Course title: Genome Structure and Diversity: Concepts and Methodologies									
Course code: BBP 146	No. of cro	edits: 3	L-T-P: 23-22-0	Learning hours: 45					
Pre-requisite course code and title (if any): None									
Department: Department of Biotechnology									
Course coordinator(s): Dr Ananc	Course instructor(s): Dr Anandita Singh								
Contact details: asingh@terisas.ac.in									
Course type: Core	Course offered in: Semester 2								

Course description:

The extraordinary diversity among living organisms is reflective of structural and functional diversity of genomes. The tree of life is strident evidence of evolutionary processes underlying biological variation. Genome elucidation studies are crucial for gaining insights into the molecular basis of morphological diversity and trait variation. This advanced course provides a conceptual framework on genome architecture and experimental methods for analysis of its components and sequences. In the first module, students will gain insights on features of diverse genomes, hierarchies of genome organisation, variability in genome complexity and content and dynamic nature of genomes at varying levels of resolution. In the second module, a critical appraisal of traditional marker techniques and modern, sophisticated genotyping platforms vis-à-vis relative efficiencies in polymorphism detection will be discussed. Introduction to next generation, genomics based, genotyping platforms will sensitize the students to frontier areas of research directed towards sustainable agriculture, generation of climate resilient crops and healthcare products. Third module is designed to inform the students, by way of interesting case studies, application of markers in sectors of plant, animal and microbial biotechnology. Through this course, students will gain a holistic perspective on "genotype-phenotype association" by integration of core principles related to diverse disciplines as molecular genetics, genomics and evolution.

Course objectives:

- 1. Building perspectives on structure and variability in genomes and its constituents
- 2. Illustrating the relationship between genotypic and phenotypic variation
- 3. Introducing versatile methodologies, concepts and applications of molecular marker techniques

Module1	Genome Structure and Organization (Prokaryotes and Eukaryotes)	L	T	P
1	Genome diversity (Viral, Bacterial, Archaeal, Eukaryotic, Auxiliary	6	6	+
	DNA structures viz. Plasmids and Organellar genome); Hierarchies of			
	Genome Organization (Genomic sequences, chromatin, nucleosomes,			
	packaging, 3D genomes and chromosome territories); Dynamic			
	genomes and variability in Genome Content (Genome sizes and			
	complexity, C-Value paradox, Unique and repeat DNA sequences;			
	Tandem and Interspersed repeats, Mobile Elements, Micro- and Mini-			
	satellites, hyper-variable VNTRs, Whole Genome Multiplications and			
	Fractionation, DNA rearrangements, SNPs and Structural variation			
	(Microscopic and sub-microscopic, Copy Number Variation, Presence			
	Absence Variation, Inversions, Mobile Element Insertion and Deletions,			
	Homologous Exchange Variation); Variability in gene categories and			
	structure (Protein coding genes, non-protein coding genes, Intron-less			
	and interrupted genes (Structure of exons, introns, variability in number,			
	size, GC-content); Intron types; poly-cistronic genes, overlapping genes			
	(+/+ and +/- strand); cis-regulatory regions (Promoter, bi-directional			
	promoters, Enhancers, Insulators, Terminators), case studies to illustrate			
	structural variations as basis for phenotypic diversity, notion of genome			
	maps			

Module2	Genome analysis by Genetic markers			
2	Molecular Markers and DNA fingerprinting techniques	12	12	
	Definition of trait, classification genetic markers, molecular basis of			
	dominant and co-dominant markers; Restriction Fragment Length Polymorphism, MAAP (Multiple Arbitrary Amplicon Profiling) and			
	other PCR based markers (DNA Amplification Fingerprinting,			
	Arbitrarily Primed PCR, Randomly Amplified Polymorphic DNA,			
	SSRs, STMS, SCARs, Inter-SSRs, Amplified Fragment Length			
	Polymorphism, Selectively Amplified Microsatellite Polymorphic Loci,			
	Inter retrotransposon amplified polymorphism, retrotransposon-			
	microsatellite amplified polymorphism, Intron spanning markers, SNP			
	based marker assays (CAPs, dCAPs, dHPLC, molecular beacons, 5'nuclease assay/TaqMan assays, FEN based Invader reactions), Eco-			
	TILLING (Targeting induced local lesions in the genome); Modern			
	Genotyping platforms Array based genotyping (Affymetrix axiom,			
	Affymetrix genechip, Illumina Infinium Bead Chip; NGS based			
	genotyping methods (GBS, DArT-seq, RAD-seq, ddRAD, REST-seq);			
	de-novo sequencing and/or WGS (PacBio. HiC. 10X Chromium, Oxford			
	nanopore, HiSeq4000/NovaSeq6000, IonTorrent)			
Module3	Applications and key concepts related to marker technology: Case			
	Studies			
3	Diversity analysis in plants Geographical diversity, center of origin,	5	4	
	domestication, gene pools, pan-genomes and super-pangenomes;			
	methods (numerical taxonomy and phenetics), conservation of plant			
	genetic resources; Diversity analysis in microbes (Microbiomes,			
	structures and functions, 16S to metagenomics); Molecular Breeding			
	(MAS, Genomics Assisted Breeding); plant variety protection; DNA			
	(Wirds, denomics resisted Diceding), plant variety protection, Divis			
	barcoding; hybrid purity tests; diagnostics (transgenics, forensics);			
	barcoding; hybrid purity tests; diagnostics (transgenics, forensics);			
	barcoding; hybrid purity tests; diagnostics (transgenics, forensics); establishing clonal fidelity; BAC fingerprinting; LD/ Haplotype			
	barcoding; hybrid purity tests; diagnostics (transgenics, forensics); establishing clonal fidelity; BAC fingerprinting; LD/ Haplotype mapping, GWAS in context to natural populations (animals and plants),			
	barcoding; hybrid purity tests; diagnostics (transgenics, forensics); establishing clonal fidelity; BAC fingerprinting; LD/ Haplotype mapping, GWAS in context to natural populations (animals and plants), human diseases (mapping human diseases, risk prediction, discovery of			

