Prof. R.S. Chauhan

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

END SEMESTER EXAMINATION-2015

B.Tech BI IV Semester

COURSE CODE: 15BIIBI411 MAX. MARKS: 45

COURSE NAME: Genetic Engineering & Genomics

COURSE CREDITS: 4 MAX. TIME: 3 HRS

Note: *All questions are compulsory. Carrying of mobile phone during examinations will be treated as case of unfair means.*

Section A

Explain the following: (6x1.5= 9)

i) Genome organization in a plant cell versus animal cell?
ii) Essential components of a plasmid vector for cloning?
iii) Why di-deoxy nucleotides are used in DNA sequencing?
iv) What determines polymorphisms in a SSR marker & how?
v) Can RNAi be used in gene therapy?
vi) Can there by discrepancy in genetic versus physical distance?

Section B

1. Can you determine protein-based biomarkers for Alzheimer's disease through proteomics? (3.5)
2. What was the need of next generation sequencing (NGS)? How NGS has benefitted over Sanger sequencing of genomes? (3.0)
3. A bacterial genome has been sequenced. How would you identify potential drug targets in that genome? (3.5)
4. Why plasmid-based libraries are constructed in whole genome sequencing through two major technologies? How and why the outcome of sequencing would differ? (3.5)

Section C

1. Why a problem of allergy or adverse effects of a drug are encountered differently among a section of population/ How those can be minimized, if information about the drug target is available? (4.0)

2. How a technological input from a bioinformatician can help to improvise next generation sequencing (NGS)? What possible computational analysis would you do to obtain results from NGS reads, contigs, transcripts and scaffolds and why? (5.0)

3. What do you understand from comparative genomics? How knowledge of comparative genomics & bioinformatics in model organisms can be used in humans? (3.5)

4. Two tissue samples, one from a cancer patient and another from a normal are provided to you. How would you determine which genes are possibly involved in cancer disease, provided no genome sequence information is available? (5.0)

5. One bacterial disease has been detected in an edible food plant species. One disease resistant variety has been identified, however, that is not edible. Can you plan a strategy to clone the disease resistance gene and suggest its utilization in the development of transgenic disease resistant variety? (5.0)