge of seed biology is a prerequisite to improve the nutritional traits in important crops like cereals and other crops. On one end of the research spectrum, tremendous efforts are being made that aim to produce prominent and bold seeds whereas on other end research is undertaken to produce soft/small/no seed trait which is considered to be a boon especially in many horticulture crops where seedless fruits are preferred (e.g., Guava, citrus, papaya etc.). In angiosperms, following double fertilization, multiple genes under the control of transcription factors (TFs) like B3, MYB, DOF and B-ZIP control seed development and maturation process. B-ZIP (basic leucine zipper) family of TFs play a pivotal role in seed biology. B-ZIPs bind to gene promoter cis-elements either as homodimer or heterodimer. In *Arabidopsis* seed maturation that involves endosperm desiccation surrounding a developed embryo/cotyledon is regulated by master TF i.e., B-ZIP53 that heterodimerizes with two other B-ZIPs namely, B-ZIP10 and B-ZIP25 and regulate seed maturation-specific genes. Seed maturation genes like albumin, cruciferin, FUSCA have G-and C-box in their promoter regions, DNA sequences that are prime binding targets of B-ZIP53 and its interacting partners. Insertion lines of B-ZIP53, B-ZIP10, and B-ZIP25 show normal seed phenotype suggesting their functional redundancies. To address this problem we have designed a dominant negative protein called A-ZIP53 that preferentially interacts and forms heterodimer with all three B-ZIPs *in vitro* and *ex vivo*. Heterodimers between A-ZIP53 and B-ZIP53, B-ZIP10, and B-ZIP25 are incompetent in binding to DNA, thus down regulating the genes that are targets of these TFs.

Research progress

Characterization of A-ZIP53 transgenic plant: We raised transgenic *Arabidopsis* that constitutively expressed A-ZIP3 dominant negative protein under 35S promoter (Pro35S::A-ZIP53). Expression of the A-ZIP53 causes altered phenotype including retarded growth, dwarfism, and late flowering compared to the wild-type *Arabidopsis* and mutants of bZIP53, bZIP25, bZIP10. Different transgenic lines in the T-1 generation were analyzed that showed differential retarded growth pattern (Figure 1). Semi-quantitative comparative mRNA expression of the A-ZIP53 was performed by the PCR of 19 transgenic lines. Expression of A-ZIP53 transcript showed good correlation with severity of phenotype.

A-ZIP53 seed morphology: To investigate the effects of A-ZIP53 on the reproductive phase of plant, A-ZIP53 expressing transgenic plants were analyzed and results compared with wild type *Arabidopsis* and insertion mutants of bZIP53, bZIP10, and bZIP25. During late growth phase, in addition to the delayed flowering time, other phenotypes were also observed including flower size, silique, and mature seed. Transgenic have significantly small flowers compared to the wild type and mutants (Figure 2). Siliques have shorter length compared to the wild type and mutants (Figure 1) and the number of siliques per 0.5 gm weight were higher compared to the wild type. Additionally, seeds were small and severely flattened compared to the wild type

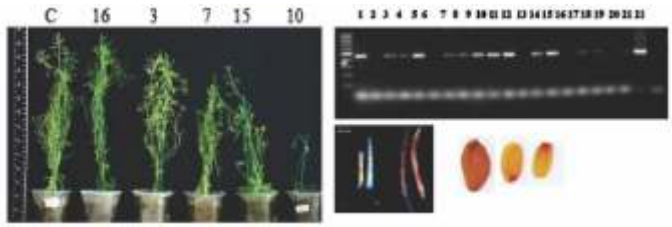

Figure1: Transgenic plants expressing different levels of A-ZIP53 transcript show an array of phenotype. Left upper panel shows genotype of 19 transgenic lines (1-19), lane 20 is a positive control and 21 is col 0 wildtype plant. Higher the transcript level more severe is the phenotype. Lower left panel shows silique and seed of wildtype col 0 and A-ZIP53 plant.

and mutants (Figure 2). Such complex phenotype can be explained, however, if we consider A-ZIP53 targeting multiple B-ZIPs or other TFs. Scanning electron microscopy revealed the morphological changes in A-ZIP53 transgenic seeds. Seeds showed severely distorted seed coat structure. The most startling observation was the presence of densely populated seed hairs or trichomes (Figure 2). To best of our knowledge, no such or similar phenotype is reported in the literature.

A-ZIP53 inhibits the expression of seed-specific genes: We used Illumina Next seq 500 NGS platform to measure the level of transcripts in transgenic and col 0 wildtype *Arabidopsis*. RNA samples from immature siliques were sequenced, which generated 20, 420, 244 reads. A cursory glance at transcripts levels demonstrated that most of the down regulated GO terms are related to genes which are involved in the gamete formation, seed development, seed maturation, seed storage protein synthesis, reproduction and other biological processes, suggesting that A-ZIP53 is specific in targeting gamete and seed-specific genes. A detailed analysis of NGS transcriptome is underway. The expression patterns of seed-specific genes were validated by qPCR. Genes responsible for seed maturation e.g., cruciferin (CRU), asparagine synthase 1 (ASN1), cruciferin (CRA), hydroxysteroid dehydrogenase 1(HSD1), seed storage albumin (2S2), proline dehydrogenase (ProDH), and the late embryogenesis accumulating 76 (LEA76), which are involved in different stages of seed development and maturation, and target of bZIP53 and its heterodimerizing bZIP partners are downregulated in A-ZIP53 plants.

Tandem mass spectrometry based proteomics was used to detect putative heterotypic interaction of A-ZIP53 in vivo: Earlier, studies from our group and others have shown that the B-ZIP53 is involved in heterotypic interaction with bZIP10, and bZIP25 *in vitro* and *in vivo.* In order to identify all interacting partners of *B-ZIP53 in vivo* we have used immunoprecipitation followed by NanoLC-tandem mass spectrometry (IP-NanoLC-MS/MS) using A-ZIP53 cell extract samples. A preliminary analysis of the proteomic data has shown the presence of additional interacting partners of B-ZIP53. An in-depth analysis of proteomic data is underway

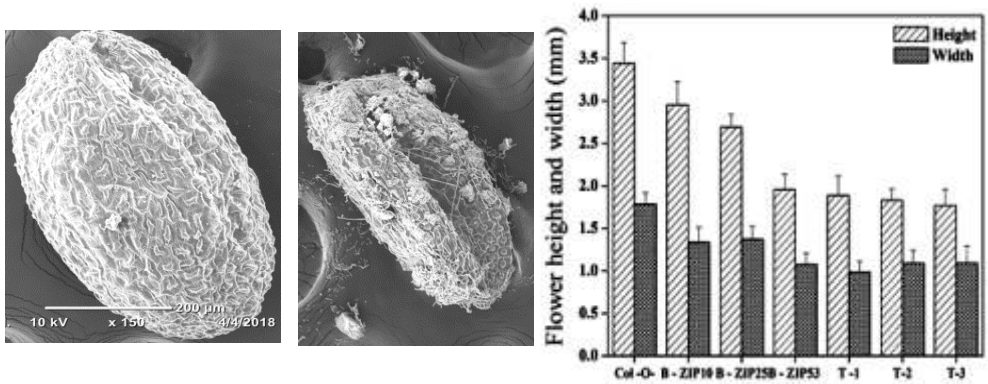

Figure 2: SEM pictures of col 0 (left) and A-ZIP53 transgenic (right) seeds. Transgenic seeds showed peculiar phenotype of shriveled seeds with long trichomes.

Salient Achievements

1) Using *Arabidopsis* as model plant we have demonstrated the efficacy of using degenerative-by-design A-ZIP53 to study biological redundancy among B-ZIP Tfs.
2) This strategy has enabled us to identify new and novel molecular targets belonging to B-ZIP TFs family that can be targeted by gene editing technologies like TALEN and CRISPR/Cas to knock-out genes that may result in small seed /soft seed phenotype in horticulture crops like citrus, guava, tomato etc.

(FOOD & NUTRITIONAL BIOTECHNOLOGY - FNB01)

FUNCTIONAL FOODS AND NUTRACEUTICAL FOR BETTER HEALTH

1.1 Beneficial Manipulation of Gut Bacteria as a Strategy for the Management of Metabolic Disorders

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Mahendra Bishnoi

Research Fellows
Paramdeep Singh
Shashank Singh
Ruchika Bhatia
Shikha Sharma

Objective 1: Development of synbiotics for the prevention of chronic diseases: Protection against inflammation

Introduction

Twenty first century has seen a drastic change in dietary habits with increased consumption of processed and Western diets that are rich in high calories. This is considered as one of the causes for the development of metabolic syndrome (MetS) and obesity. MetS is a group of at least any three out of five clinical conditions that includes obesity, hyperglycemia, hypertension, hypertriglyceridemia and lower HDL-c levels in blood. Each component of MetS is a known risk factor for the development of type 2 diabetes, atherosclerosis, and coronary artery disease. However, many individuals do not meet the criteria for diagnosis but have at least two symptoms for future MetS development, a stage termed as pre-MetS (PMetS). Recently, host's perturbed gut microbiome is recognized as one of the predisposing factors for MetS. PMetS individuals are at high risk to develop cardiovascular disorders including type II diabetes, and thus early prediction and prevention/treatment measures becomes indispensable. Several studies, including our previous ones, have linked obesity with dysbiosis of gut microbiota. Globally, researchers are trying to understand the interplay between gut microbiota and MetS and achieving gut microbial balance by either restoration or replenishment using various dietary regimens including supplementation with prebiotics and probiotics. Based on above observations, we propose to use indigenous beneficial bacteria isolated from various sources for its protective efficacy against low protein, moderate fat and high sucrose diet induced (LPMFHS) metabolic alterations.

Research Progress

Preparation of bacterial cells: Frozen cultures were activated on agar plates by incubating at 37°C for 48 h. Single colony of each strain was transferred into liquid broth and allowed to grow at 37°C for 24 h. Two subsequent transfers into fresh broth were made and bacterial pellets were suspended in sterile PBS and corresponding doses were prepared and stored along with 10% glycerol in trypticase soy broth.

Animal study: Male Wistar rats were housed in the Central Animal House Facility of Punjab University, Chandigarh, India under standard laboratory conditions with 12 h light-dark cycles. Access to food and water was provided ad libitum. All the experimental procedures were approved by Institutional Animal Ethical Committee (IAEC), PU and were conducted as per the guidelines of the Committee for the Purpose of Control and Supervision on Experiments on Animals. After acclimatization rats were randomized into (i) Control diet; (ii) low protein, moderate fat and high sucrose diet; (iii) LPMFHS – strain 1; (iv) LPMFHS + strain 2: (v) LPMFHS + Combination dose (CD) and (vi) Control- high dose of strains (per se) with n = 10 in each group except per se and CD with n=6. LPMFHS diet contain low Protein (10% kcal); medium Fat (30% kcal) and high Sucrose (52% kcal) and normal standard diet contain protein (30% kcal); fat (10% kcal) and starch (47% kcal). At the time of dosing, bacterial cells were centrifuged, washed in PBS and re-suspended in PBS. Bacterial strains were fed by oral gavage every day for 3 months.

Behavioral parameters such as depression and anxiety were determined as per established protocols. OGTT was performed before 48 h of terminating the experiment. At the completion of the study, animals were euthanized by cervical dislocation. Serum, Visceral white adipose tissue (vWAT), liver, cecum content, ileum and colon were collected; snap frozen and stored at -80°C and kept in formalin at 4°C till further analysis. Further, serum biochemical parameters and histological

alterations were evaluated.

Low protein, moderate fat and high sucrose (LPMFHS) diet did not promote weight gain and did not enhance the basal blood glucose levels relative to normal diet fed rats. However, the area under the curve in OGTT was high in LPMFHS fed mice suggesting an imbalance in glucose homeostasis. There was no significant change in insulin resistance and insulin sensitivity indices and no abnormal increase in serum insulin levels in LPMFHS diet rats (Figure 1a-1i). LPMFHS diet did not elevate serum total cholesterol and HDL-c levels. However, the levels of TAGs and LDL-c in the serum were elevated and corresponding increase in TyG and atherogenic indices in LPMFHS diet fed rats. Higher systolic blood pressure and enhanced levels of serum inflammatory markers such as lipopolysaccharide (LPS), TNF-α and IL-6 was noted in LPMFHS diet fed rats relative to normal diet fed rats. Serum leptin was also elevated in LPMFHS mice suggesting a leptin resistance state. There was a marked increase in inflammatory markers (CRP and IL-1β) in the liver homogenates.

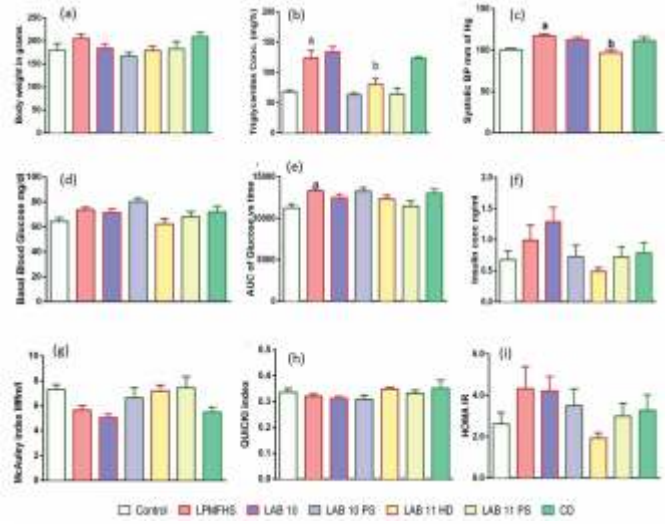

Figure 1: Effect of low protein, moderate fat and high carbohydrate (LPMFHS) diet and bacterial intervention on (a) body weight gain; (b) Triglycerides; (c) systolic blood pressure; (d) basal blood glucose levels; (e) area under the curve in OGTT; (f) Insulin level in serum; (g) McAuley Index; (h) QUICKI Index and (i) HOMA-IR assessment

Behaviour studies suggested that rats developed depression and anxiety (increased immobility time in forced swim test, decreased time spent in open arm in elevated plus maze test and decreased distance moved and number of entries into the central and middle circle in open field test) like conditions upon LPMFHS diet feeding (Figure 2a-2c). Histological studies revealed remarkable changes in the ileal and colonic architecture upon LPMFHS diet feeding suggesting breaching of intestinal epithelial integrity. All the above changes suggest that diets having poor protein, moderate fat and high carbohydrates causes pre-metabolic syndrome and if not prevented may become predisposing for full metabolic syndrome. Intervention with two bacterial strains, which are selected through *in vitro* studies, prevented the above deleterious changes.

Salient Achievement

Bacterial strains that could alleviate diet induced metabolic alterations in rats has been identified.

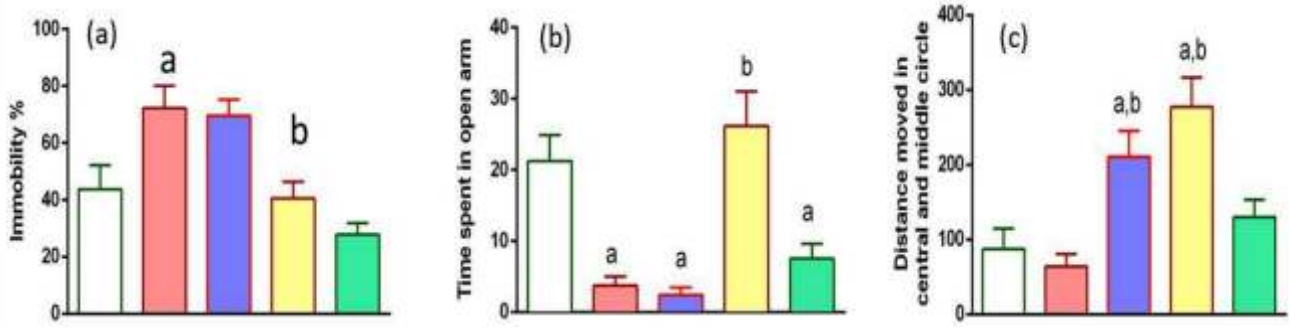

Figure 2: Effect of low protein, moderate fat and high carbohydrate (LPMFHS) diet and bacterial intervention on behavioral changes (a) Forced Swim Test for depression; (b) Elevated Plus Maze Test for anxiety and (c) Open Field Test for Anxiety

1.2 Development of novel co-biotic formulations for the improvement of metabolic health

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Research Fellows
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Pragyanshu Khare

Introduction

Obesity has emerged as an increasing health concern in India. According to recently published multi-centered study, it has been reported that around 20% (every one of five adults) of Indian adult population is overweight and obese. Based on the 2007 National Health Family Survey data, Punjab is the "heaviest" state in India with as many as 30% of males and 38% of females are obese, a significant cause of concern for this region given link of obesity to the development of other chronic illnesses like diabetes, hypertension and cancer. Dietary modification and physical exercise are considered as safest approaches for prevention of HFD-induced metabolic, redox stature and immune-related alterations. Keeping gut health in the focus, the 'modifiers of gut health' could be an interesting approach in alleviating metabolic irregularities. Dietary fibers are well known to exert the prebiotic effect and are also protective against the HFD induced obesity. Recently it has been demonstrated that the enhancement of non-digestible carbohydrate in diets provides an effective weight reduction via production of short chain fatty acids (SCFAs) and a central homeostatic mechanism. Individually several antioxidants and prebiotics have shown prevention and alleviation of HFD-induced changes, but there are very limited studies on the combination of two (antioxidant plus prebiotic, cobiotics). The present study is aimed to evaluate the synergistic and combinatorial effects of oligosaccharides with antioxidant/anti-inflammatory agents in rodent models *per se* and in disease state (obesity and related complications). Furthermore, a prototype functional food development using oligosaccharides as sugar alternative and its functional evaluation will be done.

Research Progress

Study 1: Bacteriostatic properties of a potential anti-obesity agent cinnamaldehyde (CMN) may present untoward effects on the resident gut microbiota. Here, we evaluated whether the combination of Isomalto-oligosaccharides (IMOs,sweet tasting non-digestible oligosaccharides) with CMN prevents unwanted effects of CMN on gut microbiota and associated metabolic outcomes in HFD-fed mice. Male Swiss albino mice divided into four groups (n=10), were fed on normal chow, or HFD (58% fat kcal), HFD+CMN (10 mg kg-1) and HFD+CMN (10 mg kg-1)+IMOs (1 g kg-1) for 12 weeks. Effects on HFD-induced biochemical, histological, inflammatory and genomic changes in the gastrointestinal tract, liver, and visceral white adipose tissue were studied. Cosupplementation of CMN with IMOs potentiates its preventive action against HFD-induced increase in serum LPS and abundances of selected LPS producing bacteria (Enterobacteriaceae, Escherichia Coli, *Cronobacter sp, Citrobacter sp., Klebsiella sp., Salmonella sp.).* CMN and IMOs co-administration prevented HFD-induced decrease in selected beneficial gut bacterial abundances (Bifidobacteria, *Roseburia sp.,* Akkermansia muciniphila, *Feacalibacterium sp.).* CMN's effects against HFD-induced increase in gut permeability, histological and inflammatory changes in the colon were further augmented by cosupplementation of IMOs. Similar effects were

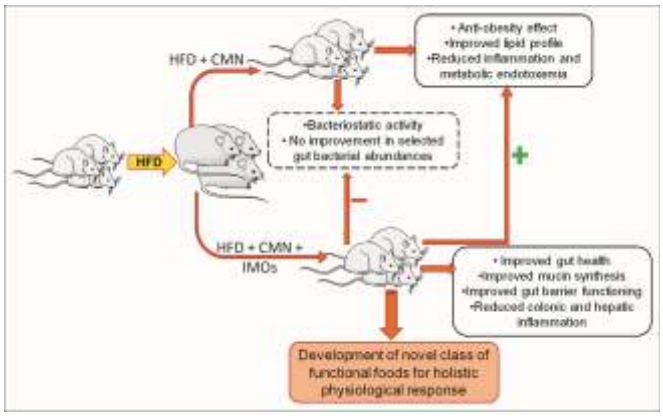


Figure 1: Coadministration of Isomalto-oligosaccharides with cinnamaldehyde potentiates its anti-obesity effect and limits the side effects of cinnamaldehyde on gastrointestinal flora.

observed in hepatic inflammatory markers. Cosupplementation of CMN with IMOs and CMN alone administration prevented HFD-induced changes in peripheral hormones and lipid metabolism-related parameters. This study provides evidence that coadministration of IMOs with CMN potentiates its anti-obesity effect and limits the side effects of CMN on gastrointestinal flora. Further, this study gives us important direction for the development of a concept-based novel class of functional foods/nutraceuticals for improved metabolic health (Figure 1).

Study 2: Cranberries are a rich source of polyphenolic antioxidants. Purified sugars or artificial sweeteners are being added to cranberry-based food products to mask tartness. Refined sugar and artificial sweeteners intake modulate gut microbiota and result in metabolic complications. We evaluated effects of IMOs with cranberry extract (CRX) on HFD-induced metabolic alterations in mice. Male Swiss albino mice were fed normal chow or HFD (58% fat kcal), and were administered either CRX (200 mg/kg) alone or in combination with IMOs (1 g/kg). Cecal short-chain fatty acids, abundances of selected (1) butyrate producing, (2) metabolically beneficial, and (3) selective lipopolysaccharides producing gram negative gut bacteria were studied. Further, gut-related histological, biochemical, genomic changes along with circulating pro-/anti-inflammatory markers and systemic obesity-associated metabolic changes were studied. Co-supplementation of CRX and IMOs significantly improved cecal SCFAs, especially butyrate levels, selected butyrate-producing bacteria (clostridial cluster XIVa bacteria) and butyrate kinase expression in HFD-fed mice. The combination also significantly improved gut beneficial bacterial abundance, gut histology and related changes (colon mucin production, gut permeability) as compared to individual agents. It also prevented HFD-induced systemic and tissue inflammation, glucose intolerance and systemic obesity-associated metabolic changes in adipose tissue and liver. The combination of CRX and IMOs appeared more effective in the prevention of HFD-induced gut derangements. Combination of CRX and IMOs could be advantageous for normalization of metabolic alterations seen in diet-induced obesity *via* beneficial modulation of gastrointestinal health (Figure 2).

