

<b>Course title:</b> Genomics and molecular genetics				
<b>Course code:</b> BBP 143		<b>No. of credits:</b> 4	<b>L-T-P:</b> 38-18-0	<b>Learning hours:</b> 56
<b>Pre-requisite course code and title (if any):</b> None				
<b>Department:</b> Department of Biotechnology				
<b>Course coordinator:</b> Dr Ramakrishnan Sitaraman			<b>Course instructor:</b> Dr Ramakrishnan Sitaraman/ Dr Anandita Singh/ Dr. Chaithanya Madhurantakam/ Dr. Shashi Bhushan Tripathi	
<b>Contact details:</b> rkraman@teriuniversity.ac.in / asingh@teriuniversity.ac.in / chaithanya.madhurantakam@teriuniversity.ac.in / shashi.tripathi@teriuniversity.ac.in				
<b>Course type:</b> Core			<b>Course offered in:</b> Semester 3	
<b>Course description:</b> The present core course seeks to provide an overview of the latest methods and technologies used in analysis of complex genomic information at a global scale. The course is divided into three segments. In the first segment, the students will be acquainted to the objectives, methodology and applications of genome sequencing projects by means of case studies. In the second segment, the course will provide an in depth review of next generation techniques such as microarrays, large-scale transcriptome and proteome analysis, and functional genomics. In the third segment, the students will be familiarized to the contemporary approaches for gene discovery and gene characterization with mutant analysis being central to functional genomics. An introduction will also be provided to methods of genome editing.				
<b>Course objectives:</b>				
<ol style="list-style-type: none"> <li>To provide an overview of current high-throughput technologies for the analysis of complex biological information.</li> <li>To promote an understanding of advanced techniques for genome-wide expression analyses.</li> <li>To integrate classical and contemporary approaches for gene discovery and characterization.</li> <li>To develop a holistic perspective on the evolution of classical and contemporary methods, and their application to the analysis of molecular genetic networks.</li> <li></li> </ol>				
<b>Course contents</b>				
<b>S.No</b>	<b>Topic</b>	<b>L</b>	<b>T</b>	<b>P</b>
<b>Module 1: Methods and strategies to analyze genomes:</b>				
<b>1</b>	<b>Genome sequencing and annotation:</b> Strategies for genome sequencing: Hierarchical sequencing, shotgun sequencing. Case Studies: The human genome, Arabidopsis and Rice genome sequencing projects (objectives, strategies and methodologies: Chromosome mapping, BAC libraries, Subclones, Contig assembly, Working Draft Sequence, Post-sequencing data processing: Quality Trimming, Sequence Assembly, Sequence Editing and Gap filling, Annotation)	5	5	0
<b>Module 2: Functional Genomics</b>				
<b>1</b>	<b>Gene Expression and the transcriptome analysis:</b> <b>Medium throughput techniques:</b> Gene Expression and the transcriptome analysis: Medium throughput techniques: Northern, Quantitative RT-PCRs, RACEs, cDNA-AFLP, Inventories for gene discovery and annotation: EST databases, full-length cDNA /ORF clones	2	2	0
<b>2</b>	<b>Microarray analysis:</b> Whole Genome arrays, cDNA arrays and Tiling Arrays – concept , design, fabrication and data analysis; Normalization techniques Applications: Genome analysis and global gene expression profiling, discovery of novel genetic pathways and targets in model organisms yeast and <i>C. elegans</i>	10	4	0
<b>3</b>	<b>Hi through put-genome wide analytical platforms:</b> Serial Analysis of Gene Expression, Digital Northern, Massively Parallel Signature Sequences, Roche's 454-FLX Sequencer, Solexa/Illumina's 1G Genome Analyser	2	2	0

