Course title: Conservation Genetics and Genomics			
Course code: BBP 144	**No. of credits:** 2	**L-T-P:** 30-0-0	**Learning hours:** 30
Pre-requisite course code and title (if any): Science graduate			
Department: Department of Biotechnology			
Course coordinator: Dr. Shashi Bhushan Tripathi		**Course instructor:** Dr. Shashi Bhushan Tripathi	
Contact details: shashi.tripathi@terisas.ac.in			
Course type: Core		**Course offered in:** Semester 2	

Course description:

The broad objective of this course is to provide the students a foundation on the concepts, tools and techniques of classical genetics, population genetics and genomics as applied in conservation of biodiversity. The students will be acquainted with various factors that affect the genetic composition of natural populations. Considering the importance of next generation sequencing in generating data for characterization of populations, a module on genome sequencing and its applications in genetic diversity assessment has been included. Further, topics on microbial genetic diversity such as 16S RNA sequencing and metagenomics have also been included.

Course objectives:

1. To introduce the students to concepts of classical and modern genetics
2. To introduce the students to concepts of population and conservation genetics
3. To familiarize the students to next generation sequencing platforms
4. Applications of next generation sequence data for characterisation of genetic resources

Course contents

Module	Topic	L	T	P
1	**Principles of Evolution and Population genetics**	6	0	0
	• Principles of evolution and Natural selection • Population attributes and structure • Gene and genotype frequency: Hardy-Weinberg Equilibrium; changes in gene frequency through natural selection, migration and random genetic drift; Population bottlenecks • Adaptive radiation; Speciation; Allopatric and Sympatric; Convergent evolution; • In-breeding depression & mating systems			
2	**Introduction to conservation genetics**	6	0	0
	• Introduction to conservation genetics, • Concepts of gene pool (primary, secondary, tertiary) • Natural variation: Phenotypic and genetic diversity including allelic richness; Analysis of genetic diversity • *In situ* and *ex situ* conservation, core collections •			
3	**Principles of Genetics and mapping**	12	0	0
	• Genetics and inheritance: Laws and exceptions • Recombination and linkage mapping • Quantitative genetics and mapping, polygenic inheritance, heritability; Linkage disequilibrium			

4	**Genomics platforms for population and conservation genetics**	6	0	0
	• Introduction to next generation sequencing platforms, Pyrosequencing, Illumina, Single molecule real time (SMRT) sequencing • 16S RNA based analysis of microbial diversity and taxonomy, metagenomics • Nuclear and Organellar DNA for conservation and diversity			
	Total	**30**	**0**	**0**

Evaluation criteria:

1. Minor test 1 - (Module 1) 30%
2. Minor test 2 - (Module 2) 30%
3. Major test (end semester) - (Modules 3 and 4) 40%

Learning outcomes:

1. Students will be able to use the principles of evolution and population genetics (Minor test 1)
2. Basic understanding of principles of germplasm conservation (Minor test 1 and Minor test 2)
3. Understanding of principles of genetics (Minor test 2 and Major test)
4. Basic understanding of next generation sequencing platforms and their application in genetic diversity analysis (Major test)

Pedagogical Approach:

1. Classroom lectures and discussions
2. Case studies and examples from original research articles

Skill Set:

1. Next generation sequencing platforms
2. Germplasm characterisation using principles of population genetics
3. 16S RNA sequencing and metagenomics analysis

Employability:

1. Forestry and wildlife research institutions
2. Academic organisations
3. Companies providing genotyping and sequencing services

Materials:

Suggested Readings

1. A Primer of Ecological Genetics. Conner, J. K. and D. L. Hartl. Sinauer Associates. 2009
2. Conservation and the Genetics of Populations. 2nd edition. Allendorf, Luikart and Aitken. 2013.
3. Adaptive radiations: From field to genomic studies. Scott A. Hodges, Nathan J. Derieg. Proceedings of the National Academy of Sciences Jun 2009, 106 (Supplement 1) 9947-9954; DOI: 10.1073/pnas.0901594106
4. Methods in Molecular Biology, vol. 376: Linkage Disequilibrium and Association Mapping: Analysis and Applications Edited by: A. R. Collins © Humana Press Inc., Totowa, NJ

Additional information (if any):

Student responsibilities:

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

Course reviewers:

1. Prof. Sandip Das, Department of Botany, University of Delhi, New Delhi
2. Dr. R. Yasodha, Scientist G, Institute of Forest Genetics and Tree Breeding, Coimbatore
3. Dr. Ram Kumar Sharma, Scientist G, Institute of Himalayan Bioresource and Technology, Palampur, Himachal Pradesh