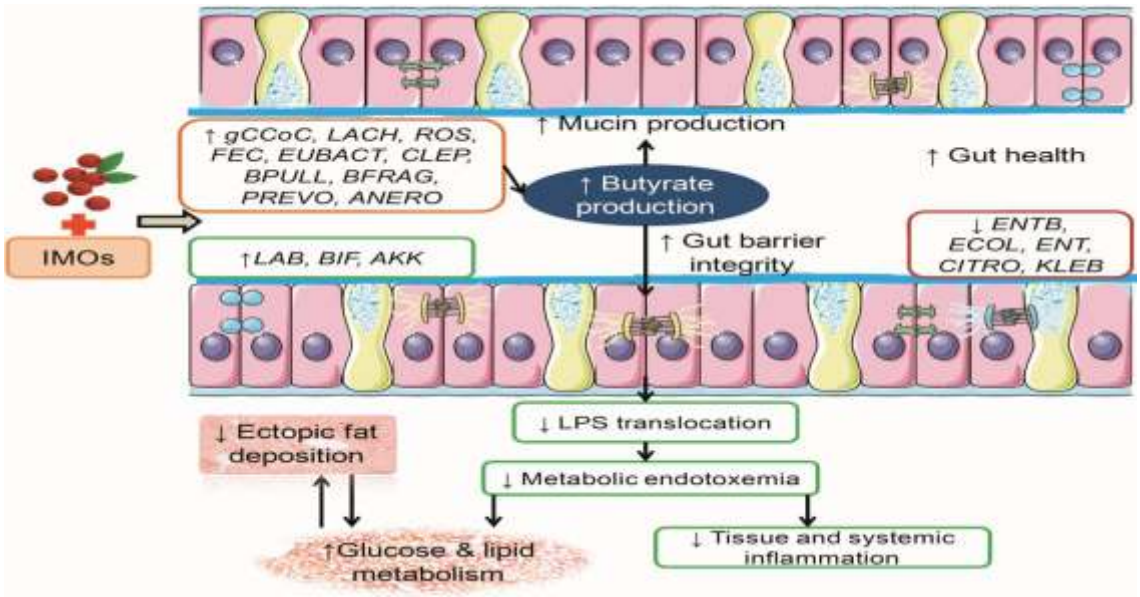


Figure 2: Combination of cranberry extract and IMOs was more effective against prevention of HFD-induced gut derangements

Salient Achievements

Proof of concept validation for using isomalto-oligosaccharides as sugar alternative in novel class of functional food development has been completed.

1.3 Production of nutraceuticals and therapeutic proteins using sustainable algae system

Investigator
Gulshan Kumar

Introduction

In the need of novel therapy, the therapeutic protein based drugs are an important class of medicines and they currently have privilege of unprecedented recognition for their therapeutic potential to treat a wide variety of fatal diseases, including cancers, acute infections, genetic disorders, etc. Therefore, the development of therapeutic protein based drugs is one of the fastest growing pharmaceutical sectors in health-care industry. In order to develop a low cost protein expression platform, microalgae are the ideal candidates which are often termed as "solar powered protein factories". The robustness of chloroplast of *Chlamydomonas reinhardtii,* eukaryotic green algae, as protein production platform has been demonstrated to produce wide range of recombinant proteins. Apart of tremendous cost advantage, production of therapeutic proteins in algae has several other advantages over traditional mammalian expression system, such as high scalability, absence of viral and other pathogens, scope for oral delivery (as algae are placed in GRAS category) and production of prokaryotic toxins which would otherwise be not possible in other eukaryotic host. The genesis of research idea is inspired by an urgent need to device strategy for production of affordable therapeutic proteins for the treatment of various fatal diseases. On the other hand, the novel identified compound with nutraceutical and pharmaceutical properties that can be used in chemoprevention and to eradicated malnutrition. Moreover the successful implementation of the research idea has significant extrapolation in developing platform for the production of prebiotics, vaccine, bioinsecticides, etc.

Research Progress

Designing, codon optimization and synthesis of Antibody (Ab)-toxin conjugate: For the proof of concept to produce protein of interest in algae, amino acid sequence of antibody Cetuximab, used for the treatment of squamous cell carcinoma, was retrieved from drug bank (www.drugbank.ca/drugs). The coding sequence was optimized according to the codon usage of *Chlamydomonas reinhardtti* chloroplast (www.kazusa.or.jp/codon). The codon optimized gene was fused genetically to *Exotoxin A* to express Ab-toxin conjugate (Figure 1).

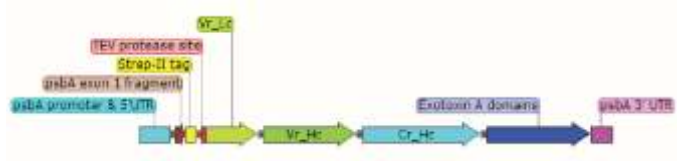


Figure 1: The gene of interest fused to psbA promoter and UTRs

Chloroplast transformation vectors preparation: A total of three chloroplast transformation vectors have been constructed to target the *psbA* locus as site of transgene integration. The *psbA* flanking sequence was used for homologus recombination for transgene integration. The constructed vectors have *psbA* gene under different promoters and UTRs, for the restoration of photosynthetic growth in CC4147 strain of *Chlamydomonas reinhardtti* (a non-photosynthetic psbA deletion mutant) and for the selection of positive transformants (Figure 2).

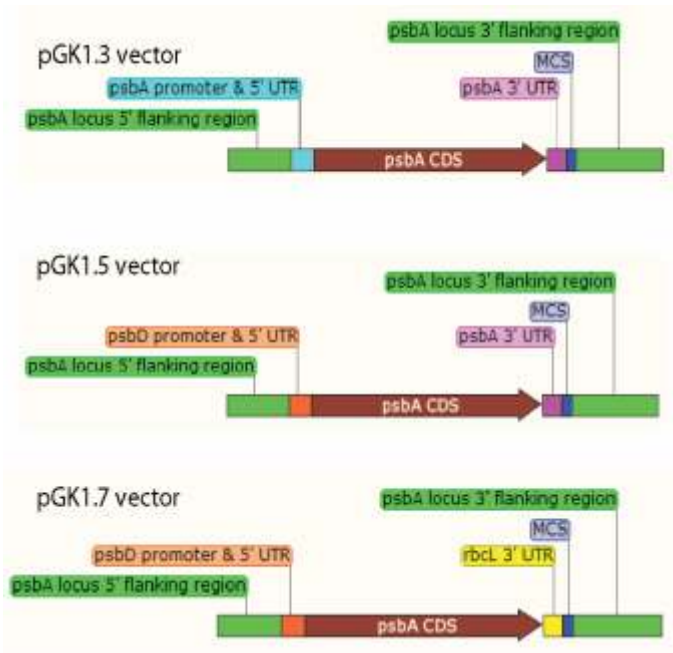


Figure 2: Chloroplast transformation vectors designed with endogenous psbA gene under different promoters and UTRs

Chloroplast Transformation constructs preparation: Using three chloroplast vectors, three constructs were prepared with chloroplast transformation cassette. The gene of interest has been incorporated in the transformation cassette using SfiI restriction

endonuclease in the multiple cloning site (Figure 3).

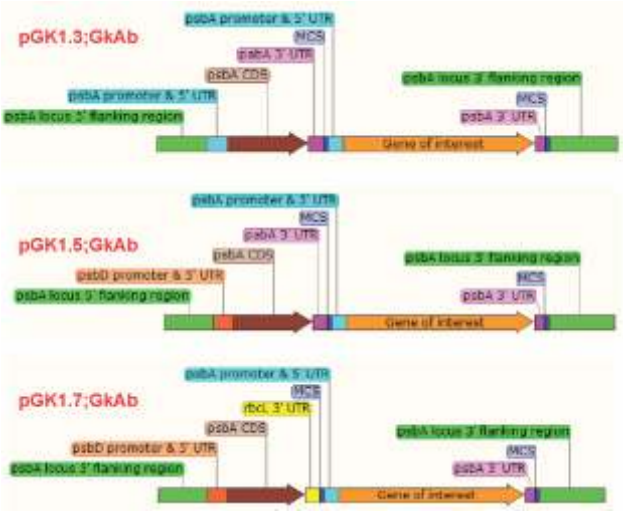


Figure 3: The transformation cassette to integrate the gene of insert at psbA locus of Chlamydomonas reinhardtti chloroplast

Transformation of Chlamydomonas Reinhardtti chloroplast: The CC4147 strain was grown in the presence of 0.5mM 5-Fluro-2'-deoxyuridine (FrDu) for two generation before transformation. The FrDu was used to reduce the genome copy number in the chloroplast of CC4147, which will later help to screen the homoplasmic lines. The chloroplast transformation was performed using plasmid coated gold particles on Biolistic PDS-1000/He particle delivery system. Three batches of experiment have been performed and several of positive transformants have been screened and subjected to further analysis .

Salient Achievements

Vectors and transformation constructs has been successfully prepared for the *Chlamydomonas reinhardtti* chloroplast transformation.

1.4 Fabricated nanomaterials in food for enhancement of micronutrients bioavailability

Principal Investigator
Nitin Singhal

Research Fellow
Stanzin Angmo

Introduction

Anemia of inflammation is the second most prevalent anemia resulting due to the activation of immune response. Though being prevalent; it still faces challenges due to poor prognosis and ineffective therapeutic ways. Chronic infection or inflammatory disorders such as rheumatoid arthritis, cancer, chronic kidney diseases and various other inflammatory disorders often results in anemia. Hepcidin, a cysteine rich hepatic peptide hormone plays a crucial role in iron sequestration hindering availability of iron to different organs for cellular functioning. The inflammatory stimulus leads to elevation of hepcidin level which in turn internalize iron mediated FPN channel resulting in blockage of iron egress from the cells, impairing iron absorption from duodenal intestine and macrophage. Therefore, it causes iron retention within the cells leading to hypoferremia, resulting in ineffective iron-mediated erythropoiesis. The genetic programming of hepcidin regulation constitutes two major pathway; IL-6/STAT3 pathway and bone morphogenetic protein (BMP)/ contraction of Sma and Mad (SMAD) pathway. Elevated hepcidin eventually binds to the FPN leading to its lysosomal degradation, thus, resulting in intracellular iron accumulation. Hence, transcriptional re-programming of hepcidin could be a novel approach in treating AI symptoms.

GDP is a natural compound and earlier we reported that apart from directly binding and inhibiting hepcidin action, GDP also attenuates inflammation-mediated IL-6/JAK//STAT3-hepcidin axis. However, to explore the mechanistic aspects behind Hamp mRNA down regulation via IL-6/JAK/STAT3 pathway, we developed a liposomal drug delivery system (NH+) encapsulating GDP (NH+GDP).Encapsulated NH+GDP with single positive charge (NH+) was found to be most compatible encapsulating delivery vehicle after all toxological studies. Further, we aimed to investigate the underlying mechanism of NH+GDP on inflammation mediated NF-B activation through IL-6/STAT3 hepcidin axis in in-vitro and in-vivo and assessed its therapeutic potential against AI.

Research Progress

NH+GDP suppresses expression of pro inflammatory mediators and IL-6/JAK/STAT3 pathway in acute mice model: In vitro studies provided a clear evidence that NH+GDP attenuates NF-B pathway activation thus, reducing pro-inflammatory mediators (IL-6, TNF-α and IL-1β) level. In correspondence, subsequently there was reduced binding of IL-6 to its receptor to down regulate IL-6/JAK/STAT3 pathway with decreased HampmRNA transcription. LPS-induced inflammation increases pro-inflammatory cytokines production (IL-6) with increase transcription of Hamp mRNA level leading to hypoferremia. To elucidate the IL-6/STAT3 pathway involved in hepcidin expression BALB/c mice were challenged with LPS (IP) for 6h followed by NH+GDP (IP) treatment for 30 minutes. In association, we found significant decrease in serum IL-6 (Figure 1A) with decreased phosphorylation of JAK2 and STAT3 activation thus, reducing transcription of Hamp mRNA level (Figure 2B-C). These results indicate that NH+GDP attenuates hepcidin expression through suppressing pro inflammatory IL-6 levels by down regulating IL6 and JAK/STAT3 activation.

NH+GDP reduces Hamp mRNA expression by suppressing IL-6/STAT3 pathway in chronic AI model: To induce the chronic AI model, BALB/c mice were challenged with LPS (IP) on the first day followed by Zymosan (IP) a week later and then sacrificed after 10 days as depicted in (Figure 2A). Next AI mice were treated with NH+GDP (IP) every 24h for 2 weeks. Treatment with NH+GDP significantly increases serum iron concentration (Figure 2B) with rise in haemoglobin level and erythrocyte number thus, correcting inflammation-induced AI state .Initially, we investigated the effect of NH+GDP on LPS-induced up regulation of serum IL-6 levels. As expected, NH+GDP markedly reduced serum IL-6 levels more than 30% (Figure 2D) with suppressed JAK2 and STAT3 phosphorylation (Figure 2E). Consistent results were observed with decreased hepcidin-25 protein expression (Figure 2F), thereby, down regulating IL-6/STAT3 pathway. Moreover, reduced Hamp expression indicates the decrease in serum ferritin level for effective iron-mediated erythropoiesis thus, improving hypoferremia

(Figure 2G). The spleen plays a significant role in chronic inflammation and immune response. Dysregulation of splenic iron is another hallmark of AI with reduced circulating iron level, thus we investigated the effects of NH+GDP on spleen during chronic AI. The tissue iron deposit and splenic iron content was reversed by NH+GDP reducing iron restrictive effect of inflammation with effective iron-mediated efflux (Figure 2H-I). These data indicate that NH+GDP successfully ameliorates inflammatory hepcidin and improves AI symptoms in chronic model thus, maintaining the normal iron homeostasis

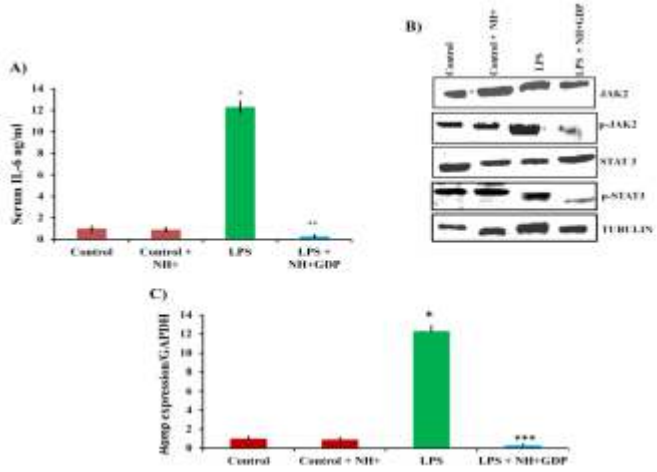


Figure 1: NH+GDP suppresses LPS–induced Hamp expression in acute model: A-B) NH+GDP significantly reduced serum IL-6 level suppressing the phosphorylation of JAK2/STAT3 pathway in hepatocytes. Tubulin was used as a internal control. C) Consistently NH+GDP decreases LPS-mediated Hamp mRNA expression relieving LPS-induced inflammation in hepatocytes. Results are normalized to GAPDH and expressed as mean ± SD for n animals (n=8/group). p values were calculated using one-way ANOVA. ***: p ⩽ 0.001 LPS+NH+GDP vs LPS**:p ⩽ 0.05 LPS+NH+GDP vs LPS and *:p ⩽ 0.01 Control vs LPS.

Pharmacodynamics and pharmacokinetics study of GDP and NH+GDP: In relevance to clinical studies, further we will investigate the role of GDP and NH+GDP in PG-APS female wistar anemic induced rats. For long-term experiment, AI condition was induced in female wistar rats by (IP) administration of PG-APS (15ug rhamnose/g of body weight), resulting in anemia within 2 week interval (1 injections/week). Meanwhile, during treatment we will analyse CBC blood parameter to check haemoglobin count. The experimental set up include eight group of female wistar rats, control, Control + GDP, Control + Liposome, Control + encapsulated GDP, Control + $FeSO_4$, Control + $FeSO_4$ + Ascorbic acid, Anemic, Anemic + $FeSO_4$,Anemic + $FeSO_4$+ Ascorbic acid, Anemic + blank liposome, Anemic + Non-encapsulated GDP (3 doses),Anemic + encapsulated GDP (3 doses),Anemic + encapsulated GDP + $FeSO_4$(3 doses),Anemic + encapsulated GDP + $FeSO_4$ + Ascorbic acid(3 doses)

To evaluate whether GDP or NH+GDP treatment could alleviate anemia in these animals, anemic rats (2 weeks post-PG-APS) were treated with GDP or NH+GDP in dose dependent concentration. Further if significant result were observed we, will check all biochemical assay, haematological parameter, tissue histology, western blotting and pharmacokinetics and pharmacodynamics parameter

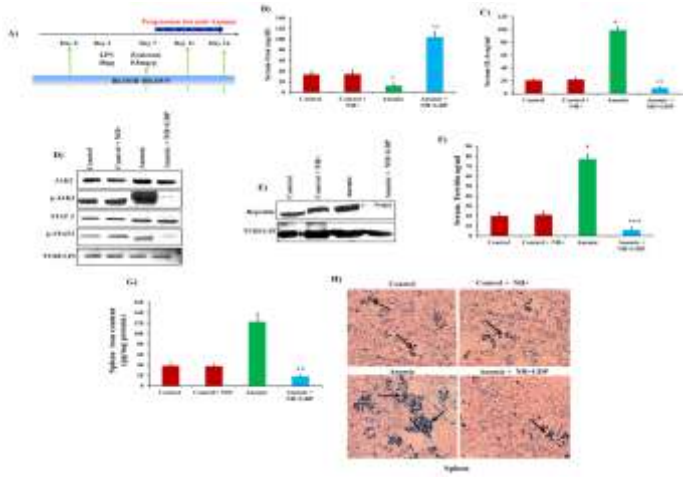


Figure 2: NH+GDP ameliorates AI in chronic model thus, maintaining normal iron homeostasis: A) Diagrammatic representation of dose interval and time progression towards anemia. B) Elevated serum iron concentration was observed with NH+GDP treated group. C) NH+GDP significantly attenuates serum IL-6 level evoked by LPS+Zymosan induced inflammation. D-E) NH+GDP suppressed phosphorylation of JAK2/STAT3 thus, decreasing inflammatory hepcidin-25 protein expression; tubulin was used as an internal control. Densitometry analysis of represented immunoblot was demonstrated in Supplementary Figure 9.Tubulin was used as a internal control. F) In parallel, significant decrease in serum ferritin level was observed in NH+GDP treated group indicating effective iron egress for erythropoiesis. G) Splenic iron level indicate decrease in iron content level after treatment with NH+GDP. H Increased iron deposit was observed in anemic state, whereas NH+GDP reversed this effect with decrease iron accumulation in spleen. Results are normalized to GAPDH and expressed relative to controls. n = 8/group.p values were calculated using One-way ANOVA. '*' withp⩽ 0.01 control vs anemic, '**'p⩽ 0.05 NH+GDP vs anemic, '***': p⩽0.001 NH+GDP vs anemic.

Salient Achievements

1) The mechanistic action of NH+GDP inactivate IL-6/JAK/STAT3 pathway thus, suppressing Hamp mRNA expression with increase cellular iron efflux in HepG2 and Caco2 co-culture cells.
2) In acute and chronic AI model, NH+GDP treatment reverses iron restrictive effect of inflammation with increase haemoglobin level and erythrocyte number thus correcting inflammation induced anemic state.

(FOOD & NUTRITIONAL BIOTECHNOLOGY - FNB02)

FOOD AND GM CROPS BIOSAFETY

2.1 Developing multi-functional gold nanorod based nanobiosensor to detect food borne bacteria

Principal Investigator
Nitin Kumar Singhal

Research Fellows
Shimayali Kaushal
NiteshPriyadarshi

Introduction

Food borne bacterial species have been identified as major cause in most of the severe pathogen related diseases. Conventional methods like plating and enzyme-linked immunosorbent assay (ELISA) are time overriding and laborious. Fast detection of bacterial species in food is proximate obligation to guarantee food safety. Advancement in nanotechnology has enabled to engender new diagnostic tools for sensitive and rapid detection of pathogens and toxins2,3. Currently our lab is developing nanobiosensor based on Carbohydrate, Aptamer and Antibody. Integration of metallic nanoparticles into biosensor has achieved recognition for its ability to increase bacterial detection. Due to their unique optical properties, plasmonic noble metals (gold and silver) containing nanomaterial-enabled colorimetric detection strategies provide rapid and sensitive sensing. AuNRs have been extensively studied, compared to monodisperse nanoparticles as biosensor due to higher sensitivity to local dielectric environment4,5. AuNRs have attracted attention because of their nontoxic nature and unique optical properties, mainly the longitudinal surface plasmon resonance (LSPR) peak which shows good shift and inhibition after aggregation in the presence of food borne bacteria. The surface plasmon greatly enhances electromagnetic fields on the gold nanorods making them useful as good sensing devices. Simple methods are available that allow for the shape control and change in chemistry on the surface of gold nanorods. It has been shown in the research study that bacterial cells produce lectins that are specific for certain carbohydrate and the bacteria depend on these lectins for their adhesion to a host tissue in order to infect them. By exploiting the sugar based adhesion properties of microorganism we can use the gold nanorods as a potential nanobiosensor to detect the food borne pathogen. Further, to increase the sensitivity and specificity, we generated aptamers against various food borne pathogens. These aptamers will be used for the multiplex detection of the pathogens in food samples. Our present study will contribute in the development of new multiplexed food borne pathogen biosensor and can have an applied impact by offering a promising solution for food quality monitoring by a time effective and economical way. This nanorod based nanobiosensor can be an ideal candidate for optical detection and killing of food borne bacteria.

Research Progress

1) Currently carbohydrate and aptamer based nanoprobe is synthesized and antibody based probe synthesis is in progress .In carbohydrate based study, Polyethylene glycol (PEG) grafted AuNRs having carboxylic group in the terminal position, are being used for fictionalization of two sugars namely, 4-aminophenyl α-D-mannopyranoside and 4-aminophenyl β-D-galactopyranoside and then further tested with lectins and bacteria to prove the specificity of synthesized nanobiosensor. A visible color change was seen in case of synthesized Glyco-AuNRs bound to specific lectin. Similarly, food borne bacteria such as *E. coli* was tested with the mannose modified AuNRs (Mann-AuNRs) and aggregation of Mann-AuNRs on E. coli surface can be easily seen whereas *P. aeruginosa* as a cross reference did not show any aggregation of Mann-AuNRs on its surface. P. aeruginosa is also used to cross check the aggregation of galactose modified AuNRs (Gal-AuNRs) on its surface and to prove the specificity of synthesized nanobiosensor. Further functionalized AuNRs can be used as photothermal agents for the selective killing of pathogenic bacteria. To kill *P. aeruginosa* and *E. coli,* we have used 200 mW 808 nm NIR light to expose bacteria attached with Glyco-AuNRs..After irradiation treatment, photothermal ablation of both bacteria was confirmed by colony counting on LB agar plate (Figure 1) and growth curve (Figure 2).In contrast, in the presence of both NIR light and Glyco-AuNRs, the number of bacterial colonies decreased

significantly. From Photothermal images shown in Figure 2, it can be seen that the temperature is increased to 59.9°C and 66.8°C (after NIR) from 32°C (before NIR) in case of E. coli and P. aeruginosa respectively when treated with both NIR and Glyco-AuNRs.