4	<b>Proteomics and integrative genomics</b> Protein separation and 2-D PAGE, Mass Spectrometry and protein identification: N-terminal sequencing, MALDI –TOF, LC-MS/MS, Tandem-MS/MS. SELDI-TOF, ICAT, I TRAQ, MUDPIT, Protein interaction maps, analysis of cellular constituents, metabolomics.	5	5	
<b>Module 3: Mutant Analysis for Functional Genomics</b>				
1	<b>Approaches and methods for mutant analysis:</b> Forward versus reverse genetics, Mutagen types, Mutant Screens, random and targeted mutagenesis	1		
2	<b>Loss-of-function mutants, Methodologies and applications:</b> Insertional Mutagenesis (T-DNA tagging, Transposon Tagging), Insertion mutagenesis in forward and reverse genetics mode, flanking sequence analysis methods for reverse genetics, systematic insertional mutagenesis for high-throughput functional genomics, Genome-wide mutant libraries and resources, TILLING (Targeted Induced Local Lesions in Genomes), DeleteAgene, Fast-neutron bombardment, RNAi based silencing techniques (Intron-hairpin constructs, artificial miRNAs)	7		
3	<b>Gain-of-function mutants, Methodologies and applications:</b> Ectopic mis-expression, Activation mutagenesis (Enhancer activation tagging, promoter activation tagging)	2		
4	<b>Functional genomics through specialized mutants:</b> Gene traps (discovery of enhancers and promoters, expression domain analysis of genes), two component systems for regulated gene expression	2		
3	<b>Genome editing:</b> Zinc-finger nucleases, Homologous Recombination, CRISPR/Cas9 system, TALENS (transcription activator-like effector nucleases)	2		
	<b>Total</b>	<b>38</b>	<b>18</b>	<b>0</b>
<b>Evaluation criteria:</b>				
1. 2 minor tests : 30% (each)				
2. 1 major test (end semester) : 40%				
<b>Learning outcomes:</b>				
1. An understanding of the methods for generation of large-scale genomic information and its analysis.				
2. A detailed knowledge of current methodologies used for transcriptomic and proteomic analyses and their applications in functional genomics.				
3. An understanding of strengths and constraints of various methodologies and ability to design optimal research strategies.				
4. An integrative problem-solving approach towards understanding biological systems.				
<b>Pedagogical Approach:</b>				
Classroom lectures and tutorials, with a major emphasis on the detailed discussion of original research articles from scientific journals in class.				
<b>Skill Set:</b>				
1. Proficiency in sequencing strategies applied in genome annotation and expression analysis				
2. Expertise in analyzing microarray experiments for genotyping and transcriptomic studies				
3. Adeptness in protein purification and identification methods				
4. Ability to analyze mass spectrometry and metabolomics data				
5. Ability to design saturation mutagenesis experiments including chemical, physical and biological mutagens including insertional mutagenesis, activation tagging, RNAi based silencing constructs				
6. Technical know-how on mutation detection and validation using PCR approaches for flanking sequence analyses and TILLING				
7. Ability to modify and edit genome sequences				
<b>Employability:</b>				
1. Agri-genomics, seed companies, crop-agri business				
2. Diagnostic centres of excellence including pathology laboratories				
3. Pharmaceutical units and nutraceutical firms				
4. Fermentation and dairy Industries				
5. Law firms and knowledge processing organizations (IP management consultancy)				

**Materials:****Required text:****Suggested readings:**

1. G. Gibson and S.V. Muse. *A Primer of Genome Science* (Sinauer Associates, Inc., Sunderland, third edition, 2009)
2. G. P. Rédei. *Genetics Manual, Current Theory, Concepts, Terms* (World Scientific, Singapore, 1998).
3. D. Leister. *Plant Functional Genomics* (Panima Publishing Corporation, New Delhi, 2004).
4. A.M. Campbell and L.J. Heyer. *Discovering Genomics, Proteomics, and Bioinformatics* (Pearson Education Inc., London, second edition, 2007).
5. S. H. Howell. *Molecular Genetics of Plant Development* (Cambridge University Press, Cambridge, 1998).
6. J. Bowmann (ed.). *Arabidopsis: An atlas of morphology and development* (Springer, Berlin, 1994).
7. S. A. Bustin. *A-Z of Quantitative PCR* (IUL Biotechnology, No. 5) (International University Line; La Jolla, 2004).
8. N.A. Barkley and M.L Wang. *Curr Genomics*, 9, 212-226 (2008).
9. S. Parinov *et al.*, *Plant Cell*, 11, 2263-2270 (1999).
10. Zhang *et al.*, *Plant Physiology*, 161, 20–27 (2013).
11. T. Cathomen, J.K. Joung, *Molecular Therapy*, 16 (2008).
12. V. K. Shukla *et al.*, *Nature*, 459, 437-441 (2009).
13. D. Carroll, *Genetics*, 188, 773–782 (2011)
14. Te-Wen Lo, *et al.*, *Genetics*, 195, 331–348 (2013).
15. I. Kardailsky *et al.*, *Science*, 286 (1999).
16. H. Puchtaa, B. Hohn, *PNAS*, 107, 11657–11658 (2010).
17. D. Weigel, *et al.*, *Plant Physiol*, 122, 1003-13 (2000).
18. Xin Li, *et al.*, *Comp Funct Genom*, 3, 158–160 (2002).
19. J. M. Alonso, J. R. Ecker, *Nature Reviews Genetics*, 7, 525-527 (2006).
20. K.A. Feldmann, *Plant J*, 1, 71-82 (1991).
21. W. Liu *et al.*, *Nature Reviews Genetics*, 14, 781-786 (2013).
22. J.F. M.Gaudry *et al.*, *Functional Plant Genomics*. (CRC Press, ed. 1, 2007).
23. D. Leister, *Plant Functional Genomics*. (CRC Press, ed. 1, 2004)
24. J. D. Sander, J Keith Joung, *Nature Biotechnology*, 32, 347–355 (2014)
25. P.S. Springer, *The Plant Cell*, 12, 1007-1020 (2000).

**Web Resources**

1. [www.tigr.org](http://www.tigr.org)
2. [www.arabidopsis.org](http://www.arabidopsis.org)
3. [www.genome.gov](http://www.genome.gov)

**Additional information (if any):****Student responsibilities:**

1. Class attendance.
2. Study of course materials as specified by the instructor.

**Course reviewers:**

1. Dr. Niranjan Chakraborty, Scientist VII, NIPGR
2. Dr. Manu Agarwal, Reader, Delhi University