MINISTRY OF EDUCATION AND TRAINING
CAN THO UNIVERSITY

SOCIALIST REPUBLIC OF VIETNAM
Independence - Freedom - Happiness

SUBJECT OUTLINE DETAILS

1. Subject: Genomics and Its Application

- **Code:** BT301C
- **Credits: 03**
- **Hours:** 45 theory hours, 90 self-study hours.

2. Management Unit:

- **Department:** Molecular Biotechnology
- **Faculty/School/Institute/Center/Department:**

Biotechnology Research and Development Institute, Can Tho university

3. Prerequisites: Biochemistry I (BC461C); Biochemistry II (BC462C); General Biology I (BS110C).

4. Subject objectives:

The purpose of this course is to provide students: (1) basic information about genomics, (2) the study of molecular markers; (3) application of genomics in plant breeding and gene mapping.

4.1. Knowledge:

Students will develop knowledge and understanding of:

4.1.1. The organiztion of genome in living organisms;

4.1.2. The principles of molecular markers in discovering genome of organisms;

4.1.3. The application of genome in plant breeding.

4.2. Skill:

4.2.1. Ability to understand genome analysis of species.

4.2.2. Apply investigative and problem-solving skills.

4.2.3. Knowing how to analyze DNA markers and read the results after analysis.

4.3. Attitude:

4.3.1. Students are encouraged to develop positive values and informed critical attitudes.

4.3.2. Being hard-working student.

4.3.3. Honesty in presenting analysis results.

5. Brief description of subject content:

Genomics describes the determination of the nucleotide sequence as well as many further analysis used to discover functional and structural gene information on all the genes of an organism. The course focus on genomic structure, genomic function,

genome mapping, genome sequencing, how to find genomic database on the web, and some applied of genome such as gene expression and micro array

6. Subject content structure:

6.1. Theory

Contents	Hours	Objectives
Chapter 1. Introduction to Genomics 1.1. Definition: Structural and Functional Genomics 1.2. Plant Genome Organization and Structure 1.3. Reassociation Kinetics technique: Tm and C_ot value 1.4. Chloroplast genome organization 1.5. Mitochondira genome organization 1.6. Expression of Gene	**4**	**4.1.1** **4.2.1** **4.2.3** **4.3.1** **4.3.2** **4.3.3**
Chapter 2. Molecular markers (part I): Protein, RFLPs, PCR, RAPDs 2.1. What is molecular markers? 2.2. Protein-based marker: Isozymes and Allozymes 2.3. DNA-based marker: RFLPs marker 2.4. PCR-based methods: factors influencing PCR' products 2.5. RAPDs marker	**4**	**4.1.2** **4.2.1** **4.2.2** **4.2.3** **4.3.1** **4.3.2** **4.3.3**
Chapter 3. Molecular markers (part II): SSRs and AFLPs markers 3.1. DNA-based marker: Sequence-Tagged sites 3.1.1. ISSR marker 3.1.2. SCARs and CAPs markers 3.2. SSRs marker and fSSRs marker assay 3.3. Other markers 3.4. AFLPs marker	**5**	**4.1.2** **4.2.1** **4.2.2** **4.2.3** **4.3.1** **4.3.2** **4.3.3**
Chapter 4. Molecular marker (part III): SNPs 4.1. What is Single Nucleotide Polymorphism (SNPs)? 4.2. SNPs marker: Strengths and Weaknesses 4.3. Why collect SNPs? 4.4. Steps in SNP documentation: Discovery, Validation, Typing 4.5. LSOPs and ASOPs 4.6. Sequence-based SNP Identification 4.7. Application of SNPs: 4.7.1. Dectect Soybean Lipoxygenase gene; 4.7.2. Soybean ESTs survey 4.7.3. Disease Resistance genes survey 4.7.4. *Waxy* gene survey in Foxtail millet	**5**	**4.1.2** **4.2.1** **4.2.2** **4.2.3** **4.3.1** **4.3.2** **4.3.3**
Chapter 5. SNPs marker (continued..) 5.1. Basic Strategies for SNP detection 5.2. Single Strand Conformation Polymorphism (SSCP)	**5**	**4.1.2** **4.2.1** **4.2.2**