2) In contrast to weak monovalent binding, multivalent interactions result in high specificity and in thermodynamic and kinetic stability. The attachment of multiple weakly binding ligands on the surface results in significantly stronger adhesion at interfaces than those that have been produced from monovalent interactions. Carbohydrate as a class of feebly binding ligands for cell surface ligands requires many individual binding events through multivalent carbohydrate protein interactions. So, considerable effort has been dedicated in constructing synthetic multivalent glycoconjugates (Figure 3). Several carbohydrates with multiple arms has been synthesized with amine and azide terminated (Figure 4) which can be used for amide coupling and click reactions respectively, that can be used to interfere with the pathogen adhesion process and serve as antibacterial agents.

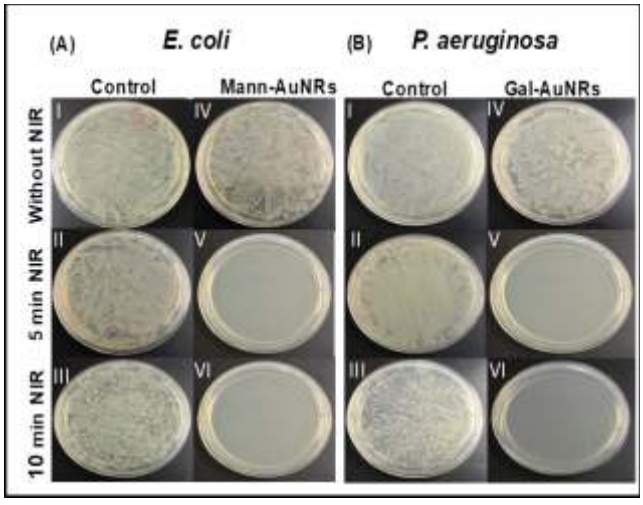


Figure 1: Images of bacterial colonies (A) E.coli (I) Control (II) Control with 5min NIR (III) Control with 10 min NIR (IV) Control incubated with Mann-AuNRs without NIR (V) Control incubated with Mann-AuNRs with 5 min NIR (VI) Control incubated with Mann-AuNRs with 10 min NIR. (B) *P. aeruginosa* (I-III) represents same as of *E. coli.* (IV) Control incubated with Gal-AuNRs without NIR (V) Control incubated with Gal-AuNRs with 5 min NIR (VI) Control incubated with Gal-AuNRs with 10 min NIR.

3) In the present study, detection using aptamers, which are ssDNA strands generated using cell-selex method (Figure 5a)6 and are specific for their respective targets. In cell selex, bacterial cells were incubated with ssDNA library which was then washed to remove unbound DNA. Bound DNA was extracted by heat denaturation method in which cells with bound DNA were heated at 95deg for 10mins followed by 10mins incubation on ice. Bound DNA was further amplified by asymetric PCR for next cycle. After last cycle, cloning was done to get multiple sequences. In this study, aptamers were generated against food borne pathogen, *Escherichia coli* and *Staphylococcus aureus* using 86 bases library. 7 cycles were performed for each pathogen. Figure 5b shows the agarose gel image of last cycle showing a band of 86 bases and the gel image of extracted plasmid after cloning. Table 1 gives the sequences obtained for *E. coli* and *Staphylococcus aureus* followed by folding image of the sequences (Figure 6).

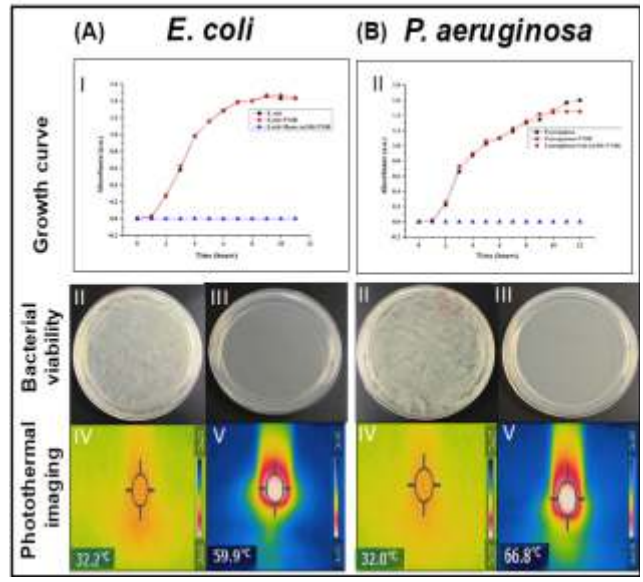


Figure 2: (A) *E. coli* (I) growth curve of Control and NIR treated samples, (II) *E. coli* without NIR treatment, (III) *E. coli* after treatment with Mann-AuNRs and NIR, (IV) Photothermal imaging of *E. coli* without Mann-AuNRs showing initial temperature, (V) Photothermal imaging of *E. coli* with Mann-AuNRs showing temperature after 5 min NIR exposure. (B) *P. aeruginosa* (I) growth curve of Control and NIR treatment, (II) P. aeruginosa without NIR treatment, (III) P. aeruginosa after treatment with Gal-AuNRs and NIR, (IV) Photothermal imaging of *P. aeruginosa* without Gal-AuNRs showing initial temperature, (V) Photothermal imaging of *P. aeruginosa* with Gal-AuNRs showing temperature after 5 min NIR exposure

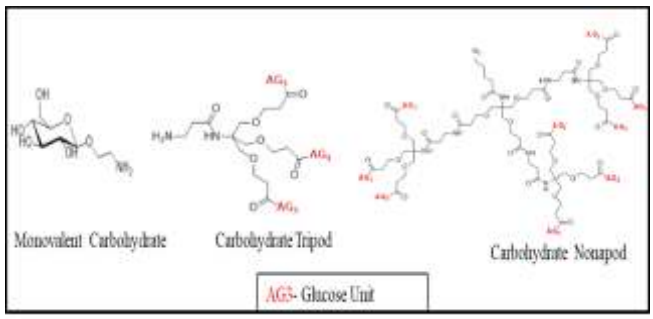


Figure 3: Synthesis of Multivalent Carbohydrate.

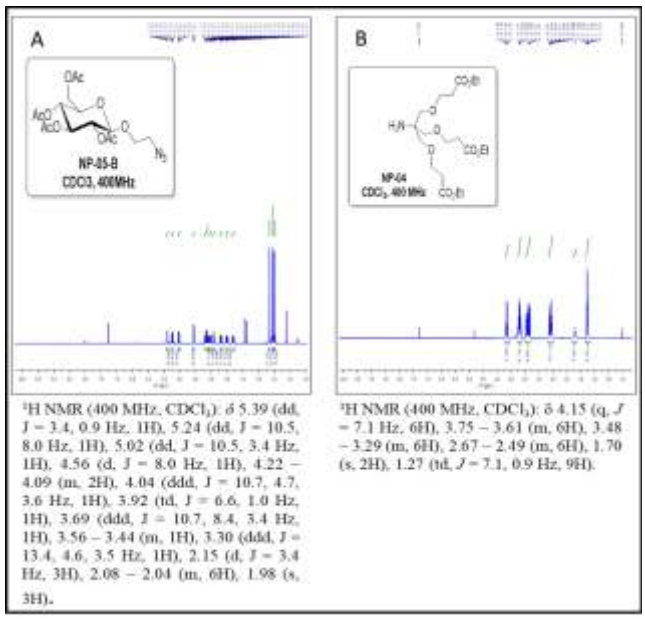


Figure 4: NMR spectra of (A)2-(acetoxymethyl)-6-(2-azidoethoxy) tetrahydro-2H-Pyran-3,4,5–triyl triacetate.(B)Diethyl 3,3'- ((2-amino-2-((3-ethoxy-3-oxopropoxy)methyl) propane-1,3-diyl) bis (oxy)) dipropanoate.

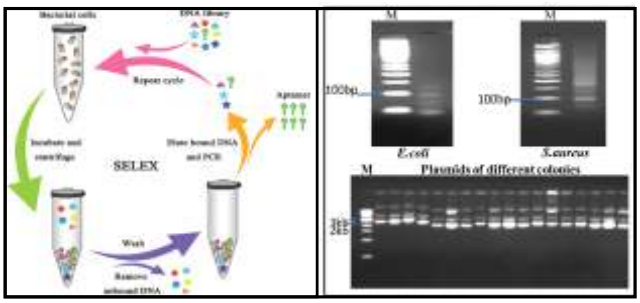


Figure 5: (a) Cell Selex method for the screening of aptamer . (b) Agarose gel image of the last cycle of screening and the gel image of the isolated plasmid.

Table 1: sequences obtained for E.coli and Staphylococcus aureus

SEQ. ID	SEQUENCE
E1	TAGGGAAGAGAAGGACATATGATCGATTACCGG AGCTGTGTCACCGGGCGCCAGTTGATGTGGTTG ACTAGTACATGACCACTTGA
E2	TAGGGAAGAGAAGGACATATGATTATGATGGGA GTAACGATTGTCCGACATGGTACCACCCCATTGA CTAGTACATGACCACTTGA
S1	TAGGGAAGAGAAGGACATATGATAGGTAGTCCC GCATTTAACCATAGGTACTGCAGCAGATTATTGA CTAGTACATGACCACTTGA
S2	TAGGGAAGAGAAGGACATATGATTGGAGAGTAG TCTGATACCCGATTATGAGCCTGTCCCTGGTTGAC TAGTACTGACCACTTGA

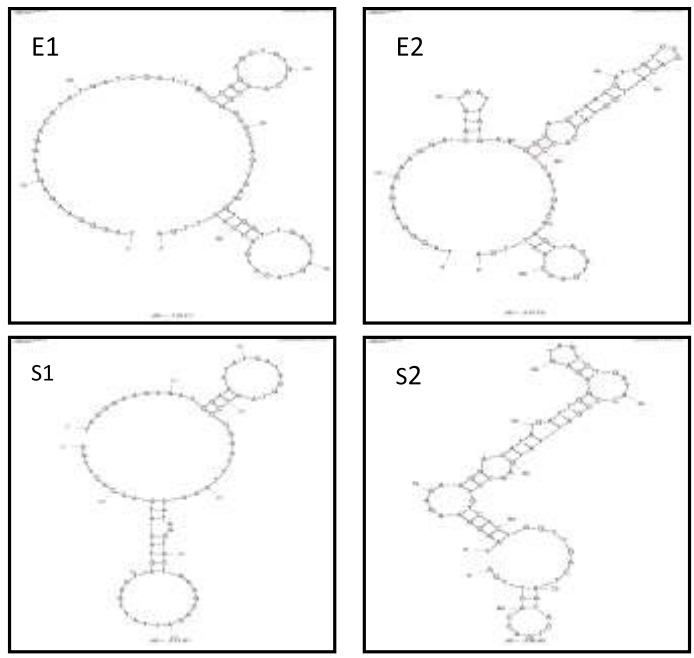


Figure 6: Folded structure of the selected sequences. E1 and E2 are E.coli sequences and S1 and S2 are of S. aureus sequences

Salient Achievements

1) The results of plating experiments indicated effective killing (>99%) of bacterial colonies within 5 min by our synthesized biosensor under NIR illumination.
2) Carbohydrate tripod synthesized with glucose and galactose unit.
3) Aptamers screened and generated against E.coli and S.aureus.

(FOOD & NUTRITIONAL BIOTECHNOLOGY - FNB03)

NUTRIGENOMICS FOR HEALTH & HUMAN WELFARE

3.1 Recombinant production of omega-3 polyunsaturated fatty acids of bacteria from high altitude lakes of Indian Himalayas

Investigator
Hena Dhar

Introduction

Eicosapentaenoic acid (C20:5 n-3, EPA) and docosahexaenoic acid (C22:6 n-3, DHA) are well known for their role in prevention and treatment of several human diseases. The major dietary sources of EPA and DHA are fish and fish oils but the increasing awareness and understanding about the health benefits of omega-3 fatty acid have prompted the search for the alternative sustainable sources of these molecules such as oleaginous microbes. Bacterial production of polyunsaturated fatty acids (PUFA) has gained interest as an alternative approach as they are the renewable source that can be easily cultured and can be genetically modified. Mostly marine bacteria including *Colwellia, Moritella, Photobacterium, Shewanella* and *Vibrio* of class Gammaproteobacteria and *Cellulophaga, Pibocella,* and *Polaribacter* of class Flavobacteria from cold and high pressure environments like ocean depths and gastrointestinal tracts of omega-3 fatty acid containing fish are known to accumulate lipids with high percentage of EPA and DHA. Production of PUFA by these bacteria is believed to be a part of survival strategy in such harsh environmental conditions. EPA and DHA can be synthesized via two pathways, the anaerobic polyketide synthase pathway for de novo synthesis directly from malonyl-CoA with no free intermediates and the aerobic desaturase and elongase pathway utilizing saturated fatty acids as precursors. In this study, high altitude lakes of Indian Himalayas, which are ideal source for psychrophilic and halophilic microorganisms due to extreme environmental conditions, are selected for exploration of PUFA-producing microbes both by culture dependent and culture-independent studies. Thereafter, heterologous expression of EPA and DHA gene cluster from the promising isolate(s) will be performed.

Research Progress

In order to explore omega-3 fatty acid producing microbes, water and sediment samples were collected from 16 locations of 4 high altitude lakes- Kiagar Tso (KT), Pangong Tso (PT), Tso Kar (TK) and Tso Moriri (TM) of Ladakh in the last week of September, 2017 (Figure 1).

In culture based microbial diversity study, a total of 665 bacteria were isolated from KT, PT, TK and TM on enriched and low-nutrient media like Zobell marine agar (MA), Tryptone Soya Agar (TSA), Nutrient agar, Reasoner's 2A, Luria Bertani agar and Yeast malt extract agar, and their dilutions (1:10, 1:50 and 1:100) at 10°C and pH 7.0, and preserved at -80°C in 25% glycerol. The total viable bacterial count in water samples on 12 different media ranged from 2.55-3.59, 2.53-3.13, 1.97-4.44 and 2.19-2.73 log10 CFU/ml in KT, PT, TK and TM, respectively. Also, 70 bacteria were isolated from the gut of two cold water fish of Himalayas- Snow trout and Rainbow trout with 6.55-6.56 and 2.72-6.54 log10 CFU/ml on 0.5% MA and TSA at 15℃, respectively. Primary screening for polyunsaturated fatty acid production was carried out by streaking bacteria on media containing 0.1% 2,3,5-triphenyltetrazolium chloride (TTC). Out of 462 isolates screened, 36 isolates capable of growing and developing red colour due to the conversion of TTC (colourless) to TF (triphenyl red formazan) were identified as putative omega-3-producing bacteria (Figure 2). Screening of remaining isolates is underway. Secondary screening for EPA and DHA will be done by fatty acid methyl ester analysis using GC-MS.

Figure 1: Sampling locations (a) Kiagar Tso (b) Pangong Tso (c) Tso Kar (d) Tso Moriri

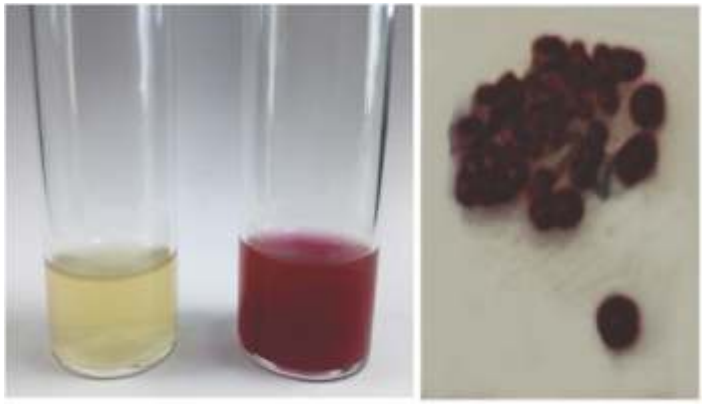


Figure 2: Screening for EPA-producing bacteria using TTC as primary test (a) Broth culture test (b) Agar plate test

For culture independent studies, community DNA from the water samples were extracted and sequenced on Illumina NextSeq500 platform using 2×150 bp chemistry. The generated reads were trimmed using Trimmomatic version 0.35 to obtain high quality clean reads ranging between 4.14 and 6.99 Gb which were then assembled into scaffolds using CLC Genomics Workbench version 9.5.2 and genes were predicted using Prodigal-2.6.3. The predicted genes were analyzed for taxonomic classification using Kaiju and for functional attributes using Cognizer. Taxonomic analysis revealed that metagenomes of all the four lakes contained 54.08-64.89% bacteria, 0.14-0.19% archaea, 0.36-1.18% eukaryota and 0.45-0.82% viruses, while 33.5-43.83% were unclassified. Among bacteria, Proteobacteria was found to be the most abundant phylum in all samples. Other major phyla included Bacteroidetes (10.1-14.6%), Actinobacteria (3.7-11.5%), Planctomycetes (1.4-4.4%) and Verrucomicrobia (1.98-3.4%) (Figure 3).

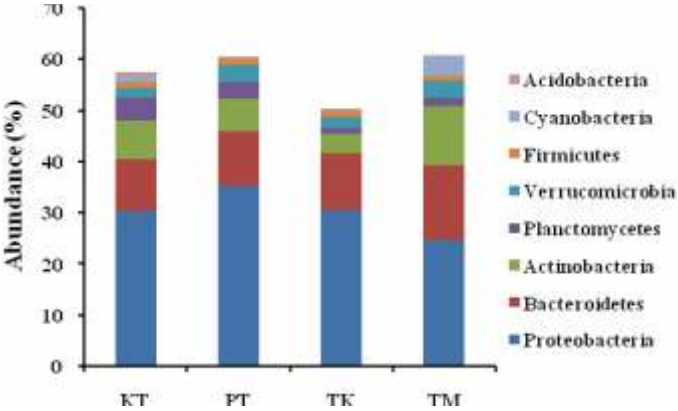


Figure 3: Stacked bar graph showing the relative abundance at Phylum level

At genus level, *Hydrogenophaga* (1.46%), *Rheinheimera* (3.21%), *Pseudomonas* (1.58%) and *Algoriphagus* (1.73%) were found to be the most abundant in the samples KT, PT, TK and TM, respectively. Moreover, the genera known for EPA and DHA production like *Shewanella, Photobacterium, Vibrio, Colwellia, Moritella* and *Psychromonas* were also observed in all samples (Figure 4).

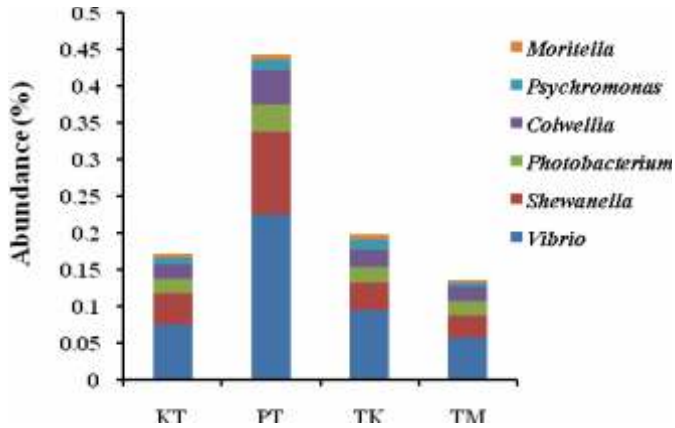


Figure 4: Abundance of known omega-3 fatty acid producing bacteria

Among 5 different databases (COG, Pfam, KEGG, FIG and GO) used for functional annotations of genes, COG was found to give the highest number of hits followed by Pfam. Functional annotations using FIG revealed the presence of 15, 6, 8 and 9 genes of omega-3 fatty acid desaturase (Δ15 desaturase), and 54, 30, 46 and 13 genes for PfaA and PfaB subunit of omega-3 fatty acid synthase in the metagenomes of KT, PT, TK and TM, respectively, indicating the presence of omega-3 fatty acid producing microbes in these niches.

Salient Achievements

1. Microbial diversity of unexplored high altitude lakes of Himalayas was studied
2. Both culture dependent and culture independent studies revealed the presence of omega-3 fatty acid producing microbes in the high altitude lakes of Indian Himalayas, which were primarily known to be present in marine environments

Bacterial culture repository

(FOOD & NUTRITIONAL BIOTECHNOLOGY - FNB04)

POST HARVEST BIOTECHNOLOGY FOR VALUE ADDITION AND INCREASING SHELF LIFE

4.1 Development of edible coating materials for the post-harvest shelf life improvement of fresh fruits

Principal Investigator
Koushik Mazumder

Research Fellows
Usman Ali
Swati Kanwar

Introduction

Absence of postharvest treatment, traditional storage on farms, infestation of microorganism and pests, non-availability of processing methods are the responsible factors for the highest rate of postharvest losses in fruit and vegetable in India. Due to limited availability of cold chain facilities especially during storage and transportation, development of coating materials to prolong the shelf life of fruits and vegetables is the high priority in this research area. Biodegradable and edible polysaccharides provide a thickening effect and have film forming ability which can be used to prepare coating materials to extend the shelf life of fruits maintaining the sensory and safety qualities. In majority of cases, the coating technology is simple and can be applied even in the farm level; therefore development of coating materials to prolong the shelf life of fruits and vegetables is the high priority, so that spoilage during transportation and marketing is reduced.

In our present study novel strategies was adopted to structurally modify polysaccharide such oat bran polysaccharide with several fatty acids to prepare hydrophobic derivatives. These hydrophobic fatty acid-polysaccharide esters were further blended with hydrophilic wheat straw polysaccharide to prepare composite formulations for shelf life improvement of the coated fresh fruits such as delaying color change, weight loss, ripening and maintaining firmness and sensory qualities during transportation and storage. Overall, we aim to develop carbohydrate based edible coating material to prolong the shelf life of perishable fruits (e.g. peach and apple).

Research Progress

In our study, wheat straw arabinoxylan (AX) and oat bran β-glucan (BG) were extracted with a yield of ~15% and 8% respectively, the lab scale extraction cost of AX and BG were in the range of ~ Rs. 10/g and 25/g. Furthermore, novel strategy was adopted to modify the oat bran polysaccharide via esterification with several fatty acids to improve their hydrophobic character and blended with wheat straw polysaccharide to prepare composite films. The composite coating material containing wheat straw arabinoxylan (AX) and stearic acid esterified-β-glucan (AX-SABG, 60:40) exhibited best functional properties such as caused significant reduction in water vapor transmission (~67%), improved mechanical strength (~12 MPa; MPa: megapascal), thermal stability (> 200°C) and film transparency.