Evaluation criteria:

- 1. Minor test 1: 30%
- 2. Minor test 2: 30%
- 3. Major test (end semester) : 40%

Learning outcomes:

- 1. An understanding on structure and variability in genomes and its constituents (Minor test1, Minor test 2 and Major test)
- 2. Ability to rationalize deployment of genotyping techniques for relevant applications (Minor test1, Minor test 2 and Major test)
- 3. Understanding genetic and molecular basis of phenotypic variation (Minor test 1, Minor test 2 and Major test)

Pedagogical Approach:

Classroom lectures with a major emphasis on the detailed discussion of original research articles

Skill Set:

- 1. Generating and interpreting DNA fingerprints and profiles for forensics
- 2. Developing natural and synthetic microbiomes as biofertilizers, biopesticides, healthcare products
- 3. Testing Hybrid purity
- 4. Diagnosing varieties, cultivars, accessions and land races
- 5. Ascertaining clonal fidelity for tissue culture raised regenerants
- 6. Applying MAS (Marker Assisted Selection) strategies in breeding programmes
- 7. Introducing transgenes for development of new plant varieties
- 8. DNA bar-coding technology
- 9. Evaluating gene-flow in transgenic field trials
- 10. Formulating appropriate conservation strategies
- 11. Innovating genome interrogation methods for unarticulated research problems

Employability:

- 1. Forensic Science laboratories, molecular diagnostic testing laboratories
- 2. Genotyping and sequencing companies
- 3. Agri-biotechnology and seed companies
- 4. Tissue culture and horticulture companies
- 5. Law firms and knowledge processing organizations (IP management consultancy)
- 6. Regulatory bodies and funding agencies

Materials:

Suggested readings (Representative)

- 1. Krieg, N.R., Ludwig, W., Whitman, W.B., Hedlund, B.P., Paster, B.J., Staley, J.T., Ward, N. and Brown, D. (eds., 2010). Bergey's Manual of Systematic Bacteriology, 2nd ed., vol. 4, Springer-Verlag, New York, NY
- 2. Dale, J.W., Schantz, M.V. and Plant, N. (2011). From Genes to Genomes: Concepts and Applications of DNA Technology. Third edition. John Wiley & Sons, UK.
- 3. Brown, T. A. (2017). Genomes 4. CRC Press, Taylor & Francis Group, USA.
- 4. Krebs J.E, Goldstein E.S., Kilpatrick S. T. (2018) Lewin's GENES XII. Jones and Bartlett Learning. USA
- 5. Meksem K., Kahl G. (2005) The Handbook of Plant Genome Mapping: Genetic and Physical Mapping, Wiley-VCH Verlag GmbH & Co. KGaA, Weinheim
- 6. Varshney R., Pandey M., Chitikineni A (2018) Plant Genetics and Molecular Biology. Advances in Biochemical Engineering / Biotechnology series number 164. Springer Nature, Switzerland
- 7. Varshney R., Roorkiwal M., Sorells M (2017) Genomic Selection for Crop improvement: New Molecular Breeding strategies for crop improvement. Springer Nature, Switzerland
- 8. Research and review articles on relevant topics
- 9. Scherer, S., & Visscher, P. (2016). Genome-Wide Association Studies: From Polymorphism to Personalized Medicine (K. Appasani, Ed.). Cambridge: Cambridge University Press. doi:10.1017/CBO9781107337459

Student responsibilities:

- 1. Class attendance
- 2. Study of course materials as specified by the instructor
- 3. Self-study

Course reviewers:

1. Prof. Surekha Katiyar-Agarwal Department of Plant Molecular Biology University of Delhi, South Campus, New Delhi- 110021, India

2. Dr. Neeti Sanan Misra Group Leader: Plant RNAi, International Centre for Genetic Engineering and Biotechnology Aruna Asaf Ali Marg New Delhi-110 067, India