5.3. WebSNAPER 5.4. CAPs and dCAPs 5.5. SNP genotyping in a Luminex System: DH, SBCE, ASPCR, OL		**4.2.3** **4.3.1** **4.3.2** **4.3.3**
Chapter 6. Genetic Diversity 6.1. Mutation: definition, types of mutation, DNA damage repair 6.2. Genetic diversity 6.2.1. Overview 6.2.2. Genetic Primers 6.2.3. Measuring Genetic Diversity 6.2.4. Values of Heterozygosity 6.2.5. Processes eroding genetic diversity 6.2.6. Applications	**4**	**4.1.3** **4.2.1** **4.2.2** **4.2.3** **4.3.1** **4.3.2** **4.3.3**
Chapter 7. Genetic Mapping 7.1. What is a Genetic map? 7.2. Types of markers for mapping 7.3. Types of Maps 7.4. Terminology: Genetic map unit; Points and Intervals; Mapping population 7.5. Steps in Genetic Mapping 7.6. QTLs mapping 7.7. Positional Cloning: Chromosome walking; Candidate genes, BAC sequencing 7.8. Marker Assisted Selection (MAS)	**5**	**4.1.3** **4.2.1** **4.2.2** **4.2.3** **4.3.1** **4.3.2** **4.3.3**
Chapter 8. Linkage Disequilibrium (LD) 8.1. What is LD? 8.2. Linkage versus LD 8.3. How is LD measured? 8.4. Association Analysis 8.5. Mapping QTLs- The Traditional way 8.6. What is Association map?	**4**	**4.1.3** **4.2.1** **4.2.2** **4.2.3** **4.3.1** **4.3.2** **4.3.3**
Chapter 9. Forward Genetics 9.1. Important Mutant population for gene function analysis 9.2. Methods for Generation of Mutant Population 9.2.1. Insertional Mutagenesis 9.2.2. Deletion Mutagenesis 9.3. Gene Cloning 9.4. Isolation of genes from a insertion mutant collection 9.4.1. Plasmid rescue 9.4.2. IPCR 9.4.3. TAIL-PCR 9.5. Isolation of genes from deletion mutation population or germplasm: Chromosome walking	**5**	**4.1.3** **4.2.1** **4.2.2** **4.2.3** **4.3.1** **4.3.2** **4.3.3**
Chapter 10. Reverse Genetics 10.1. Methods to assign putative gene function of ESTs	**4**	**4.1.3** **4.2.1**

10.2. Approaches 10.3. Biological Function Analysis of Identified mutants 10.4. Isolation of mutants from deletion mutant collection		**4.2.2** **4.2.3** **4.3.1** **4.3.2** **4.3.3**

7. Teaching method:

- Teaching and explaining each lecture.
- Providing supplements, case studies, homeworks.

8. Duties of student:

Students have to do the following duties:

- Lecture/Class attendance: not allow to be absent more than 20% of lectures.
- Laboratory Attendance: mandatory.
- Discussion problems and doing homeworks: mandatory

9. Assessment of student learning outcomes:

9.1. Assessment

No.	Point components	Rules and Requirement	Weights	Objectives
1	Midterm exam	Tests	40%	Evaluating knowledge of half program
2	Final exam	Tests	60%	Evaluating knowledge of whole course

9.2. Grading

- Grading components and final test scores will be marked on a scale of 10 (0 to 10), rounded to one decimal place.
- Subject score is the sum of all the components of the evaluation multiplied by the corresponding weight. The subject score is marked on a scale of 10 and rounded to one decimal place, then is converted to A-B-C-D score and score on a scale of 4 under the academic provisions of the University.