To evaluate the efficacy of the coating formulation for the post-harvest shelf life improvement, AX-SABG coating material (1-4%) was surface coated on fresh peaches (Sharbati variety). The study on the post-harvest quality parameters showed non-coated peaches exhibited weight loss (Figure-1) of ~21% during storage period of 6 days at 20°C and 80% relative humidity (RH) whereas significant lowering in fruit weight loss of ~15-16% and 13-15% were observed for AX-SABG (1-4%) and commercially available shellac (1-4%) coatings respectively. The study also revealed that AX-SABG coating formulation effectively maintained fruit texture and firmness (~11-12 N, N= Newton) compared to non-coated (~7.0 N) and shellac (~7.5-8.0 N) coated peaches. (Figure-2)These results suggested AX-SABG coating material (1-4%) significantly improved the shelf-life of the coated peaches by reducing weight loss and delayed fruit softening during the storage condition. (Figure 3)

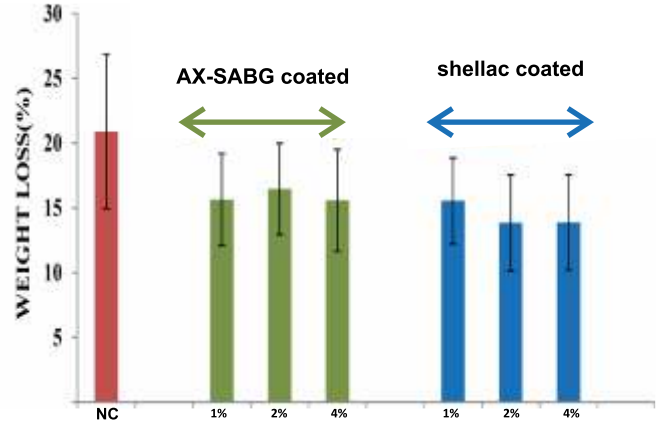


Figure 1: Measurement of weight loss of peaches under storage at 20°C and 80% RH for 6 days (NC: Non-coated peaches).

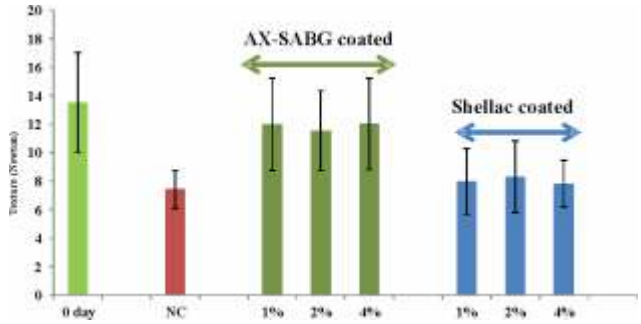


Figure 2: Measurement of texture/ firmness of peaches under storage at 20°C and 80% RH for 6 days (0 day: fresh peaches immediately after harvesting; NC: Non-coated peaches).

Figure3: Images of un-coated peaches (A) and coated with 1% AX-SABG coating formulation (B) after 6 days at 20°C and 80% relative humidity.

The detailed studies for the post-harvest shelf life improvement of apple were conducted on three varieties of apples (Royal Delicious, Kinnaur; Royal Delicious, Kashmir and Rich Red, Kinnaur) at different storage conditions. The study on Royal Delicious, Kinnaur variety revealed that AX-SABG coating (1-4%) significantly reduced fruit weight loss (~6.1-11.0%) compared to non-coated apples (~7.8-13.8%) during storage period of 60 days at 22°C and 65% RH. The ability of AX-SABG coating to reduce weight loss was very much comparable to that of commercially available shellac coating (~5.7-10.3%). Similarly, AX-SABG effectively maintained fruit firmness during storage; only 3.1-5.2% reduction in fruit firmness was observed during storage period up to 30 days. The study also suggested AX-SABG coating formulation maintained the sensory quality parameters (sweetness, firmness, sourness and flavor) of the coated apples during storage. Our initial study showed AX-SABG coating formulation has the ability to extend the post-harvest shelf life of Royal Delicious apples (Kinnaur) up to 45 days compared to the normal shelf life of no-coated apples in the range of 15-30 days.

Figure 4: Images of un-coated apples (A) and coated with 1% AX-SABG (B) at 45 days at 22°C and 65% relative humidity.

Further detailed studies on postharvest quality improvement of AX-SABG coating formulation on different varieties of apples (e.g. Royal Delicious, Kashmir variety and Rich red, Kinnaur variety) are under progress.

Salient Achievements

1) In our study polysaccharides from secondary agricultural by-products (e.g. wheat straw) was extracted to produce edible coating materials for the shelf-life improvement of perishable fruits.
2) The studies of the post-harvest qualities of perishable fruits suggested AX-SABG coating formulation significantly improved the shelf life by reducing fruit weight loss, softening and delaying ripening compared to non-coated fruits. This study suggested that the edible fruit coating material based on AX-SABG has potential as an alternative to commercially available animal based shellac coating in India.

New Initiatives

New Initiative-I

Metabolic engineering of triacylglycerol (TAG) metabolism pathway to trigger oil content stability in plant leaves and seeds

Metabolic engineering of triacylglycerol (TAG) metabolism pathway to trigger oil content stability in plant leaves and seeds: Rice bran oil (RBO) is extracted from rice bran as a by-product of milling (separation of husk) and is available as a food grade vegetable oil. RBO is emerging as a popular oil as it is typically high in oleic and linoleic fatty acids and contains naturally occurring antioxidants with health beneficial effects. However, during the normal practice of RBO extraction, the physical barriers that sequester the endogenous lipases away from the oil are disrupted, and these enzymes become activated by the moisture introduced in the milling process. Hence, RBO preparations have high free fatty acid (FFA) content, and this continues to increase during storage reaching 40-60% by 30 days after milling, which spoils the oil via oxidative rancidity.

Similarly, the most difficult problems that nutrition and animal scientists face is the fate of FAs in the rumen. When essential fatty acids, like linoleic (C18:2) and α-linolenic acid (C18:3), enter the rumen, the process of bio-hydrogenation begins. Rumen microbes immediately begin the process of saturating these FAs. In respect to lipid metabolism, the two major processes that occur in the rumen are hydrolysis of ester linkages in triacylglycerol by microbial lipases followed by bio-hydrogenation of unsaturated fatty acids (converted to saturated fatty acids) and subsequently incorporated into milk fat. Hence, rumen lipolysis and bio-hydrogenation greatly reduces the quantity of dietary unsaturated FAs reaching the small intestine of the dairy cows.

The issues that this research will address is to overcome the common problem of spoiling by endogenous and microbial lipases, which occurs when rice grain is milled and plant fatty meal consumed by dairy cattle. Therefore, solution that I propose to develop is to alter the genetics of plant, by protecting the TAG products from lipase degradation. In addition, applying this strategy to leaf tissue will have the added benefit of increasing the energy-content of this tissue, which can be used as a source of sustainable energy production

New Initiative-II

Understanding and improving nutrient partitioning during rice grain filling

Understanding and improving nutrient partitioning during rice grain filling: Rice is staple food for not only India but also for global population. Rice is mainly eaten as polished grains, which mainly contain starchy endosperm part of the seed. The polishing is necessary for long term storage of the grains, however this process removes its outer layers (i.e. aleurone layer and seed coat) and embryo, both of which are major reservoirs of various minerals, vitamins and essential mineral oils, thus it reduces total nutritional value of rice. In order to overcome this problem, it is important to identify regulator genes responsible for nutrient partitioning in different parts of the grain. For this purpose, this project aim to employ a high-resolution, cell-type specific, transcriptomics approach to identify the genes which could be potentially involved in loading of specific nutrient in specific cell-types in developing seeds. Laser-Capture Microdissection (LCM) or Fluroscence Activated Cell-sorting (FACS) approach would be used for collecting specific cell-types from developing seeds at the grain filling stage. Ultimately, gene products which work as barrier to micronutrient loading into endosperm would be identified through analysis of their loss of function mutants. Fortunately, such mutant collection are available for rice (Guotian Li et al., 2017), which would expedite the functional analysis part.

EXISTING MOUs FOR COLLABORATION & NETWORKING

1. NABI and Institute of Nano Science and Technology (INST) signed an MOU on June 13th, 2017 to undertake the joint research work in the areas of mutual interest.

2. NABI signed an MOU with Borlaug Farmers Association for South Asia on November 17th, 2017 for licensing of knowhow of "Colored wheat (Black, Blue and Purple developed by NABI) with high anthocyanin content" to BAFASA for production of bakery products like bread, biscuit and chappati etc.

3. NABI signed an MOU was signed with Farmgrocer Products Pvt. Ltd., Ambala on November 17th, 2017 for licensing of knowhow of "Colored wheat (Black, Blue and Purple developed by NABI) with high anthocyanin content" to BAFASA for production of bakery products like bread, biscuit and chappati etc.
4. NABI signed an MOU was signed with ITC Ltd, Guntur on December 28th, 2017 for commercialization of anthocyanin bio-fortified colored wheat and high amylose/resistance starch wheat.

5. NABI signed an MoU was signed with Metahelix Life Sciences Ltd, Bangalore on January 12th, 2018 for commercialization of anthocyanin bio-fortified colored wheat and high amylose/resistance starch wheat.

6. An MoU was signed with Regional Centre for Biotechnology, Faridabad on February 22nd, 2018 to recognize NABI as a centre for conducting Ph.D. degree programme for human resource development in the areas of Agricultural, Food and Nutritional biotechnology.

7. An MoU was signed with C-DAC Pune on March 14th, 2018 to strengthen the application of computers in genomics and computational biology.

EXTRAMURAL GRANTS AND FUNDINGS

Sr.No.	Name of PI	Budget Grant	Project Title	Funding Agency	Period of Project	
		(Rs. in Lac)			From	To
1.	Dr. T.R Sharma	Rs.1,36,33,000	Genome and transcriptome sequencing of aromatic rices from North-Eastern region	DBT	October 2016	October 2019
2-	Dr. Nitin Kumar Singhal	Rs. 45,40,500	Developing glycoconjugates capped multifunctional gold nanorod based nanobiosensor for detection of multiple food borne bacteria	DBT	February 2015	February 2018
3.	Dr. Monika Garg	Rs.1,59,34,400	A genomics-assisted synthetic hexaploid wheat gene isolation and pre-breeding platform for improved heat tolerance and sustainable production	DBT	May 2015	April 2018
4.	Dr. Kanthi Kiran	Rs. 19,39,000	Metagenomic and functional characterization of Soy-based fermented foods of North-Eastern region	DBT	January 2017	Nov 2020
5.	Dr. Siddharth Tiwari	Rs.1,79,20,000	Transfer and evaluation of Indian anana with Pro-vitamin A (PVA) constructs. This project is a part of the Multi-Institutional core project entitled development and transfer of technology from Queensl and University of Technology (QUT), Australia to India for biofortification and disease resistance in Banana.	BIRAC	Nov 2012	Nov 2019
6.	Dr. Ajay K Pandey	Rs.52,27,600	Utilizing genome editing tools for nutritional improvement In wheat	DBT	June 2017	June 2020
7.	Sh. Shrikant S Mantri	Rs. 22,22,000	Connections: A comprehensive biological relationships resources and tools for automated literature mining	DBT	June 2017	June 2020
8.	Dr. Ajay K Pandey	Rs. 42,19,600	Functional characterization and implications of plant inositol pyrophosphate kinase	DBT	July 2017	July 2020
9.	Dr. Kanthi Kiran	Rs. 57,80,000	Enhanced rice millilng and maximised valorisatioin of rice milling by product	DBT	June 2017	June 2019
10.	Dr. Mahendra Bishnoi	Rs. 47,34,440	Pharmacological mimicking of cold via cold thermo-receptors	DBT	August 2017	August 2019
11.	Dr. Koushik Mazumder	Rs.2,75,05,000	Setting up of secondary agriculture/food processing entrepreneurial network in Punjab Phase-I	BIRAC	March 2018	March 2020
12.	Dr. Siddharth Tiwari	Rs. 55,92,160	CRISPR/Cas mediated genome editing of genes for high pro-vitamin A accumulation and its stability in banana	DBT	March 2018	March 2022

PARTICIPATION IN NATIONAL/INTERNATIONAL CONFERENCES/ WORKSHOPS

1. Dr. Monika Garg was invited to deliver a talk on understanding colored wheat at international conference on "Advancements in Science and Technology (ICAST 2107) held during April 20th – 21st, 2017 at Rayat Bahra University, Punjab.
2. Ms. Navneet Kaur presented an oral talk on "Metabolic Engineering for Enhanced Production of Provitamin A in Banana" in Agri Genomics India 2017 conference organized by SELECTBIO during July 20th – 21st, 2017 at Hotel Hyatt Regency Chandigarh.
3. Dr. Siddharth Tiwari, Dr. Praveen Awasthi and Ms. Shivani attended the "Agri Genomics India 2017" conference organized by SELECT BIO during July 20th – 21st, 2017 at Hotel Hyatt Regency Chandigarh.
4. Dr. Koushik Mazumder attended and delivered a talk on "Biopolymer Based Coating Applications for Shelf Life Improvement in Fruit Crops" during young faculty training program at PAU, Ludhiana, Punjab on July 28th, 2017.
5. Dr. Siddharth Tiwari was invited for a talk on "Transgenics in Fruit Crop Improvement - Concerns and Potential" on July 28th, 2017 at Department of Fruit Science, Punjab Agricultural University (PAU), Ludhiana, Punjab.
6. Dr. Monika Garg attended the "56th All India Wheat and Barley Research Workers" meet held during August 25th – 28th, 2017 at Varanasi, UP.
7. Dr. Mahendra Bishnoi attended the "3rd USQ-Functional Foods Festival (Healthy Living Symposium)" held during September 6th - 9th, 2017 at the Empire Theatre, Toowoomba.
8. Sh. Shrikant Mantri participated in DBT-EMBL conference held during October 12th -13th, 2017 at New Delhi.
9. Dr. Monika Garg and Ms. Payal Sharma was invited to attend the "India International Science Festival 2017: Science for New India" held during October 13th – 16th, 2017 at Chennai, Tamil Nadu.
10. Dr. Monika Garg was invited to deliver a talk (oral presentation) on "Colored Wheat as a Novelty Crop: Understanding Potential Health Benefits" at the international conference on Biotechnology and Healthcare held during October 26th – 27th, 2017 at PJTSAU, Hyderabad.
11. Sh. Shrikant Mantri participated in GIAN course, "Conservation and Evolution in Developmental Gene Regulatory Networks: A Systemic View" held during November 1st -8th, 2017 at IISER Mohali.
12. Dr. Nitin Singhal attended the "Nano Science & Nano Technology- Biological Sciences" conference held during November 6th - 11th, 2017at INST, Mohali
13. Dr. Gulshan Kumar attended and delivered a lecture at national conference on "Plant Physiology: Emerging Role of Plant Physiology for Food Security and Climate Resilient Agriculture" held during November 23rd - 25th, 2017 at Indira Gandhi Krishi Viswavidyalaya (IGKV), Raipur.
14. Dr. Mahendra Bishnoi attended the "10th Asia Pacific Conference on Clinical Nutrition (APCCN) Adelaide" held during November 26th - 29th, 2017 at SA, Australia.
15. All the Faculty of NABI attended the "Nobel Laureate Har Gobind Khorana Memorial Symposium on Genes, Genomes and Membrane Biology" held during December 3rd - 5th, 2017 at National Agri-Food Biotechnology Institute (NABI), Mohali, India.
16. Ms. Navneet Kaur received the best poster award in the "Nobel Laureate Har Gobind Khorana Memorial Symposium on Genes, Genomes & Membrane Biology" held during December 3rd - 5th, 2017 at National Agri-Food Biotechnology Institute (NABI), Mohali. Title of the poster was "Establishment and Application of Genome Editing towards Banana biofortification".
17. Ms. Shivani presented a poster in the Nobel Laureate Har Gobind Khorana Memorial Symposium on "Genes, Genomes & Membrane biology" held during December 3rd - 5th, 2017 at National Agri-Food Biotechnology Institute (NABI), Mohali. Title of the poster was "A Step towards the Development of Marker-free Technology in Banana".
18. Dr. Monika Garg attended the heat stress wheat meeting at the international conference on "Climate Resilient Crops" held during December 10th – 12th, 2017 at Nanded, Maharashtra.
19. Dr. Joy K. Roy presented a talk entitled "NGS to Detect eQTL" at Centre for Advanced Faculty Training (CAFT) in Plant Biotechnology during "Next Generation Sequencing and its Application in Crop

Sciences" symposia held from December 1st to 21st, 2017 at ICAR-NRCPB, New Delhi.

20. Dr. Joy K. Roy presented a talk on "Agricultural Biotechnology for Sustainable Crop Production" at 21st Punjab Science Congress held during February 7th - 9th, 2018 at PAU, Ludhiana
21. Dr. Siddharth Tiwari was invited to deliver a talk on "Research Initiatives in Agricultural Biotechnology by NABI" in the state level bio-safety capacity building workshop held on February 16th, 2018 at Punjab Agricultural University (PAU), Ludhiana.
22. Dr. Pramod Kandoth attended the "8th Conclave of Ramalingaswami Fellows" organized by NIPGR, New Delhi on behalf of DBT, India held during February 15th-17th, 2018.
23. Sh. Shrikant Mantri participated in India-EMBO Symposium on "Big-data in Biomedicine", held during February 25th -27th, 2018 at New Delhi.
24. Dr. Kanthi Kiran and his research group presented a poster entitled "Isomaltoligosaccharide Metabolism by the Human Lactic Acid Bacterial Strains" at 4th Biennial Conference of PAi and International Symposium on "Probiotic Therapy: Translating to Health and Clinical Practice" held in February 2018 at AIIMS, New Delhi.
25. Dr. Kanthi Kiran and his research group received a best poster award at 4th Biennial Conference of PAi and International Symposium on "Probiotic Therapy: Translating to Health and Clinical Practice" held in February 2018 at AIIMS, New Delhi. Title of the poster was "*Weissella cibaria* Strains Attenuate LPS Induced Pro-inflammatory Stress in Murine Macrophages & Human Epithelial Cells"
26. Dr. Kanthi Kiran and his research group presented a poster entitled "Screening for Immunomodulatory Microbes from Soy Based Fermented Foods" at 4th Biennial Conference of PAi and International Symposium on "Probiotic Therapy: Translating to Health and Clinical Practice" held in February 2018 at AIIMS, New Delhi.
27. Dr. Monika Garg attended the conference on "Technological Empowerment of Women: Commemorating the International Women's Day" held during March 8th – 9th, 2018 at New Delhi.
28. Sh. Shrikant Mantri organized "NABI Computational Biology Workshop 2018", during March 12th -14th, 2018 at National Agri-Food Biotechnology Institute (NABI), Mohali.
29. Dr. Joy K. Roy presented a talk on "Plant Genome Analysis using Association Mapping Approach" at "NABI Computational Biology Workshop 2018" held during March 12th - 14th, 2018 at NABI, Mohali.
30. Dr. Monika Garg attended the 13th International Gluten Workshop on "Rapid Development and Characterization of Chromosome Specific Translocation Line of Thinopyrumelongatum with Improved Dough Strength" held during March 15th – 17th, 2018 at Mexico City, Mexico.
31. Dr. Gulshan Kumar attended "ICGEB workshop 2018: Smart Metabolic Engineering of Plants for Drug Biosynthesis" held during March 16th to 17th, 2018 at ICGEB, New Delhi, India.
32. Dr. Monika Garg attended the international visitor week of CIMMYT held during March 18th – 23rd, 2018 at Obregon, Mexico.
33. Dr. Siddharth Tiwari attended the brainstorming workshop on "Prospects & Way-forward for Strengthening Tissue Culture Industry in Punjab" held on March 21st, 2018 at MGSIPA Complex, Sector 26, Chandigarh.
34. Dr. Joy K. Roy presented a talk on "Genomic Selection in Plant Breeding" on March 08th, 2018 in the ICAR-HRM programme 2017-18 on "Genomics Assisted Breeding for Crop Improvement" held during March 1st to 21st, 2018 at ICAR-IARI, New Delhi.
35. Dr. Koushik Mazumder attended one day colloquium BIOPOSIUM, organized by the Department of Biotechnology on March 27th, 2018 at Thapar Institute of Engineering & Technology, Punjab.

