

M.F.Sc. Fish Biotechnology (2nd Semester)

Course: FBT-510 “Molecular Taxonomy and Phylogenetics” (2+1) Lecture Plan (Theory)

S. No.	Unit	Topics	Lecture Plan
1	Unit I Molecular Basis of Evolution	Overview of genome structure	01
2		Sources of genetic variation (Recombination, Mutations, Indels, Gene duplication)	02
3		Fast and slow- evolving sequences; Homologous, Paralogous and Orthologous genes,	02
4		Concept of Neutral theory of molecular evolution	01
5	Unit II Evolution and Speciation	Allopatric, Sympatric and Parapatric speciation,	01
6		Factors responsible for speciation Phylogenetic species concept, Phylogenetic trees,	01
7		Concept of monophyly, paraphyly and polyphyly, Species delimitation, Gene trees and species trees	02
8		DNA barcoding and concept, BOLD SYSTEMs and WORMS; Principle, Methodology, Application and limitations	03
9	Unit III Genetic distance measures	Observed and expected distances, Pair-wise distances	02
10		Inter and intra specific distances;	02
11	Unit IV Concepts in phylogeny	Phylogenetic species concept, Phylogenetic trees	02
12		Concept of monophyly, Paraphyly and polyphyly	02 02
13	Unit V Phylogenetic tree construction	Phylogenetic reconstruction using distance-based methods (UPGMA, Neighbour-Joining), Principle, Methodology, Interpretation of results and limitations.	03
14	Unit VI Phylogenetic analyses	Phylogenetic reconstruction using character Based Methods, Maximum Parsimony, Maximum Likelihood and Bayesian Inferences,	04
15		Mesquites, Genepops, Phylogenetic tree importances.	02
Total			32

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Course Teacher

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Course: FBT-510 “Molecular Taxonomy and Phylogenetics” (2+1) Lecture Plan (Practical)

S. No.	Practical	Practical Plan
1	DNA sequence analysis	01
2	Genomic databases, GenBank search and dataset download	01
3	EMBOSS tools	02
4	Blast Tools	02
5	Sequence alignment and editing	01
6	Data partition,	01
7	Selection of the best substitution model.	01
8	Use of Neighbour-Joining, Maximum Likelihood and Bayesian inference.	01
9	Re-analysis and interpretation of reference data	02
10	Bioinformatic tools (MEGA, Phylip) for phylogenetic tree reconstruction	02
11	Bioinformatic tools (PAUP, Mr Bayes and Fig Tree) for phylogenetic tree reconstruction	03
	Total	17

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