10. Materials:

Materials information	Code number
[1]. Genomics and Its Application Handout	File-BiRDI website
[2]. Lesk, A.M., 2007. Introduction to Genomics. Oxford University Press	BiRDI Library ISBN 978 0199296958
[3]. Primrose, S.P., 2003. Principles of Genome Analysis and Genomics. 3rd Edition , Blackwell Publishing.	BiRDI Library ISBN 1-40510-120-1

11. Self-study Guide:

Week	Content	Theory (hours)	Practice (hours)	Students' duties
1	**Chapter 1. Introduction to Genomics** 1. Structural and Functional Genomics 2. Plant Genome Organization Structure	**8**		Reading Chapter 1 and Chapter 2 [Material 2]; Part I-

	3. Chloroplast genome organization 4. Mitochondira genome organization			Chapter 1 and Chapter 2 [Material 3]
2	**Chapter 2. Molecular markers (part I): Protein, RFLPs, PCR, RAPDs** 1. Protein-based marker: Isozymes and Allozymes 2. DNA-based marker: RFLPs marker 3. PCR and factors influencing PCR' products 4. RAPDs marker	**8**		Reading Chapter [Material 2]; Chapter 3 and Chapter 4 [Material 3]
3	**Chapter 3. Molecular markers (part II): SSRs and AFLPs markers** 1. Sequence-Tagged sites 2. SSRs marker and fSSRs marker assay 3. Other markers 4. AFLPs marker	**10**		Reading Chapter 2 [Material 3];
4	**Chapter 4. Molecular marker (part III): Single Nucleotide Polymorphism** 1. What is SNPs? 2. SNPs marker: Strengths and Weaknesses 3. Why collect SNPs? 4. LSOPs and ASOPs 5. Sequence-based SNP Identification 6. Application of SNPs	**10**		Reading Part II-Chapter 4 [Material 2]; Chapter 5 [Material 3].
5	**Chapter 5. SNPs marker (continued..)** 1. Basic Strategies for SNP detection 2. Single Strand Conformation Polymorphism (SSCP) 3. WebSNAPER 4. CAPs and dCAPs 5. SNP genotyping in a Luminex System: DH, SBCE, ASPCR, OL	**10**		Reading Part II-Chapter 4 [Material 2];
6	**Chapter 6. Genetic Diversity** 1. Mutation and DNA damage repair 2. Genetic diversity 3. Measuring Genetic Diversity 4. Values of Heterozygosity 5. Processes eroding genetic diversity 6. Applications	**8**		Reading Part III-Chapter 7 [Material 2];
7	**Chapter 7. Genetic Mapping** 1. What is a Genetic map? 2. Types of markers for mapping 3. Types of Maps 4. Steps in Genetic Mapping 5. QTLs mapping 6. Positional Cloning 7. Marker Assisted Selection (MAS)	**10**		Reading Part II-Chapter 4 [Material 2];

8	**Chapter 8. Linkage Disequilibrium (LD)** 1. What is LD? 2. Linkage versus LD 3. How is LD measured? 4. Association Analysis 5. Mapping QTLs- The Traditional way 6. What is Association map?	**8**		Reading Part I- Chapter 1 [Material 2];
9	**Chapter 9. Forward Genetics** 1. Important Mutant population for gene function analysis 2. Methods for Generation of Mutant Population 3. Gene Cloning 4. Isolation of genes from a insertion mutant collection 5. Isolation of genes from deletion mutation population or germplasm: Chromosome walking	**10**		Reading Chapter 6 [Material 3];
10	**Chapter 10. Reverse Genetics** 1. Methods to assign putative gene function of ESTs 2. Approaches 3. Biological Function Analysis of Identified mutants 4. Isolation of mutants from deletion mutant collection	**8**		Reading Chapter 6 [Material 3]

Can Tho, April/25/2014

ON BEHALF OF RECTOR
DEAN/ DIRECTOR

HEAD OF DEPARTMENT