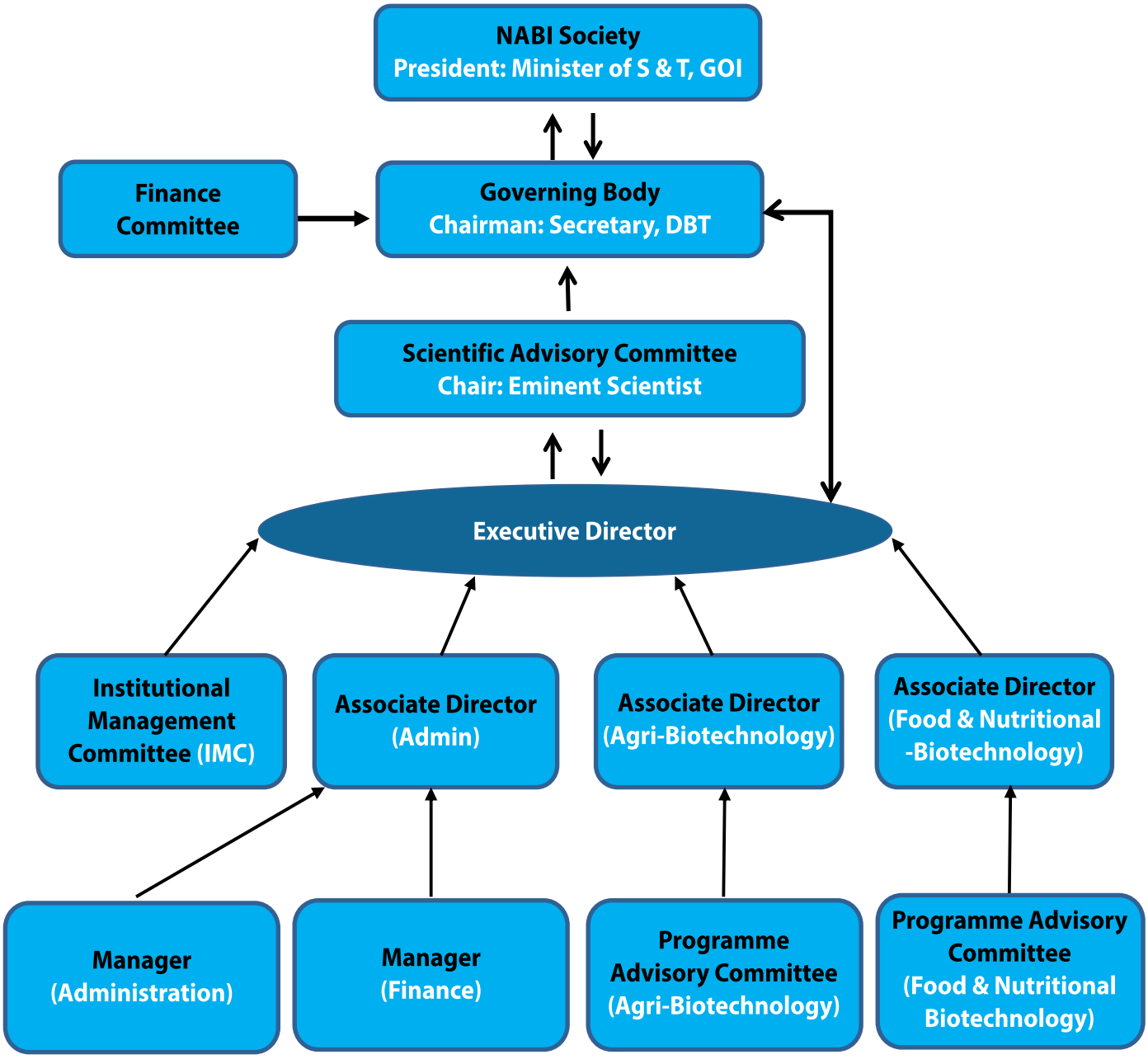
Visitors at NABI

1. Dr. Swarup Roy Choudhury, Post Doctoral Research Associate, Donald Danforth Plant Science Center, St. Louis, USA delivered a talk entitled "Heterotrimeric G-protein Signaling in Plants" on May 17th, 2017.
2. Dr. Vandana Sharma, Staff Scientist, Sanford Burnham Prebys Medical Discovery Institute, California, USA delivered a talk entitled "A tale of two Ms - Mannose and Microbiome" on July 14th, 2017.
3. Dr. Suresh kumar Ramasamy, Assistant Professor - AcSIR and Ramanujan Fellow, CSIR-NCL, Pune delivered a talk entitled "Mechanism and Application of Recently Identified Protein Targeting Pathways in Plants and Plant Pathogens" on September 15th, 2017
4. Dr. Prateek Tripathi, Research Associate, The Scripps Research Institute, California, USA was invited to deliver a talk on "Understanding the Mechanistic Links Between the Circadian Clock and Plant Metabolism for Crop Improvement" on 25th September 2017.
5. Dr. Rob Burgess, Vice President, Global Business Development, Ray Biotech Inc., USA delivered a talk entitled "Introduction to Multiplex Array Systems" on October 24th, 2017.
6. Dr. Pinky Ray chaudhuri, Associate Manager – Incubation, NCL Innovation Park, Dr. Homi Bhabha Road, Pashan, Pune delivered a talk entitled "Science Entrepreneurship: A Venture Center Perspective" on November 20th, 2017.
7. Prof. Gurmukh S. Johal, Professor, Department of Botany and Plant Pathology, Purdue University, USA delivered a talk entitled "A Probable Immunostat in Maize Comprising an Auto Active NLR and a RIN-family Inhibitor" on November 16th, 2017.
8. Prof. Uttam L Raj Bhandary, Lester Wolfe Professor of Biology, MIT, Cambridge, USA delivered the 3rd HarGobind Khorana Lecture on December 6th, 2017.
9. Prof. Kulvinder S. Gill, Department of Crop and Soil Sciences, Washington State University, USA delivered a talk entitled "The Ph1 gene, Homology Search, Chromosome Pairing and Alien Introgression" on December 8th, 2017.
10. Prof. Lindsay Browan, Professor of Biomedical Sciences, University of Southern Queensland, Toowoomba, Australia visited and delivered a lecture at NABI on February 21st, 2018
11. Dr. P. S. Vijaya Kumar, Scientist C, Institute of Nano Science and Technology, Mohali delivered a talk entitled "Targeted Cargo Delivery in Medicine and Agriculture with the Assistance of Nanoscience" on February 23rd, 2018.
12. Dr. Sudhakar Srivastava, Post-Doctoral Fellow, Ben Gurion University, Israel delivered a talk entitled "Novel role of Arabidopsis Aldehyde Oxidases in plants: Aldehyde Detoxification and thereby Premature Senescence Prevention" on March 9th, 2018.

Important Institutional Activities

1) Dr. Harsh Vardhan, Union Minister for Science and Technology, Earth Sciences and Environment, Forest and Climate Change inaugurated the new Administrative and Research buildings of National Agri-Food Biotechnology Institute, Mohali on August 6th, 2018. Dr. K. Vijay Raghavan, the then Secretary, DBT and other dignitaries from tri-city were also present on the occasion.
2) NABI along with his co-partners (Institute of Nano Science and Technology, Punjab State Council for Science and Technology and Indian Institute of Science Education and Research, Mohali) organized a three day Har Gobind Memorial Symposium on "Genes, Genomes and Membrane Biology" from December 3rd - 5th, 2017. During the symposium close to 32 speakers presented their research work. Twenty eight overseas speakers also participated and presented their work. A total of 320 researchers including young scientist, faculty and students from different parts of the country participated in the meeting. Multiple sessions dealing with cell signalling and gene regulation, GPCRs and membrane protein, structural biology, translation and post translational modifications and plant biology were organised. Some of the eminent scientists like Prof. Uttam Raj Bhandary (MIT, USA), Prof. Dieter Soll (Yale Univ., USA), Prof. Marsha Rosner (UNiv. of Chicago, USA) and Dr. Michael Gait (MRC, Cambridge-UK) attended and presented their scientific work during the symposium.
3) One day brainstorm session on "Development of Biofortified and Protein Rich Wheat" was organized on March 5th, 2018 under the Chairmanship of Dr. R. S. Paroda, Chairman, NABI-SAC. Multiple eminent scientist/researchers presented their work and relevant discussion was made in an effort to bring the concerted effort to address the issues pertaining to biofortificaiton in cereals crops.
4) A three day "Computational Biology Workshop" was organized at NABI from March 12th -14th, 2018. Around 50 leading experts, scholars and researchers from various scientific institutes of India attended this workshop.

GOVERNANCE


NABI Society
President: Minister of S & T, GOI
Finance Committee
Governing Body
Chairman: Secretary, DBT
Scientific Advisory Committee
Chair: Eminent Scientist
Executive Director
Institutional Management Committee (IMC)
Associate Director (Admin)
Associate Director (Agri-Biotechnology)
Associate Director (Food & Nutritional -Biotechnology)
Manager (Administration)
Manager (Finance)
Programme Advisory Committee (Agri-Biotechnology)
Programme Advisory Committee (Food & Nutritional Biotechnology)

MANAGEMENT OF THE INSTITUTE

A. Members of NABI Society

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Ministry of Science & Technology,
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Secretary
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(Chairperson – Governing Body)

Sh. C.P Goyal
Joint Secretary
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Joint Secretary
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(Member Secretary)

C. Finance Committee

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(Chairman)

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Sh. Suneet Verma
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C. Scientific Advisory Committee (SAC)

Dr. R. S. Paroda
(Former Director General – ICAR)
Trust for Advancement of Agricultural Sciences
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Former Vice Chancellor
University of Delhi, Benito Juarez Road
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Office-in-charge
Division of Genomic Resources
ICAR – National Bureau of Plant Genetics Resources
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Dr. Geeta Trilok Kumar
Director
Institute of Home Economics
Delhi University, F-4 Haus Khas Enclave
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Department of Gastro Enterology
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Department of Plant Molecular Biology University of Delhi South Campus
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Dr. Arun Sharma
Outstanding Scientist (Food Technology)
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(Chairman)

Dr. M.R Dinesh
Director
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Prof. Nagendra Kumar Singh
Project Director
ICAR – National Research Centre on Plant Biotechnology
LBS Centre, Pusa Campus
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Dr. A.K. Singh
Head & Principal Scientist (Genetic Division)
ICAR - Indian Agricultural Research Institute
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Dr. Navtej Singh Bains
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E. Programme Advisory Committee (PAC): Food and Nutritional Biotechnology

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Kharagpur–721302, Kolkata

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Professor
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Dr. V.K. Batish
Former Head & Emeritus Scientist
Molecular Biology Unit
National Dairy Research Institute
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Dr. K. Madhavan Nair
Scientist - F and Head
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Biophysics Division
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Professor and Chairperson
Department of Food Technology
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Dr. Farooq Masoodi
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Dr. Rita Singh Raghuvanshi
Professor and Dean
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F. Building Committee

Dr. V.S. Chauhan
Former Director
International Centre for Genetic Engineering and Biotechnology
New Delhi - 110067
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Sh. C.P Goyal
Joint Secretary
Department of Biotechnology
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New Delhi - 110003

Sh. B. Anand
AS & FA
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(From March 6th, 2018 till date)

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Chief Executive Officer
Center of Innovative and Applied Biopreocessing
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Sh. S.L Kaushal
Former Chief Architect
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Mohali – 160062, Punjab

Er. N.K. Verma
Former Chief Engineer
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New Delhi - 110001

Dr. Jagdeep Singh
Registrar
Central University of Punjab Education
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Former Chief Town Planner
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Dr. R.S. Khandpur
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Dr. Vamsi Krishna
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Administrative Officer
National Agri-Food Biotechnology Institute
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Mohali – 140306, Punjab
(Member Secretary)

RESEARCH PUBLICATIONS OF FACULTY AT NABI

1. Aggarwal S, Kumar A, Bhati KK, Kaur G, Shukla VK, Tiwari S and Pandey AK (2018). RNAi-mediated downregulation of inositol pentakisphosphate kinase (IPK1) in wheat grains decreases phytic acid levels and increases Fe and Zn accumulation. Frontiers in Plant Science.doi: 10.3389 / fpls.2018. 00259.
2. Banerjee A, Rudra SG, Mazumder K, Nigam V and Bandopadhyay R (2018). Structural and functional properties of exopolysaccharide excreted by a novel Bacillus anthracis (Strain PFAB2) of hot spring origin. Indian Journal of Microbiology 58, 39-50.
3. Biswal BK, Sadany ME, Kumari D, Sagar P, Singhal NK, Sharma S, Stobdan T and Shanmugam VK (2018). –Twin Function of ZeinZinc Coordination Complex: Wheat Nutrient Enrichment and Nanoshield against Pathogenic Infection. ACS Sustainable Chemistry & Engineering 6 (5), 5877-5887.
4. Dhaliwal J, Singh DP, Singh S, Pinakka AK, Boparai RK, Bishnoi M, Kondepudi KK and Chopra K (2018). Lactobacillus plantarum MTCC 9510 protects from chronic unpredictable and sleep deprivation stress-induced behavior, biochemical and selected gut microbial aberrations in mice. Journal of Applied Microbiology. Doi: 10.1111/jam.13765.
5. Garg M, Sharma N, Sharma S, Kapoor P, Kumar A, Chunduri V and Arora P (2018). Biofortified crops generated by breeding, agronomy, and transgenic approaches are improving lives of millions of people around the world. Frontiers in Nutrition 5:12, 1-33. Doi:10.3389/fnut.2018.00012.
6. Kaur G, Dogra V, Kumar R, Kumar S, Bhanjana G, Dilbaghi N and Singhal NK (2018). DNA interaction, anti-proliferative effect of copper oxide nanocolloids prepared from metallosurfactant based microemulsions acting as precursor, template and reducing agent. International Journal of Pharmaceutics. 535 95-105.
7. Kaur N, Alok A, Shivani, Kaur N, Pandey P, Awasthi P and Tiwari S (2018). CRISPR/Cas9 mediated efficient editing in phytoene desaturase (PDS) demonstrates precise manipulation in banana cv. Rasthali genome. Functional & Integrative Genomics, 18:89-99. doi:10.1007/s10142-017-0577-5
8. Mittal R, Kumar A, Singh DP, Bishnoi M and Nag TC (2018). Ameliorative potential of rutin in combination with nimesulide in STZ model of diabetic neuropathy: targeting Nrf2 /HO-1/NF-kB and COX signalling pathway. Inflammopharmacology 26(3):755-768.
9. Kumari M, Devanna BN, Singh PK, Rajashekara H, Sharma V, Sharma TR (2018). Stacking of blast resistance orthologue genes in susceptible indica rice line improves resistance against Magnaporthe oryzae.3 Biotech, 18: doi.org/10.1007/s 132050 1710 625.
10. Kisko M, Shukla V, Kaur M, Bouain N, Chaiwong N, Lacombe B, Pandey AK and Rouached, H (2018). Phosphorus transport in arabidopsis and wheat: emerging strategies to improve P pool in seeds. Agriculture 8, 27.
11. Patel SN, Singh V, Sharma M, Sangwan RS, Singhal NK and Singh SP (2018). Development of a thermostable and recyclable magnetic nanobiocatalyst for bioprocessing of fruit processing residues and D-allulose synthesis. Bioresource Technology 247 633-639.
12. Rahim MS, Sharma H, Parveen A and Roy JK (2018). Trait mapping approaches through association analysis in plants. Advances in Biochemical Engineering/ Biotechnology - Springer. Doi: 10.1007/10_2017_50.
13. Sarma SM, Singh DP, Singh P, Khare P, Mangal P, Singh S, Bijalwan V, Boparai RK, Kaur J, Mantri S, Boparai RK, Mazumder K, Bishnoi M, Bhutani KK and Kondepudi KK (2018). Finger millet arabinoxylan protects mice from high-fat diet induced lipid derangements, inflammation, endotoxemia and gut bacterial dysbiosis. International Journal of Biological Macromolecules 106, 994-1003.
14. Sharma G, Chopra K, Puri S, Bishnoi M, Rishi P and Kaur IP (2018). Topical delivery of TRPsiRNA-loaded solid lipid nanoparticles confer reduced pain sensation via TRPV1 silencing, in rats. Journal of Drug Target 26(2):135-149.
15. Singh S, Bhatia R, Singh A, Singh P, Kaur R, Khare P, Purama RK, Boparai RK, Rishi P, Ambalam P, Bhadada S, Bishnoi M, Kaur J and Kondepudi KK (2018). Probiotic attributes and prevention of LPS-induced pro-inflammatory stress in RAW264.7 macrophages and human epithelial cell line (Caco-2) by newly isolated Weissella Cibaria strains. Food & Function 9(2) 1254-1264.

16. Sharma S, Chunduri V, Kumar A, Kumar R, Khare P, Kondepudi KK, Bishnoi M, and Garg M (2018). Anthocyanin bio-fortified colored wheat: Nutritional and functional characterization. PLoS One, 13(4):e0194367.
17. Tanaka H, Nabeuchi C, Kurogaki M, Garg M, Saito M, Ishikawa G, Nakamura T and Tsujimoto H (2018). A novelcompensating wheat–Thinopyrumelongatum Robertsonian translocation line with a positive effect on flour quality. Breeding Science. 67: 509-517 Doi:10.1270/jsbbs.17058.
18. Vaish S, Awasthi P, Tiwari S, Tiwari SK, Gupta D and Basantani MK (2018). In silico genome-wide identification and characterization of glutathione S-transferase gene family in Vigna radiata. Genome, 61:311–322.doi:10.1139/ gen-2017-0192 Yadav A
19. Sunkaria A, Singhal N and Sandhir R (2018). Resveratrol loaded solid lipid nanoparticles attenuate mitochondrial oxidative stress in vascular dementia by activating Nrf2/HO-1 pathway. Neurochemistry International 1-16.
20. Arora S , Mahato AK, Singh S, Mandal P, Bhutani S, Dutta S, Kumawat G, Singh BP, Chaudhary AK, Yadav R, Gaikwad K, Sevanthi AM, Datta S, Raje RS, Sharma TR and Singh NK (2017). A high-density intraspecific SNP linkage map of pigeonpea (Cajanas cajan L. Millsp.). PLoS ONE 12(6): e0179747.
21. Baboota RK, Khare P, Mangal P, Singh DP, Bhutani KK and Kondepudi KK, Kaur J and Bishnoi M (2018). Dihydrocapsiate supplementation prevented high fat diet induced adiposity, hepatic steatosis, glucose intolerance and gut morphological alterations in mice. Nutrition Research. 51, 40-46.
22. Bhanjana G, Dilbaghi N, Singhal NK, Kim K and Kumar S (2017). Zinc oxide nanopillars as an electrocatalyst for direct redox sensing of cadmium. Journal of Industrial and Engineering Chemistry 25, 192-200.
23. Deol PK, Khare P, Singh DP, Soman G, Bishnoi M, Kondepudi KK and Kaur IP (2017). Managing colonic inflammation associated gut derangements by systematically optimised and targeted ginger extract-Lactobacillus acidophilus loaded pharmacobiotic alginate beads. International Journal of Biological Macromolecules. 105(Pt 1):81-91.
24. Jain P, Shah K, Sharma N, Kaur R, Singh J, Vinson C and Rishi V (2017). A-ZIP53, a dominant negative reveals the molecular mechanism of heterodimerization between bZIP53, bZIP10 and bZIP25 involved in Arabidopsis seed maturation. Scientific Reports volume 7, 14343 doi:10.1038/ s41598-017-14167-5.
25. Kumari M, Rai AK, Devanna BN, Singh1 PK, Kapoor R, Rajashekara H, Prakash G, Sharma V, Sharma TR (2017). Co-transformation mediated stacking of blast resistance genes Pi54 and Pi54rh in rice provides broad spectrum resistance against Magnaporthe oryzae.Plant Cell Reports 36:1747–1755.
26. Kaila T, Chaduvla PK, Rawal HC, Saxena S, Tyagi A, Mithra SVA, Solanke AU, Kalia P, Sharma TR, Singh NK and Gaikwad K (2017). Chloroplast genome sequence of clusterbean (Cyamopsis tetragonoloba L.): genome structure and comparative analysis. Genes (Basel) 8(9) pii: E212. (doi: 10.3390/ genes8090212).
27. Kumar A, Garg M, Kaur N, Chunduri V, Sharma S, Misser S, Kumar A, Tsujimoto H, Dou QW and Gupta RK (2017). Rapid development and characterization of chromosome specific translocation line of Thinopyrumelongatum with improved dough strength. Frontiers in Plant Science 8:1593, 1-13. Doi:10.3389/ fpls.2017.01593.
28. Mahato AK, Sharma N, Singh A, Srivastav M, Jaiprakash, Singh SK, Singh AK, Sharma TR, Singh NK (2017). Leaf transcriptome sequencing for identifying genic-SSR markers and SNP Heterozygosity in crossbred mango variety 'Amrapali' (Mangifera indica L.). PLoS ONE 11(10): e0164325.
29. Ramakrishna Ch, Singh S, Sangala R, Padaria JC, Mohanty S, Sharma TR and Solanke AU (2017). The membrane tethered transcription factor EcbZIP17 from finger millet promotes plant growth and enhances tolerance to abiotic stresses. Scientific Reports, DOI:10:1138/541598-018-19766-4.
30. Sharma BB, Kalia P, Singh D and Sharma TR (2017). Introgression of black rot resistance from brassica carinata to Cauliflower (Brassica oleracea botrytis Group) through embryo rescue. Frontiers in Plant Science 8:1255.
31. Shivani, Awasthi P, Sharma V, Kaur N, Kaur N, Pandey P and Tiwari S (2017). Genome-wide analysis of transcription factors during somatic embryogenesis in banana (Musa spp.) cv. Grand Naine. PLoS ONE 12(8): e0182242. doi:10.1371/ journal.pone. 0182242.
32. Singh DP, Singh J, Boparai RK, Zhu J, Mantri S, Khare P, Khardori R, Kondepudi KK, Chopra K and Bishnoi M (2017). Isomalto-oligosaccharides, a prebiotic, functionally augment green tea effects against high fat diet-induced metabolic alterations via preventing gut dysbacteriosis in mice. Pharmacological Research 123, 103-113.
33. Singh DP, Singh S, Bijalwan V, Kumar V, Khare P, Baboota RK, Singh P, Boparai RK, Singh J, Kondepudi

KK, Chopra K and Bishnoi M (2017). Co-supplementation of isomalto-oligosaccharides potentiates metabolic health benefits of polyphenol-rich cranberry extract in high fat diet-fed mice via enhanced gut butyrate production. European Journal of Nutrition, Doi: 10.1007/s00394-017-1561-5.

34. Singh DP, Khare P, Bijalwan V, Baboota RK, Singh J, Kondepudi KK, Chopra K and Bishnoi M (2017). Coadministration of isomalto-oligosaccharides augments metabolic health benefits of cinnamaldehyde in high fat diet fed mice. Biofactors 43(6):821-835.
35. Sharma TR, Devanna BN, Kiran K, Singh PK, Arora K, Jain P, Tiwari IM, Dubey H, Saklani B, Kumari M, Singh J, Jaswal R, Kapoor R, Pawar DV, Sinha S, Bisht DS, Solanke AU and Mondal TK (2017). Status and prospects of next generation sequencing technologies in crop plants. Current Issues in Molecular Biology 27:1-36.
36. Singh A, Sharma AK, Singh NK and Sharma TR (2017). PpTFDB: A pigeonpea transcription factor database for exploring functional genomics in legumes. PLoS ONE 12(6): e0179736.
37. Tiwari IM, Jesuraj A, Kamboj R, Devanna BR, Botella JR & Sharma TR (2017). Host delivered RNAi, an efficient approach to increase rice resistance to sheath blight pathogen (Rhizoctonia solani). Scientific Reports 7: 7521.

Patents

1. A process of preparation of glycol-conjugates capped nanomaterial based novel biosensor for selective detection and ablation of food borne bacteria and uses thereof. (Application no. TEMP/E1/26661/2017- DEL).

HUMAN RESOURCE
(As on March 31st, 2018)

I. Research Faculty

S. No	Name	Designation	Date of Joining
	Regular Faculty		
1	Dr. T.R Sharma	Executive Director	09-01-2017
2	Dr. Vikas Rishi	Scientist F	01-03-2012
3	Dr. Joy K. Roy	Scientist E	09-08-2010
4	Dr. Ajay K. Pandey	Scientist E	14-11-2011
5	Dr. Siddharth Tiwari	Scientist D	28-07-2010
6	Sh. Shrikant S. Mantri	Scientist D	18-08-2010
7	Dr. (Mrs.) Monika Garg	Scientist D	30-11-2010
8	Dr. Kanthi Kiran	Scientist D	02-09-2011
9	Dr. Mahendra Bishnoi	Scientist D	16-12-2011
10	Dr. Koushik Mazumder	Scientist D	01-02-2012
11	Dr. Nitin K. Singhal	Scientist D	02-03-2012
	Other Faculty		
12	Dr. Praveen Awasthi	Project Scientist	05-09-2016
13	Dr. Hena Dhar	Inspire Faculty	25-04-2017
14	Dr. Gulshan Kumar	Inspire Faculty	11-05-2017
15	Dr. Hasthi Ram	Inspire Faculty	10-08-2017
16	Dr. Pramod Kaitheri Kandoth	Ramalingaswami Fellow	17-08-2017
17	Dr. Rupam Kumar Bhunia	Inspire Faculty	01-01-2018

II. Technical and Engineering Support

S. No	Name	Designation	Date of Joining
1	Ms. Aakriti Gupta	Senior Technical Assistant	22-02-2011
2	Sh. Jagdeep Singh	Senior Technical Assistant	01-03-2011
3	Sh. Jaspreet Singh	Assistant Engineer	19-03-2012
4	Sh. Sushant Vatsa	Assistant Engineer	02-04-2012
5	Dr. Mainpal Singh	Senior Technical Assistant	24-12-2012
6	Sh. Atul Kesarwani	Senior Technical Assistant	21-01-2013
7	Sh. Kamalendra	Senior Technical Assistant	18-03-2013
8	Sh. Pankaj Pandey	Senior Technical Assistant	29-04-2013

III. Administration

S. No	Name	Designation	Date of Joining
1	Sh. S. Krishnan	Manager (Administration)	0-03-2010
2	Sh. Suneet Verma	Manager (Finance)	15-09-2011
3	Sh. Hardip Singh	Administrative Officer	29-09-2014
4	Sh. Sabir Ali	Management Assistant (Admin.)	21-01-2011
5	Ms. Hema Pharswan	Management Assistant (Accounts)	01-04-2011
6	Sh. Ashish Arora	Management Assistant (Admin.)	15-06-2012
7	Sh. Arun Kumar	Management Assistant (Public Relation)	21-06-2012
8	Ms. Anukiran Bagga	Library Assistant	19-12-2012
	Contractual Staff		
9	Mr. Shyam Kumar	Maintenance & Facility Supervisor	07-12-2016

IV. HUMAN RESOURCE DEVELOPMENT

(i) National Post Doctoral Fellows:

S. No	Name	Area of Research	Date of Joining
1	Dr. Himanshu Sharma	Agri-Biotechnology	05-08-2016
2.	Dr. Aanchal Aggarwal	Food and Nutritional Biotechnology	06-04-2017
3.	Dr. Parul Goel	Agri-Biotechnology	25-04-2017
4.	Dr. Preeti Arya	Agri-Biotechnology	01-05-2017
5.	Dr. Akshay Nag	Agri-Biotechnology	01-06-2017

(ii) Ph.D Awarded

S. No	Name	Area of Research	Awarding University/Institute
Student awarded Ph.D degree:			
1	Sh. Jitendra Kumar	Development of virus induced gene silencing vector and its application in studying gene function in wheat (Triticum aestivum l.)	Barkatullah University,
2	Sh. Yogesh Gupta	Gene discovery for seedlessness in *Annona* species	Panjab University, Chandigarh, Punjab
3	Ms. Anuradha Singh	Expression analysis of starch biosynthesis pathway genes and their effects on starch quality.	Guru Jambheshwar University of Science & Technology, Hisar, Haryana
4	Sh. Rohit Kumar	Allelic variation in puroindolines in Indian wheat cultivars, their association with hardness and starch granule properties.	Panjab University, Chandigarh, Punjab
5	Sh. Ritesh Kumar Baboota	Studies on modulation of adipogenesis, obesity and related complications by capsaicin	UIET Panjab University, Chandigarh
6	Sh. Kaushal Kumar Bhati	Isolation and functional characterization of ABCC-MRP genes from wheat *(Triticum aestivum L.)* involved in phytic acid transport	Panjab University, Chandigarh, Punjab
7	Sh. Dhirendra Pratap Singh	Pharmaconutritional studies on prebiotic-antioxidant cobiotics in high fat diet- induced alterations	UIPS, Panjab University, Chandigarh

(iii) Research Scholars

S no.	Name of the Student	Position at Present	Date of Joining
1	Sh. Ashish Kumar Pathak	Senior Research Fellow	08-08-2012
2	Ms. Sipla Aggarwal	Senior Research Fellow	16-08-2012
3	Sh. Raja Jeet	Senior Research Fellow	12-03-2012
4	Ms. Stanzin Angmo	Senior Research Fellow	11-02-2013
5	Sh. Shashank Singh	Senior Research Fellow	22-02-2013
6	Sh. Vishnu Shukla	Senior Research Fellow	01-10-2015
7	Ms. Mandeep Kaur	Senior Research Fellow	20-06-2013
8	Ms. Shivani	Project Fellow	11-05-2013
9	Sh. Aman Kumar	Senior Research Fellow	05-08-2013
10	Ms. Navneet Kaur	Project Fellow	30-08-2013
11	Sh. Koushik Shah	Senior Research Fellow	05-09-2013
12	Sh. Dhirendra Pratap Singh	Senior Research Fellow	11-09-2013
13	Sh. Pragyanshu Khare	Research Associate-1	16-02-2018
14	Sh. Pankaj Kumar	Senior Research Fellow	25-02-2014
15	Sh. Usman Ali	Senior Research Fellow	13-03-2014
16	Ms. Flowerika	Senior Research Fellow	04-04-2014
17	Sh. Venkatesh Chunduri	Junior Research Fellow	25-09-2014
18	Ms. Saloni Sharma	Senior Research Fellow	30-09-2014
19	Ms. Ankita Mishra	DST- Inspire Fellow/SRF	13-02-2015
20	Ms. Shwetha Rathee	Junior Research Fellow	31-08-2015
21	Ms. Nishtha Sharma	Senior Research Fellow	01-09-2015
22	Sh. Paramdeep Singh	Junior Research Fellow	02-09-2015
23	Sh. Anshu Alok	Senior Research Fellow	01-01-2016
24	Ms. Shimayali Kaushal	Senior Research Fellow	21-01-2016
25	Sh. Vishal Singh	Senior Research Fellow	23-02-2016
26	Ms. Amandeep Kaur	Senior Research Fellow	08-03-2016
27	Ms. Neha Thakur	Senior Research Fellow	16-03-2016
28	Sh. Vijay Kumar	Senior Research Fellow	22-03-2016
29	Sh. Nitesh Priyadarshi	Junior Research Fellow	19-08-2016
30	Ms. Afsana Parveen	Junior Research Fellow	31-08-2016
31	Ms. Raminder Kaur	DST- Inspire Fellow/JRF	01-09-2016
32	Sh. Ashish Kumar	Junior Research Fellow	01-09-2016

33	Ms. Gazaldeep Kaur	Junior Research Fellow	07-11-2016
34	Ms. Shahirina Khan	Junior Research Fellow	21-11-2016
35	Sh. Anil Kumar	Junior Research Fellow	28-11-2016
36	Ms. Nandita Thakur	Senior Research Fellow	17-08-2017
37	Ms. Anita Kumari	Senior Research Fellow	12-02-2017
38	Sh. Akshay Singh	Senior Research Fellow	08-05-2017
39	Ms. Nitika Rana	Junior Research Fellow	11-05-2017
40	Ms. Ruchika Bhatia	Junior Research Fellow	11-05-2017
41	Sh. Pankaj Kumar Singh	Research Associate-1	18-05-2017
42	Ms. Shikha Sharma	Junior Research Fellow	05-06-2017
43	Ms. Poonam Sagar	Junior Research Fellow	21-06-2017
44	Ms. Ruchi Bansal	Junior Research Fellow	23-06-2017
45	Sh. Rajdeep Jaswal	Junior Research Fellow	18-07-2017
46	Ms. Abhilasha Indoria	Junior Research Fellow	19-07-2017
47	Ms. Vinita Sharma	Junior Research Fellow	24-07-2017
48	Ms. Shivani Sharma	Senior Research Fellow	01-08-2017
49	Sh. Anuj Shukla	Senior Research Fellow	21-08-2017
50	Ms. Kirti Devi	Junior Research Fellow	05-09-2017
51	Sh. Siddhanth Chaturvedi	Junior Research Fellow	11-09-2017
52	Ms. Swati Kanwar	Junior Research Fellow	13-09-2017
53	Ms. Sunaina Kaul	Junior Research Fellow	22-09-2017
54	Sh. Prateek Jain	Research Associate-1	31-01-2018
55	Ms. Aakansha Bhardwaj	Junior Research Fellow	06-02-2018
56	Ms. Ritika Gupta	Junior Research Fellow	20-02-2018
57	Ms. Aakriti Chauhan	Junior Research Fellow	27-02-2018

(iv) Project Assistants

S no.	Name	Designation	Date /of Joining
1.	Ms. Priya Arora	Project Assistant – II	15-06-2015
2.	Sh. Mohd. Saba Rahim	Project Assistant – II	07-09-2015
3.	Ms. Navjot Kaur	Lab/ Field Project Assistant	20-06-2016
4.	Sh. Pankaj Kumar	Project Field Assistant	03-05-2017
5.	Ms. Nidhi	Project Assistant – II	06-02-2018

(V) Trainees

S no.	Name	Designation	Date of Joining
1	Ms. Gagandeep kaur	Trainee	02-01-2017
2	Ms. Akshdeep	Trainee	02-01-2017
3	Ms. Gurpreet Sharma	Trainee	02-01-2017
4	Ms. Aysha Saifi	Trainee	02-01-2017
5	Ms. Anjali Dhall	Trainee	02-01-2017
6	Ms. Mandeep Kaur	Trainee	02-01-2017
7	Ms. Karuna Jain	Trainee	02-01-2017
8	Ms. Khyati Wadhawan	Trainee	02-01-2017
9	Ms. Neha	Trainee	02-01-2017
10	Ms. Nidhi	Trainee	02-01-2017
11	Ms. Ritul Sharma	Trainee	02-01-2017
12	Sh. Saahil Chandel	Trainee	02-01-2017
13	Ms. Shivani Sharma	Trainee	02-01-2017
14	Ms. Shweta	Trainee	02-01-2017
15	Ms. Tanya Sharma	Trainee	02-01-2017
16	Ms. Gurdev Kaur	Trainee	25-07-2017
17	Ms. Sweta Kumari	Trainee	25-01-2018
18	Ms. Manisha Kumari	Trainee	05-01-2018
19	Ms. Nishi Kumari	Trainee	25-01-2018
20	Ms. Mohini Pal Choudhoury	Trainee	10-01-2018
21	Ms. Srishti Singh	Trainee	05-01-2018
22	Ms. Manvinderpreet Kaur	Trainee	05-01-2018
23	Ms. Sneha Suman	Trainee	08-01-2018
24	Ms. Ojasvi Singh	Trainee	05-01-2018
25	Sh. Kartik Rohilla	Trainee	05-01-2018
26	Ms. Laxmi Kumari	Trainee	08-01-2018
27	Ms. Silky Gandhi	Trainee	12-01-2018
28	Ms. Alisha	Trainee	02-01-2018
29	Ms. Alisha Doda	Trainee	02-01-2018
30	Ms. Amritpreet Kaur	Trainee	02-01-2018
31	Ms. Gaganpreet Kaur	Trainee	02-01-2018
32	Ms. Harleen kaur	Trainee	02-01-2018
33	Ms. Moyna kalia	Trainee	02-01-2018
34	Ms. Simran Bhatia	Trainee	02-01-2018
35	Ms. Ravinderjit kaur	Trainee	02-01-2018
36	Ms. Kiran Sankhyan	Trainee	15-01-2018

PHOTO GALLERY

Celebration of World Environment Day: June 5th, 2017

Faculty, staff and students participating in tree plantation drive during World Environment Day.

A tree plantation drive was organized in the NABI campus during the World Environment Day. Different varieties of trees were planted to make campus look clean and green.

Inauguration of Research & Administrative Buildings: August 6th, 2017

Hon'ble Union Minister for Science and Technology, Earth Sciences and Environment, Forest & Climate Change Dr. Harsh Vardhan inaugurating the Research & Administrative Buildings of NABI.

Hon'ble Union Minister for Science and Technology, Earth Sciences and Environment, Forest & Climate Change Dr. Harsh Vardhan planting a tree at NABI premises.

Prof. K. Vijay Raghavan, the then Secretary, DBT planting a tree at NABI premises.

From the left: Dr. Vamsi Krishna, Scientist, DBT; Dr. T.R Sharma, Executive Director, NABI; Dr. Harsh Vardhan, Hon'ble Minister of S&T, Earth Sciences and Environment, Forest & Climate Change and Dr. R.S. Sangwan, the then CEO, CIAB releasing the vision document of NABI.

Dr. T.R Sharma, Executive Director, NABI presenting a memento and shawl to Dr. Harsh Vardhan, Hon'ble Minister for Science & Technology, Earth Sciences and Environment, Forest & Climate Change

Har Gobind Khorana Symposium: December 3rd – 5th, 2017

On the dais (from left): Dr. J.K Arora, Executive Director, PSCST, Punjab; Dr. Rajinder Ranu, Emeritus Professor, Colorado State University; Prof. Uttam Raj Bhandari, MIT, USA; Dr. T.R Sharma, Executive Director, NABI and Dr. Ashok Ganguli, the then Director, INST, Mohali.

Prof. Uttam Raj Bhandary, MIT, US lighting the lamp along with other organisers from NABI, INST and PSCST and IISER

Prof. Dieter Soll, Yale University, US and Prof. Uttam Raj Bhandari, MIT, US interacting with participants.

Dr. Marsha Rosner, Professor, University of Chicago, US delivering a talk entitled "Rewiring signalling pathways in cancer cells".

Prof. Mathew S. Sachs presenting a talk entitled "Gene regulation through the control of Ribosome movement".

From the left: Prof. J.P Khurana, Delhi University; Prof. C.M Gupta, Former Director, CSIR-CDRI, Lucknow; Prof. Dieter Soll, Yale University, US; Dr. Rajinder Ranu, Emeritus Professor, Colorado State University, US; Prof. Uttam Raj Bhandari, MIT, US; Dr. T.R Sharma, Executive Director, NABI; Prof. Aseem Z. Ansari, University of Wisconsin-Madison, US and Dr. Umesh Varshney, IISc, Bangalore posing for a photograph.

Republic Day Celebrations at NABI: January 26th, 2018

Dr. T.R Sharma, ED, NABI hoisted the National flag.

Dr. T.R Sharma, ED, NABI addressing staff and their family members.

Eighth Foundation Day: February 18th, 2018

On the dais (from left) – Dr. T.R Sharma, Executive Director, NABI; Prof. G. Padmanaban, Former Director, IISc, Bangalore and Dr. B.S Dhillon, VC, PAU, Ludhiana.

Prof. G. Padmanaban was the Chief Guest & lighting the lamp. Dr. B.S Dhillon was the Guest of Honour.

Prof. G. Padmanaban delivering a foundation day lecture on "Agri-Biotechnology for Food, Nutrition and Health Security".

Dr. B.S Dhillon addressing the gathering.

Dr. T.R Sharma presenting a memento and shawl to Prof. G. Padmanaban.

Dr. T.R Sharma presenting a memento and shawl to Dr. B.S Dhillon.

Visit of Dr. Renu Swarup, Secretary, DBT to NABI

Dr. Renu Swarup, Secretary-DBT, planting a tree at NABI campus.

Dr. Renu Swarup, Secretary - DBT visiting NABI lab building.

FINANCIALS

S S P J & Co.
(Formerly Sandeep Pawan Jain & Associates)
CHARTERED ACCOUNTANTS
(Peer Reviewed firm)
Firm Registration No. 018083N

AUDITORS' REPORT

TO THE MEMBERS OF NATIONAL AGRI-FOOD BIOTECHNOLOGY INSTITUTE

1. We have audited the attached Balance Sheet of NATIONAL AGRI-FOOD BIOTECHNOGY INSTITUTE as at March 31, 2018, the Income and Expenditure Account and Receipt & Payments Account for the year ended on that date annexed thereto. These financial statements are the responsibility of the Institution's Management. Our responsibility is to express an opinion on these financial statements based on our audit.

2. We conducted our audit in accordance with auditing standards generally accepted in India. Those standards require that we plan and perform the audit to obtain reasonable assurance about whether the financial statements are free of material misstatements. An audit includes, examining, on test basis evidence supporting the amount & disclosures in the financial statements. An audit also includes assessing the accounting principles used and significant estimates made as well as evaluating the overall financial statement presentation. We believe that our audit provides a reasonable basis for our opinion.

3. We have obtained all the information and explanation, which, to the best of our knowledge and belief, were necessary for the purpose of audit. In our opinion proper books of accounts as are necessary have been kept so far as it appears from our examination of those books.

4. In our opinion, and to the best of our information and according to the explanations given to us, **subject to our observation in paragraphs 5 below**, the financial statements give a true and fair view, in conformity with the accounting principles generally accepted in India:

   a) In the case of Balance Sheet, of the state of affairs of the Bank as at March 31, 2018 and
   b) In the case of Income & Expenditure Account, of the Income/ Loss of the Institution for the year ended on that date

5. *The Institution has accounted for Leave encashment expense on cash basis instead of making provision in respect of unavailed earned leave of the staff at the end of the year as per Accounting Standard-15 "Accounting for Retirement Benefits' issued by Institute of Chartered Accountants of India (Refer Para J of Accounting Policies).*

For S S P J & Co.
Chartered Accountants
Firm Registration No.018083N

(CA Suresh Kumar Goyal)
Partner
Membership No 099279

Place: Mohali
Dated: 14.06.2018

- **Delhi Office:** 105, Roots Tower, Plot No. 7, Laxmi Nagar District Centre, Laxmi Nagar, Delhi-110092
- Chandigarh Office: #1276, Basement, Sector 21B, Chandigarh-160022
- **Landline:** 0172-2541276; Handheld: +91 9417006611; Email: suresh@spjca.in ; Web: www.spjca.in
- **Office also at:** Bathinda, Faridabad, Noida, Mansa and Ambala

FORM OF FINANCIAL STATEMENTS (NON PROFIT ORGANIZATION)

NATIONAL AGRI-FOOD BIOTECHNOLOGY INSTITUTE

NABI Campus, Knowledge City, Sector 81, PO Manauli, SAS Nagar, Mohali.

BALANCE SHEET AS ON 31st MARCH 2018

(Amount in Rs.)

CORPUS/ CAPITAL FUND AND LIABILITIES	Schedule	Current Year	Previous Year
Corpus/Capital Fund	1	1,61,16,90,492	1,57,82,18,398
Reserves and Surplus	2	1	1
Earmarked / Endowment / Project Grants	3	3,30,93,323	1,20,23,802
Secured Loans and Borrowings	4	-	-
Unsecured Loans and Borrowings	5	-	-
Deferred Credit Liabilities	6	-	
Current Liabilities and Provisions	7	1,90,04,003	1,25,73,232
TOTAL		**1,66,37,87,819**	**1,60,28,15,433**
ASSETS			
Fixed Assets	8	1,44,80,34,379	17,38,20,814
Capital Work in Progress	8	88,03,700	1,30,21,69,210
Investments- from Earmarked/Endowment funds	9	-	-
Investments - Others	10	-	-
Current Assets, Loans & Advances etc.	11	20,69,49,740	12,68,25,409
TOTAL		**1,66,37,87,819**	**1,60,28,15,433**
Significant Accounting Policies	24		
Contingent liabilities and notes on accounts	25		

As per our separate report of even date attached

M/S S S P J & CO.
CHARTERED ACCOUNTANTS

(SUNEET VERMA)
MANAGER FINANCE

(DR. T. R. SHARMA)
EXECUTIVE DIRECTOR

(CA SURESH KUMAR GOYAL)
PARTNER
Membership No. 099279

Dated: 14/06/2018
Place: Mohali

सुनीत वर्मा / Suneet Verma
वित्त प्रबंधक / Manager (Finance)
राष्ट्रीय कृषि-खाद्य जैव प्रौद्योगिकी संस्थान
National Agri-Food Biotechnology Institute
भारत सरकार / Govt. of India
जैवप्रौद्योगिकी विभाग / Deptt. of Biotechnology
मोहाली, पंजाब / Mohali, Punjab-140306

डॉ० तिलक राज शर्मा
Dr. T. R. Sharma
कार्यकारी निदेशक/Executive Director
राष्ट्रीय कृषि-खाद्य जैव प्रौद्योगिकी संस्थान
National Agri-Food Biotechnology Institute
जैव प्रौद्योगिकी विभाग, भारत सरकार
Department of Biotechnology, Govt. of India
मोहाली (पंजाब), भारत
Mohali (Punjab), India

FORM OF FINANCIAL STATEMENTS (NON-PROFIT ORGANISTIONS)
NATIONAL AGRI-FOOD BIOTECHNOLOGY INSTITUTE
NABI Campus, Knowledge City, Sector 81, PO Manauli, SAS Nagar, Mohali.

INCOME AND EXPENDITURE ACCOUNT
FOR THE YEAR ENDED 31st MARCH 2018

(Amount in Rs.)

INCOME	Schedule	Current Year	Previous Year
Income from Sales/Services	12	-	-
Grants in aid /subsidies	13	11,00,00,000	9,00,00,000
Fees/subscriptions	14	-	-
Income from Investments (Income on investment from earmarked/endowment funds transferred to funds)	15	-	-
Income from Royalty, Publication etc.	16	-	-
Interest Earned	17	52,91,098	64,53,011
Other Income	18	69,59,529	9,18,064
Increase/decrease in stock of finished goods & work-in -progress	19		-
TOTAL(A)		**12,22,50,627**	**9,73,71,075**
EXPENDITURE			
Establishment Expenses	20	3,48,15,392	2,56,77,045
Other Administrative Expenses	21	4,62,87,034	4,55,45,167
Research & Development Expenditure (Incl. Grants, Subsidies etc)	22	3,99,38,812	2,93,18,110
Interest	23	-	-
Depreciation (net total at the year end-corresponding to schedule 8)		16,77,37,300	3,00,15,106
TOTAL(B)		**28,87,78,538**	**13,05,55,428**
Balance being surplus/ (deficit) carried to Capital Fund (A-B)		-16,65,27,911	-3,31,84,353
Significant Accounting Policies	24		
Contingent liabilities and notes on accounts	25		

As per our separate report of even date attached

M/S S S P J & CO.
CHARTERED ACCOUNTANTS

(SUNEET VERMA)
MANAGER FINANCE

Dated: 14/06/2018
Place: Mohali

सुनीत वर्मा / Suneet Verma
वित्त प्रबंधक / Manager (Finance)
राष्ट्रीय कृषि खाद्य जैव प्रौद्योगिकी संस्थान
National Agri-Food Biotechnology Institute
भारत सरकार / Govt. of India
जैवप्रौद्योगिकी विभाग / Deptt. of Biotechnology
मोहाली, पंजाब / Mohali, Punjab-140306

(DR. T. R. SHARMA)
EXECUTIVE DIRECTOR

डॉ० तिलक राज शर्मा
Dr. T. R. Sharma
कार्यकारी निदेशक/Executive Director
राष्ट्रीय कृषि-खाद्य जैव प्रौद्योगिकी संस्थान
National Agri-Food Biotechnology Institute
जैव प्रौद्योगिकी विभाग, भारत सरकार
Department of Biotechnology, Govt. of India
मोहाली (पंजाब), भारत
Mohali (Punjab), India

(CA SURESH KUMAR GOYAL)
PARTNER
Membership No. 099279

Form of Financial Statements for the Central Autonomous Bodies (Non- Profit Organizations and similar Institutions)

NATIONAL AGRI FOOD BIOTECHNOLOGY INSTITUTE

NABI Campus, Knowledge City, Sector 81, PO Manauli, SAS Nagar, Mohali.

RECEIPTS AND PAYMENTS ACCOUNT FOR THE PERIOD/YEAR ENDED ON 31.03.2018

(Amounts in Rs.)

RECEIPT	Current Year	Previous Year	PAYMENT	Current Year	Previous Year
(A) Opening Balance			**(A) Establishment Expenses**		
a) Cash in Hand			1. Manpower Salaries and Fellowships	3,17,66,256	2,34,20,206
b) Bank Balances			2. Expenses on Employees Retirement & terminal benefits	24,99,484	19,27,448
i) In current accounts					
ii) In deposit Accounts	6,05,99,512	7,27,42,633	**(B) Other Administrative Expenses**		
iii) In Savings Accounts	54,35,214	3,82,295	1. Cartage & Carriage inward	27,692	22,164
			2. Honorarium /Sitting Fee	1,87,896	1,87,729
(B) Grant-in-Aid			3. Electricity, power and Water charges	1,65,46,857	1,14,96,818
(a) Grant from DBT	31,00,00,000	69,00,00,000	4. Rent of Interim Facility and Guest House	-	1,48,74,718
			5. Vehicles Running & maintenance	1,44,325	88,190
			6. Postage, Telephone & communication charges	9,63,285	5,99,751
(C) Interest Incomes			7. Printing & stationery	7,08,375	4,56,474
(a) Interest Income	49,34,147	69,98,967	8. Travelling & conveyance expenses	21,45,349	21,04,816
			9. Outsourcing Manpower Exp	1,08,83,688	49,41,471
(D) Other Incomes			10. Legel & Professional charges	42,204	21,556
			11. Advt. & publicity	20,65,327	3,63,182
(a) Tender Fees	1,09,310	1,48,523	12. Repair & Maintenance Building	37,78,903	22,70,007
(b) Sample Analysis	-	23,766	13. Office & Admn Expenses	12,86,271	6,24,979
(c) Guest House Income	3,91,500	60,550	14. Guest House Expenditure	9,89,222	3,67,876
(d) RTI Fee	110	30	15. Shifting Expenses	5,31,355	48,85,184
(e) Project Income	13,59,770	4,90,285	16. Watch & Ward Expenses	29,83,277	28,88,012
(f) Training fee	3,45,424		17. Hostel Expenses	8,48,958	17,864
(g)Staff quarter Licence fee	2,87,963		18. Inauguration Day Expenses	4,51,602	
(h) Hostel Licence Fee	6,28,571				
(i) Application fee	1,73,540		**(C) Research & Development Expenditure**		
(j) Rental Income	4,32,803		1. Chemicals & Consumables	2,23,19,949	1,60,39,628
(k) Technology Transfer	1,50,000		2. Fellowships	52,17,440	55,62,431
(l) Misc. Income	4,89,178	50,131	3. Computer Software & Accessories	20,74,912	22,20,298
			4. Research Work Expenses	76,652	78,995
			5. Field Expenses	50,35,292	27,11,445
			6. Patent Filling Expenses	91,600	1,61,400
(E) Other Projects Receipt	5,84,90,130	3,26,75,139	7. Workshops and seminars	3,36,906	1,78,575
			8. Research Publication Expenses	6,94,196	3,02,792
(F) Other Receipt			9. Sequencing Expenses	17,96,487	15,09,529
(a) Security Deposit	14,70,880	1,35,132	10. Recognition & Membership Fee	10,10,200	
(b) Earnest Money Deposit	11,05,759		11. Campus Plantation Expenses	5,41,930	
(c) Advance for advance/Securities		7,91,575			
(d) Creditors payable		44,95,972	**(D) Non-Recurring Expenditures**		
(e)GST Payable	50,942		1. Development of Main Campus	11,21,52,471	59,58,38,280
			2. Scientific Equip & Research Acce	4,61,85,245	66,57,325
			3. Computers & Books	14,92,128	94,000
			4. Furniture & Fixture	2,14,48,005	31,91,524
			5. Office Equipment	4,78,814	1,12,200
			6. Library Books & Periodicals	3,45,483	5,671
			(E) Other Payments		
			(a) External Project Expenses	3,62,65,262	3,46,51,321
			(b) TDS Refund receivable	9,200	40,340
			(c) Earnest Money Deposit Paid		74,491
			(d) Har Gobind Khorana Memorial workshop	1,40,000	
			(e) Creditors payable	8,86,395	
			(F) Loan & Advances		
			(a) Advance to NIPER		4,250
			(b) Advance to Employees	14,198	5,16,864
			(c) Secured Advance to M/s Pyramid Builders	9,20,356	
			(d) Advance to NICSI	84,39,258	14,50,468
			(e) Advance to CDAC	72,12,000	
			(f) Security for Gas Connection to M/s Chahal Gas Agency	26,250	
			(g) Deposit with M/s Rites Ltd.		
			(G) Closing Balance		
			a) Cash in Hand		
			b) Bank Balances		
			i) In Deposit Accounts	9,22,29,990	6,05,99,512
			ii) In Savings Accounts	1,63,808	54,35,214
Grand Total	**44,64,54,753**	**80,89,94,998**	**Grand Total**	**44,64,54,753**	**80,89,94,998**

In terms of separate report of even date attached

M/S S S P J & CO.
CHARTERED ACCOUNTANTS

(SUNEET VERMA)
MANAGER FINANCE

(DR. T.R. SHARMA)
EXECUTIVE DIRECTOR

(CA SURESH KUMAR GOYAL)
PARTNER
Membership No. 092278

Dated: 14/06/2018
Place: Mohali

सुनीत वर्मा / Suneet Verma
वित्त प्रबंधक / Manager (Finance)
राष्ट्रीय कृषि खाद्य जैव प्रौद्योगिकी संस्थान
National Agri-Food Biotechnology Institute
भारत सरकार / Govt. of India
जैवप्रौद्योगिकी विभाग / Deptt. of Biotechnology
मोहाली, पंजाब / Mohali, Punjab-140306

डॉ० तिलक राज शर्मा
Dr. T. R. Sharma
कार्यकारी निदेशक/Executive Director
राष्ट्रीय कृषि-खाद्य जैव प्रौद्योगिकी संस्थान
National Agri-Food Biotechnology Institute
जैव प्रौद्योगिकी विभाग, भारत सरकार
Department of Biotechnology, Govt. of India
मोहाली (पंजाब), भारत
Mohali (Punjab), India

FORM OF FINANCIAL STATEMENTS (NON-PROFIT ORGANISTIONS)

NATIONAL AGRI-FOOD BIOTECHNOLOGY INSTITUTE

NABI Campus, Knowledge City, Sector 81, PO Manauli, SAS Nagar, Mohali.

SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31.03.2018

SCHEDULE-1
CORPUS/CAPITAL FUND

(Amount In Rs.)

Particulars	Current Year	Previous Year
Balance as at the beginning of the year	1,57,82,18,398	1,01,14,02,751
Add : Contributions towards corpus/capital fund	20,00,00,000	60,00,00,000
Add : Fixed Assets Created out of Project Grants	5	-
Less/(Deduct) : Expenditure over Income transferred from the income & expenditure A/c	-16,65,27,911	-3,31,84,353
BALANCE AS AT THE YEAR -END	**1,61,16,90,492**	**1,57,82,18,398**

SCHEDULE-2
RESERVES AND SURPLUS

Particulars	Current Year	Previous Year
1.Capital Reserves: Land provided by Punjab Govt.	1	1
2.Revaluation Reserve		-
3.Special Reserve		-
4.General Reserve		
TOTAL	**1**	**1**

M/S S S P J & CO.
CHARTERED ACCOUNTANTS

(SUNEET VERMA)
MANAGER FINANCE

(DR. T. R. SHARMA)
EXECUTIVE DIRECTOR

(CA SURESH KUMAR GOYAL)
PARTNER
Membership No. 099279

सुनीत वर्मा / Suneet Verma
प्रबंधक / Manager (Finance)
राष्ट्रीय कृषि खाद्य जैव प्रौद्योगिकी संस्थान
National Agri-Food Biotechnology Institute
भारत सरकार / Govt. of India
जैवप्रौद्योगिकी विभाग / Deptt. of Biotechnology
मोहाली, पंजाब / Mohali, Punjab-140306

डॉ० तिलक राज शर्मा
Dr. T. R. Sharma
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राष्ट्रीय कृषि-खाद्य जैव प्रौद्योगिकी संस्थान
National Agri-Food Biotechnology Institute
Department of Biotechnology, Govt. of India
मोहाली (पंजाब), भारत
Mohali (Punjab), India

Dated: 14/06/2018
Place: Mohali

Schedule-3- EARMARKED/ENDOWMENT/PROJECT GRANTS

Sr. No.	Project Name	Additions				Utilization /expenditure							REFUND	NET BALANCE AT THE YEAR END
		a) Opening balance of the Fund	b) Additions during the Year	c) Accrued Interest / Interest Recd. on Investment	TOTAL (a+b+c)	i) Capital Expenditure	ii) Revenue Expenditure					TOTAL EXP		
							Fellowships	Chemical & Consumable	Contingency Exp/Travel etc	Overhead Exp	TOTAL			
1	Development and Transfer of Technology from Queensland University of Technology, Australia to India for Bio-fortification and Disease Resistane in Banana (GAP 02)	94,95,654	27,30,400	2,44,855.00	1,24,70,709	18,75,478	22,20,878	9,55,292	38,766		32,14,936	50,90,414		73,80,295
2	Nutrigenomic approach to understand the role of TRP channel activating food components in adipose Tissue inflammation (GAP 08)	-24,413	-	-	-24,413						-	-		-24,413
3	Identification, cloning and Functional characterization of MIOX from Wheet (GAP 13)	1,66,222			1,66,222			1,10,961			1,10,961	1,10,961	55,261	-
4	Developing glycoconjugates capped multifunctional gold nanorod based nanobiosensor for detection of multiple food borne bacteria (GAP 14)	4,73,485	2,46,515	12,928	7,32,928		2,29,406	2,99,211	25,567		5,54,184	5,54,184		1,78,744
5	A genomics-assisted synthetic hexaploid wheat gene isolation and pre-breeding platform for improved heat tolerance and sustainable production (GAP 15)	11,57,927	10,99,459	24,827	22,82,213		7,06,032	8,96,518	2,41,181		18,43,731	18,43,731		4,38,482
6	Metagenomic and Functional Characterization of Soy-based Fermented Foods of Northeastern Region (GAP 16)	6,94,660	2,48,000	18,436	9,61,096		2,66,935	3,13,159	22,177		6,02,271	6,02,271		3,58,825
7	Genome and Transcriptome Sequencing of Aromatic rices from North Eastern Region (GAP 17)		93,06,000	1,96,357	95,02,357	9,98,000	5,92,233	39,86,198	30,952	1,00,000	47,09,383	57,07,383		37,94,974
8	Utilizing genome editing tools for nutritional improvement In wheat (GAP 18)		17,79,200	28,164	18,07,364		4,05,548	8,65,400	14,034		12,84,982	12,84,982		5,22,382
9	Connections: A Comprehesive biological relationships resources and tools for automated literature mining (GAP 19)		7,24,000	18,857	7,42,857				8,443		8,443	8,443		7,34,414
10	Functional Characterization and Implications of Plant Inositol Pyrophosphate Kinase (GAP 20)		14,93,200	16,594	15,09,794		2,47,122	8,11,392	37,243	50,000	11,45,757	11,45,757		3,64,037
11	Enhanced rice millilng and maximised valorisatioin of rice milling by product (GAP 21)		30,30,000	26,347	30,56,347		2,04,066	19,17,418	13,253	20,000	21,54,737	21,54,737		9,01,610
12	Pharmacological mimicking of cold via cold thermo-receptors (GAP 22)		23,67,220	32,520	23,99,740		79,500	5,24,332	21,484	1,79,020	8,04,336	8,04,336		15,95,404
13	Setting up of Secondary Agriculture/ Food Processing Entreprenurial Network in Punjba-Phase-I (GAP 23)		1,18,49,000	17,280	1,18,66,280						-	-		1,18,66,280
14	CRISPR/Cas mediated genome editing of genes for high pro-vitamin A accumulation and its stability in banana (GAP 24)		25,28,960	-	25,28,960					1,00,000	1,00,000	1,00,000		24,28,960
15	Department of Biotechnology (DBT) JRF/SRF fellowships	-4,62,214	26,03,180		21,40,966		15,67,346	2,60,391			18,27,737	18,27,737	10,803	3,02,426
16	Council of Scientific & Industrial Research (CSIR) JRF/SRF Fellowships	-7,79,100	9,50,021		1,70,921		61,600	29,973			91,573	91,573		79,348
17	Indian Council of Medical Research (ICMR) JRF/SRF Fellowships	24,262	23,18,451		23,42,713		21,68,814	1,28,246			22,97,060	22,97,060		45,653
18	UGC Fellowhsip	-1,27,080			-1,27,080						-	-		-1,27,080
19	JC Bose Fellowship	-4,36,036	10,95,222		6,59,186		3,00,000	9,39,437	10,014	1,20,000	13,69,451	13,69,451		-7,10,265
20	DST INSPIRE Fellowship	1,27,702	7,30,599		8,58,301		6,05,236		24,385		6,29,621	6,29,621		2,28,680
21	National Post Doc Fellowship	4,52,733	49,43,738		53,96,471		32,00,704	6,20,238		6,00,000	44,20,942	44,20,942	6,39,211	3,36,318
22	Ramalingaswamy Fellowship		21,10,000		21,10,000		6,55,794		7,60,236	50,750	14,66,780	14,66,780		6,43,220
23	DST INSPIRE Faculty Fellowship		57,00,000		57,00,000	2,87,372	23,47,613	10,72,694	97,292	1,40,000	36,57,599	39,44,971		17,55,029
24	Indo Australia EMCR Fellowship Grant	12,60,000			12,60,000		10,76,024		1,83,976		12,60,000	12,60,000		-
	Total	1,20,23,802	5,78,58,153	6,36,965	7,05,13,932	31,60,850	1,69,34,851	3,67,70,069	19,29,003	13,59,770	3,35,54,484	3,67,15,334	7,05,275	3,30,93,323

Dated: 14/06/2018
Place: Mohali

(MANEET VERMA)
Manager, Finance

For National Agri-Food Biotechnology Institute

Dr. T. R. Sharma
Executive Director

Page 5 of 19

M/S B J & CO.
Chartered Accountants
(CA SURENDRA KUMAR GOYAL)
Partner

SCHEDULE-4
SECURED LOANS & BORROWINGS

(Amount in Rs.)

Particulars	Current Year	Previous Year
1.Central Government		-
2.State Government(specify)		-
3.Financial Institutions		
4.Banks:		
5.Other Institutions & agencies		-
6.Debentures & bonds		-
7.Others(specify)		-
TOTAL		-

SCHEDULE-5
UNSECURED LOANS & BORROWINGS

(Amount in Rs.)

Particulars	Current Year	Previous Year
1.Central Government		-
2.State Government(specify)		-
3.Financial Institutions		
4.Banks:		
5.Other Institutions & agencies		-
6.Debentures & bonds		-
7.Others(specify)		-
TOTAL		-

SCHEDULE-6
DEFERRED CREDIT LIABILITIES

(Amount in Rs.)

Particulars	Current Year	Previous Year
1. Acceptances secured by hypothecation of capital equipment		-
2. Others		-
TOTAL	-	-

M/S S S P J & CO.
CHARTERED ACCOUNTANTS

(SUNEET VERMA)
MANAGER FINANCE

(DR. T. R. SHARMA)
EXECUTIVE DIRECTOR

(CA SURESH KUMAR GOYAL)
PARTNER
Membership No. 099279

Dated: 14/06/2018
Place: Mohali

सुनीत वर्मा / Suneet Verma
Manager (Finance)
National Agri-Food Biotechnology Institute
भारत सरकार / Govt. of India
जैवप्रौद्योगिकी विभाग / Deptt. of Biotechnology
मोहाली, पंजाब / Mohali, Punjab-140306

डॉ॰ तिलक राज शर्मा
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Department of Biotechnology, Govt. of India
मोहाली (पंजाब), भारत
Mohali (Punjab), India

SCHEDULE-7

CURRENT LIABILITIES & PROVISIONS

(Amount in Rs.)

Particulars	Current Year	Previous Year
A)CURRENT LIABILITIES		
1. Sundry Creditors		
a) For goods/Equipment	54,64,913	63,51,308
b) For Securities	19,22,926	4,52,046
c) Earnest Money Deposit	17,59,649	6,53,890
2. Interest accrued but not due on:		
a) Secured Loans/Borrowings		
b) Unsecured Loans/Borrowings		
3. Statutory Liabilities		
a) Overdue		
4. Other Current Liabilities		
a) Manpower (Salary) Payable	22,95,172	18,31,630
b) Other Expenses Payable	52,88,328	17,09,503
c) TDS Payable	2,98,875	1,79,704
d) Fellowship Payable	19,23,198	13,95,151
e) GST Payable	50,942	
TOTAL(A)	**1,90,04,003**	**1,25,73,232**
B) PROVISIONS		
1. Gratuity		
2. Superannuation/Pension		-
3. Leave Encashment		-
TOTAL(B)		-
TOTAL(A+B)	**1,90,04,003**	**1,25,73,232**

M/S S S P J & CO.
CHARTERED ACCOUNTANTS

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MANAGER FINANCE

(DR. T. R. SHARMA)
EXECUTIVE DIRECTOR

(CA SURESH KUMAR GOYAL)
PARTNER
Membership No. 099279

सुनीत वर्मा / Suneet Verma
वित्त प्रबंधक / Manager (Finance)
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जैव प्रौद्योगिकी विभाग, भारत सरकार
Department of Biotechnology, Govt. of India
मोहाली (पंजाब), भारत
Mohali (Punjab), India

Dated: 14/06/2018
Place: Mohali

NATIONAL AGRI-FOOD BIOTECHNOLOGY INSTITUTE

NABI Campus, Knowledge City, Sector 81, PO Manauli, SAS Nagar, Mohali

SCHEDULE-8 FIXED ASSETS

Sl.No.	Description		GROSS BLOCK					DEPRECIATION			NET BLOCK	
Sl.No.		Depreciation Rate	Cost/Valuation as at beginning of the year	Additions during the year	Additions during the year	Deduction during the year	Cost/Valuation at the year end	As at the beginning of the year	Depreciation during the year	Total at the year end	As at the Current Year End	As at the Previous Year End
			1st April 2017	UPTO 30.09.17	AFTER 30.09.17	2017-18	31st March 2018	1st April 2017	2017-18	31st March 2018	31st March 2018	31st March 2017
A	FIXED ASSETS											
I	LAND		1				1				1	1
II	BUILDINGS											
	a)On Freehold Land	10.00%	83,57,674	1,37,93,66,991	2,75,04,868	-	1,41,52,29,533	34,22,551	13,98,05,457	14,32,28,008	1,27,20,01,525	49,35,123
	b)On Leasehold Land	10.00%	-	-	-		-	-	-	-	-	-
	c)Ownership Premises	10.00%	-	-	-	-	-	-	-	-	-	-
	d)Other Superstructures	10.00%	-		-	-	-	-	-	-	-	-
			-				-					
III	PLANT, MACHINERY & EQUIPMENT		-				-					
	EQUIPMENTS	15.00%	36,67,40,976	10,66,317	1,01,04,906	-	37,79,12,199	20,58,04,014	2,50,58,360	23,08,62,374	14,70,49,825	16,09,36,962
IV	VEHICLES	15.00%	6,62,497			-	6,62,497	4,33,180	34,398	4,67,578	1,94,919	2,29,317
V	FURNITURE & FIXTURES	10.00%	68,17,699	14,43,446	2,01,47,907	-	2,84,09,052.25	18,39,296.00	16,49,581	34,88,877.00	2,49,20,175	49,78,403
VI	COMPUTER/PERIPHERALS	40.00%	2,10,73,365	12,47,221	2,44,907	-	2,25,65,493	2,06,38,507	7,21,814	2,13,60,321	12,05,172	4,34,858
VII	LIBRARY BOOKS	60.00%	4,86,232		3,45,483	-	8,31,715	4,83,964	- 2,08,651	6,92,615	1,39,100	2,268
VIII	OFFICE EQUIPMENT	10.00%	40,08,311	94,214	3,84,600	-	44,87,125	17,04,439	2,59,039	19,63,478	25,23,647	23,03,872
	TOTAL OF CURRENT YEAR (A)		42,92,20,120	1,38,32,18,189	5,87,32,671	-	1,85,00,97,615	23,43,25,951	16,77,37,300	40,20,63,251	1,44,80,34,364	17,38,20,804
B	Fixed Asset Created from Projects Grants:											
	EQUIPMENTS		6.00		5		11				11	6
	COMPUTER/PERIPHERALS		4.00				4				4	4
	TOTAL OF FIXED ASSETS PROCURRED		10	-	5		15	-	-	-	15	10
	TOTAL (A+B)		42,92,20,130	1,38,32,18,189	5,87,32,676	-	1,85,00,97,630	23,43,25,951	16,77,37,300	40,20,63,251	1,44,80,34,379	17,38,20,814
XI	PREVIOUS YEAR											
	a) Expenditure on Assets/Fixed Assets		-	-	-	-	-	-	-	-	-	-
	b) Expenditure on Plan Activities		-	-	-	-	-	-	-	-	-	-
	TOTAL OF PREVIOUS YEAR		-		-	-	-	-	-	-	-	-
XII	CAPITAL WORK-IN-PROGRESS											
	a) Main Campus At Sec 81		1,30,21,69,210	25,000	87,78,700	1,30,21,69,210	88,03,700	-	-	-	88,03,700	1,30,21,69,210
	d) Equipment		-	-	-	-	-	-	-	-	-	-
							-	-	-	-	-	-
	TOTAL OF CURRENT YEAR (CWIP) (C)		1,30,21,69,210	25,000	87,78,700	1,30,21,69,210	88,03,700	-	-	-	88,03,700	1,30,21,69,210
	GRAND TOTAL (A+B+C)		1,73,13,89,340	1,38,32,43,189	6,75,11,376	1,30,21,69,210	1,85,89,01,330	23,43,25,951	16,77,37,300	40,20,63,251	1,45,68,38,079	1,47,59,90,024

For National Agri-Food Biotechnology Institute

सुनीत वर्मा / Suneet Verma
वित्त प्रबंधक / Manager (Finance)
राष्ट्रीय कृषि खाद्य जैव प्रौद्योगिकी संस्थान
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जैवप्रौद्योगिकी विभाग / Deptt. of Biotechnology
मोहाली, पंजाब / Mohali, Punjab-140306

(SUNEET VERMA)
Manager Finance

डॉ० तिलक राज शर्मा
Dr. T. R. Sharma
कार्यकारी निदेशक/Executive Director
राष्ट्रीय कृषि-खाद्य जैव प्रौद्योगिकी संस्थान
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Department of Biotechnology, Govt. of India
मोहाली (पंजाब), भारत
Mohali (Punjab), India

(DR. T. R. SHARMA)
Executive Director

M/S S S P J & CO.
Chartered Accountants

(CA SURESH KUMAR GOYAL)
Partner

Dated: 14/06/2018
Place: Mohali

SCHEDULE-9

INVESTMENTS FROM EARMARKED/ENDOWMENT FUNDS

(Amount in Rs.)

Particulars	Current Year	Previous Year
1. In Government Securities		-
2. Other approved securities		-
3. Shares		-
4. Debentures & Bonds		-
5. Subsidiaries & Joint Ventures		-
6. Others Fixed Deposits (to be specified)		-
TOTAL	-	-

SCHEDULE-10

OTHER INVESTMENTS

(Amount in Rs.)

Particulars	Current Year	Previous Year
1. In Government Securities		-
2. Other approved securities		-
3. Shares		-
4. Debentures & Bonds		-
5. Subsidiaries & Joint Ventures		-
6. Others(to be specified)		-
TOTAL		-

M/S S S P J & CO.
CHARTERED ACCOUNTANTS

(SUNEET VERMA)
MANAGER FINANCE

(DR. T. R. SHARMA)
EXECUTIVE DIRECTOR

(CA SURESH KUMAR GOYAL)
PARTNER
Membership No. 099279

Dated: 14/06/2018
Place: Mohali

सुनीत वर्मा / Suneet Verma
वित्त प्रबंधक / Manager (Finance)
राष्ट्रीय कृषि खाद्य जैव प्रौद्योगिकी संस्थान
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मोहाली, पंजाब / Mohali, Punjab-140306

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Department of Biotechnology, Govt. of India
मोहाली (पंजाब), भारत
Mohali (Punjab), India

SCHEDULE-11

CURRENT ASSETS, LOANS & ADVANCES

(Amount in Rs.)

Particulars	Current Year	Previous Year
A) CURRENT ASSETS		
1. Inventories		
a) Stores & Spares		
b) Loose Tools		
c) Stock-in-trade		
2. Sundry Debtors		
3. Cash balances in hand		
4. Bank balances:		
a) With Scheduled Banks:		
-On Current accounts		
-On Fixed Deposit accounts	9,22,29,990	6,05,99,512
-On Savings accounts		
(i) State Bank of India A/c	1,63,808	54,35,214
TOTAL(A)	**9,23,93,798**	**6,60,34,726**
B) LOANS, ADVANCES AND OTHER ASSETS		
1. Loans		
2. Advances and other amounts recoverable		
a) On Capital Account		
b) Advances		
(i) Deposite with M/s RITES Ltd	9,36,17,560	5,67,13,528
(ii) Deposit with NICSI	98,89,726	14,50,468
(iii) Deposit with CDAC	72,12,000	
(iv) Secured Advance to M/s Pyramid Builders	9,20,356	
c) Recoupable form Govt. Agencies		
(i) NIPER	6,222	6,222
(ii) DBT (Brain Storming Project)	-	2,21,904
(iii) Hargobind Khurana Memorial Symposium	1,40,000	
(iv) INST	2,58,958	
(v) CIAB	36,847	
d) Advance to Employees	27,698	13,500
e) Others(specify)		
(i) Security for Gas Connection to M/s Chahal Gas	26,250	-
(ii) Deposit with PSPCL	44,581	44,581
(iii) TDS Receivable	60,963	51,763
(v) PSEB Elelct Security for Main Campus	11,12,090	11,12,090
(vi) Advance to Fellows	2,14,305	5,45,192
3.Income accrued:		
a) on investments from earmarked/endowment funds		
b) Interest On Saving A/c and Fixed Deposits	9,88,386	6,31,435
c) on loans & advances		
d) others(Accrued Interest from GAPs)		
4. Claims Receivable		
TOTAL(B)	**11,45,55,942**	**6,07,90,683**
TOTAL(A+B)	**20,69,49,740**	**12,68,25,409**

M/S S S P J & CO.
CHARTERED ACCOUNTANTS

(SUNEET VERMA)
MANAGER FINANCE

(DR. T. R. SHARMA)
EXECUTIVE DIRECTOR

(CA SURESH KUMAR GOYAL)
PARTNER
Membership No. 099279

Dated: 14/06/2018
Place: Mohali

सुनीत वर्मा / Suneet Verma
प्रबंधक / Manager (Finance)
कृषि खाद्य जैव प्रौद्योगिकी संस्थान
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जैवप्रौद्योगिकी विभाग / Deptt. of Biotechnology
मोहाली, पंजाब / Mohali, Punjab-140306

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Department of Biotechnology, Govt. of India
Mohali (Punjab), India

SCHEDULE-12
INCOME FROM SALES/SERVICES

(Amount in Rs.)

Particulars	Current Year	Previous Year
1. Income from sales		
2. Income from services		-
TOTAL		-

SCHEDULE-13
GRANTS/SUBSIDIES

(Amount in Rs.)

Particulars	Current Year	Previous Year
(Irrevocable Grants & subsidies received)		
1. Central Government	11,00,00,000	9,00,00,000
2. State Government		-
3. Government Agencies		-
4. Institutional /welfare bodies		-
5. International Organisations		-
6. Others (to be specified)		-
TOTAL	11,00,00,000	9,00,00,000

SCHEDULE-14
FEES/SUBSCRIPTIONS

(Amount in Rs.)

Particulars	Current Year	Previous Year
1. Entrance Fees		-
2. Annual Fees / subscriptions		-
3. Seminar/program fees		-
4. Consultancy fees		-
5. Others		-
TOTAL		-

SCHEDULE-15
INCOME FROM INVESTMENTS

(Amount in Rs.)

Particulars	Current Year	Previous Year
1. Interest		-
a)On Govt. securities		
b)Other Bonds/Debentures		
2. Dividends:		-
a)On shares		
b)On Mutual Fund securities		
3. Rents		-
4. Others (specify)		-
TOTAL		-

M/S S S P J & CO.
CHARTERED ACCOUNTANTS

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MANAGER FINANCE

(DR. T. R. SHARMA)
EXECUTIVE DIRECTOR

(CA SURESH KUMAR GOYAL)
PARTNER
Membership No. 099279

Dated: 14/06/2018
Place: Mohali

सुनीत वर्मा / Suneet Verma
वित्त प्रबंधक / Manager (Finance)
राष्ट्रीय कृषि खाद्य जैव प्रौद्योगिकी संस्थान
National Agri-Food Biotechnology Institute
भारत सरकार / Govt. of India
जैवप्रौद्योगिकी विभाग / Deptt. of Biotechnology
मोहाली, पंजाब / Mohali, Punjab-140306

डॉ० तिलक राज शर्मा
Dr. T. R. Sharma
कार्यकारी निदेशक/Executive Director
राष्ट्रीय कृषि-खाद्य जैव प्रौद्योगिकी संस्थान
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Department of Biotechnology, Govt. of India
मोहाली (पंजाब), भारत
Mohali (Punjab), India

SCHEDULE-16

INCOME FROM ROYALTY/PUBLICATIONS, ETC.

(Amount in Rs.)

Particulars	Current Year	Previous Year
1. Income from Royalty		-
2. Income from Publications		-
3. Others(specify)		-
TOTAL		-

SCHEDULE-17

INTEREST EARNED

(Amount in Rs.)

Particulars	Current Year	Previous Year
1)On Term Deposits		
a)With Scheduled Banks:		
i) Actual Received	41,12,138	57,93,006
ii) Accrued as on 31.03.2018	9,88,386	6,31,435
b)With Non-Scheduled Banks:		
2)On Savings Accounts:		
a)With Scheduled Banks:	1,90,574	27,733
b)With Non-Scheduled Banks:		
3)On Loans		
a)Employees/staff		
b) Interest on Mobilisation Advnace/Escrow Acc		
4)Interest on Debtors & other Receivables		
a) Interest on refund of Income Tax		837
TOTAL	**52,91,098**	**64,53,011**

M/S S S P J & CO.
CHARTERED ACCOUNTANTS

(SUNEET VERMA)
MANAGER FINANCE

(DR. T. R. SHARMA)
EXECUTIVE DIRECTOR

(CA SURESH KUMAR GOYAL)
PARTNER
Membership No. 099279

Dated: 14/06/2018
Place: Mohali

सुनीत वर्मा / Suneet Verma
वित्त प्रबंधक / Manager (Finance)
राष्ट्रीय कृषि खाद्य जैव प्रौद्योगिकी संस्थान
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Mohali (Punjab), India

SCHEDULE-18
OTHER INCOME

(Amount in Rs.)

Particulars	Current Year	Previous Year
1. Profit on sale/disposal of assets		
a) Owned Assets		
b) Assets acquired out of grants,or received free of		
2. Export Incentives realized		
3. Overhead Income from Extenal Projects	13,59,770	4,90,285
4. Miscellaneous Income		
a) Tender Fees	1,09,310	1,48,523
b) Sample Analysis	-	23,766
c) Guest House (Income)	3,91,500	60,550
d) RTI Fee	110	30
e) Training Fee	3,45,424	
f) Staff Quarters Licence Fee	2,94,303	
g) Hostel fee	6,48,739	
h) Application fee	1,73,540	
i) Rental income	6,91,761	
j) Technology transfer	1,50,000	
k) LD Charges	23,05,894	1,44,779
l) Misc Income	4,89,178	50,131
TOTAL	**69,59,529**	**9,18,064**

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Mohali (Punjab), India

SCHEDULE-19

INCREASE/(DECREASE) IN STOCK OF FINISHED GOODS & WORK IN PROGRESS

(Amount in Rs.)

Particulars	Current Year	Previous Year
1. Closing Stock	-	-
a) Finished Goods	-	-
b) Work-in-progress	-	-
2) Less: Opening stock	-	-
a) Finished Goods	-	-
b) Work-in-progress	-	-
NET INCREASE/(DECREASE)(1-2)	-	-

SCHEDULE-20

ESTABLISHMENT EXPENSES

(Amount in Rs.)

Particulars	Current Year	Previous Year
1. Manpower Salaries, Wages and Allowances	3,23,15,908	2,37,33,629
2. Expenses on Employees Retirement & terminal benefits	24,99,484	19,43,416
TOTAL	**3,48,15,392**	**2,56,77,045**

SCHEDULE-21

OTHER ADMINISTRATIVE EXPENSES

(Amount in Rs.)

Particulars	Current Year	Previous Year
1. Cartage & Carriage inward	27,692	22,164
2. Honorarium /Sitting Fee	1,87,896	1,87,729
3. Electricity, power and Water charges	1,79,00,379	1,07,82,677
4. Rent of Interim Facility and Guest House		1,46,67,871
5. Vehicles Running & maintenance	1,44,325	88,190
6. Postage,Telephone & communication charges	9,57,171	5,92,118
7. Printing & stationery	7,08,375	4,56,474
8. Travelling & conveyance expenses	20,58,731	21,63,004
9. Outsourcing Manpower Exp	1,10,70,671	48,52,251
10. Legel & Professional charges	53,041	21,593
11. Advt. & publicity and display Expenses	21,47,050	3,55,534
12. Repair, Operation & Maintenance of Building	38,10,477	22,64,684
13. Office & Admn Expenses	12,87,360	6,19,090
14. Guest House Expenditure	10,49,818	3,66,400
15. Shifting Expenses	5,24,551	48,91,988
16. Watch & Ward Expenses	30,14,922	31,95,536
17. Hostel Expenses	8,92,973	17,864
18. Inauguration Day Expenses	4,51,602	
TOTAL	**4,62,87,034**	**4,55,45,167**

M/S S S P J & CO.
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(SUNEET VERMA)
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(DR. T. R. SHARMA)
EXECUTIVE DIRECTOR

(CA SURESH KUMAR GOYAL)
PARTNER
Membership No. 099279

Dated: 14/06/2018
Place: Mohali

सुनीत वर्मा / Suneet Verma
वित्त प्रबंधक / Manager (Finance)
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Mohali (Punjab), India

SCHEDULE-22

RESEARCH & DEVELOPMENT EXPENDITURE (INCL. GRANTS, SUBSIDIES ETC.)

(Amount in Rs.)

Particulars	Current Year	Previous Year
1. Chemical & Consumables	2,23,63,014	1,62,08,216
2. Fellowship	55,56,101	57,21,465
3. ICT Services & Consumables, Software , Accessories etc	20,74,912	22,20,298
4. Research Work Expenses	76,652	79,000
5. Field Expenses (Ploughing, RM & Other Job work)	53,87,328	27,11,445
6. Patent Filling Expenses	91,600	1,61,400
7. Workshops & Seminars	5,73,810	1,78,575
8. Research Publication Expenses	4,43,044	5,53,944
9. Sequencing Expenses	18,20,221	14,83,767
10. Recognition & Membership Fee	10,10,200	
11. Plantation & Horticulture Expenses	5,41,930	
TOTAL	**3,99,38,812**	**2,93,18,110**

SCHEDULE-23

INTEREST

(Amount in Rs.)

Particulars	Current Year	Previous Year
1. On Fixed loans		
2. On Other Loans		
3. Others (Specify)		
TOTAL		

M/S S S P J & CO.
CHARTERED ACCOUNTANTS

(SUNEET VERMA)
MANAGER FINANCE

(DR. T. R. SHARMA)
EXECUTIVE DIRECTOR

(CA SURESH KUMAR GOYAL)
PARTNER
Membership No. 099279

Dated: 14/06/2018
Place:Mohali

सुनीत वर्मा / Suneet Verma
वित्त प्रबंधक / Manager (Finance)
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Department of Biotechnology, Govt. of India
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Mohali (Punjab), India

FORM OF FINANCIAL STATEMENTS

NATIONAL AGRI FOOD BIOTECHNOLOGY INSTITUTE

Knowledge City, Sector 81, PO Manauli, S.A.S. NAGAR, MOHALI

SCHEDULE 24

SIGNIFICANT ACCOUNTING POLICIES

A) ACCOUNTING CONVENTION

The Financial Statements are prepared on the basis of historical cost convention, unless otherwise stated and on the accrual method of accounting as per the Common Format of Accounting for all Central Autonomous Bodies.

B) INVENTORY VALUATION

Expenditure on purchase of chemicals, consumables, glassware, publications, stationery and other stores are accounted for as revenue expenditure, immediately on purchase of these items.

C) INVESTMENTS

There are no investments other than fixed deposits in the bank. No brokerage or other expenses have been incurred in making such investments.

D) FIXED ASSETS

Fixed assets are created out of grants received from DBT and valued at cost of acquisition inclusive of inward freight, duties and taxes and incidental and direct expenses related to acquisition. However, the value of Fixed Assets created out of the completed /closed external funded projects have been taken at the nominal value of Rupee one for each article. The Land which is allotted free of cost by Govt. of Punjab for setting up of NABI has been taken as nominal value of Re. 1.

E) DEPRECIATION

Depreciation on fixed assets has been charged as per the rate prescribed in the Income Tax Act-1961 on written down value method. However, no depreciation has been charged on the Fixed Assets created out of the completed /closed external funded projects as their value has been taken at the nominal amount.

F) MISCELLANEOUS EXPENDITURE

There is no deferred revenue expenditure during 2017-18.

G) ACCOUNTING FOR SALES

Being an Institution there is no sales during the year under consideration.

S P J & CO. Chartered Accountants FRN-018083N

H) GOVERNMENT GRANTS/ SUBSIDIES

As the Institute is funded by the Department of Biotechnology (DBT), Ministry of Science and Technology, (Govt. of India) and the grants are treated as irrevocable, the same has been accounted for on sanction and receipt basis. During the FY 2017-18, recurring grants amounting to Rs. 11,00,00,000/- has been sanctioned for the purpose as shown in schedule-13. Non-recurring Grants amounting to Rs. 20,00,00,000/- sanctioned by DBT have been shown as addition to Corpus/ Capital Fund (schedule-1).

I) Expenses payable up to 31st March, 2018 pertaining to FY 2017-18 have been shown under expenses payable (schedule-7). Any expenditure which has not been claimed or for which bill has not been received pertaining to any expenditure relevant to the FY 2017-18, the same will be accounted for in the year of claim.

J) RETIREMENT BENEFITS

The Institute is covered under New Pension Scheme of Government of India and is registered with the agency approved by Ministry of Finance. Institute is regularly depositing the monthly pension contribution (both employee and employer share) with appropriate authority. The expenditure of Rs. 1,09,725/- on account of encashment of earned leave has been taken in account on cash basis.

K) FOREIGN CURRENCY TRANSACTIONS

Foreign Currency Transactions are accounted for at the rate of exchange prevailing on the dates of such transactions. Assets and Consumables acquired against foreign currency are recorded at the amount actually paid on their import.

For National Agri-food Biotechnology Institute

Manager Finance

Dated: 14/06/2018

Place: Mohali

सुनीत वर्मा / Suneet Verma
वित्त प्रबंधक / Manager (Finance)
राष्ट्रीय कृषि खाद्य जैव प्रौद्योगिकी संस्थान
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Executive Director

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Department of Biotechnology, Govt. of India
मोहाली (पंजाब), भारत
Mohali (Punjab), India

For S S P J & CO.
Chartered Accountants

(CA SURESH KUMAR GOYAL)
Partner
Membership No. 099279

FORM OF FINANCIAL STATEMENTS

NATIONAL AGRI-FOOD BIOTECHNOLOGY INSTITUTE

Knowledge City, Sector 81, PO Manauli, S.A.S. Nagar, Mohali

SCHEDULE 25

NOTES ON ACCOUNTS

The financial statement of accounts is prepared in three parts (i) The Balance Sheet (ii) Income & Expenditure Account and (iii) Receipt & Payment Accounts

1. Receipt and Payment Accounts

The Receipt & Payment Account carries the figures of actual receipts & actual payments of the Institute during the financial year 2017-18. It is virtually a copy of cash book / Institute's accounts. The total receipt as shown in receipt & payment account comes to Rs. 38,04,20,027/- which include Rs. 31,00,00,000/- as Recurring and Non-recurring grants from DBT, grant of Rs. 5,84,90,130/- for externally funded projects and Rs. 1,19,29,897/- from other receipts. Total amount of Rs. 35,40,60,955/- has been released as payments during the financial year 2017-18.

2. The Income and Expenditure Account

The Income and Expenditure accounts are prepared on accrual basis. The total income is Rs.12,22,50,627/- out of which includes Rs. 11,00,00,000/- Recurring Grant from DBT and rest is from Interest & Other Resources.

Total expenditure (before depreciation) comes to Rs.12,10,41,238/- and depreciation of Rs. 16,77,37,300/- has been charged in the current FY 2017-18. A sum of Rs. 16,65,27,911/- being excess of expenditure over income has been transferred to Corpus/ Capital Fund (Schedule-1).

3. Fixed Assets

Fixed assets are valued at cost of acquisition inclusive of inward freight, duties and taxes and incidental and direct expenses related to acquisition. During the FY 2017-18, a sum of Rs. 27,82,777/- has been earned as interest on deposits with RITES, which has been adjusted against Main campus building capitalized during the year (Schedule-8) as per the recommendations of 11th Finance Committee meeting held on 08-10-2015.

During the FY 2017-18, an occupation certificate of NABI buildings has been received from GMADA, Mohali vide GMADA-S.D.O/2017/28498 dated 4th July 2017 being the building works have been completed. A sum of Rs.130,21,69,210/- has been capitalized in fixed assets by transferring from Capital Work in Progress (Main Campus, Sector-81, Mohali) to Building Account being the construction work completed.

4. Depreciation

Depreciation on fixed assets has been charged as per the rate prescribed in the Income Tax Act-1961 on written down value method, however, no depreciation has been charged on the Fixed Assets created out of the completed / closed external funded projects as their value has been taken at the nominal amount. Depreciation on Library Books has been charged @ 60%.

5. Current Assets, Loans and Advances

In the opinion of the management the current assets, loans & advances of the institute have a realizable value in the ordinary course at least to the extent shown in the accounts and the provisions of liabilities are adequate.

6. Land

The Government of Punjab has provided approx. 35 acres of land in Knowledge City at Sector-81, Mohali to the Institute, free of cost, for setting up of NABI Campus. Therefore, the cost of NABI land has been taken as nominal value of Re. 1 and corresponding accounting effect has been given in Schedule-2.

7. Exemption u/s 35(i)(ii) of The Income Tax Act,1961

The institute has been granted exemption u/s 35(i)(ii) of the Income Tax Act,1961 in the Category of 'Scientific Research Association vide notification no 21/2013 dated 20th March,2013.

8. **Externally Aided Project**

As on 31st March 2018, there is a balance of Rs. 3,30,93,323/- in the externally funded project accounts. The balance will be spent in accordance with the terms and conditions of the projects. An interest of Rs.6,36,965/- has been credited to the externally funded projects as shown in Schedule 3.

9. There are no losses from casualties such as flood and fire.

10. Previous year figures have been re-grouped and rearranged where ever considered necessary to make them comparable with those of current year.

11. Government Grants have been recognized on the basis of sanctions issued by the Govt. of India.

For National Agri-food Biotechnology Institute

Manager Finance

Dated: 14/06/2018

Place: Mohali

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मोहाली, पंजाब / Mohali, Punjab-140306

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For S S P J & CO.
Chartered Accountants

(CA SURESH KUMAR GOYAL),
Partner
Membership No. 099279

NATIONAL AGRI-FOOD BIOTECHNOLOGY INSTITUTE

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