JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT TEST -2 EXAMINATION- 2016

B. Tech IV Semester (Bioinformatics)

COURSE CODE: 15B11BI411

MAX. MARKS: 25

COURSE NAME: Genetic Engineering & Genomics

**COURSE CREDITS: 04** 

MAX. TIME: 1.5 HR

Note: All questions are compulsory. Carrying of mobile phone during examinations will be treated as case of unfair means. Assume suitable data if required.

- Q. 1. An EST coding for a portion of a protein with a therapeutic potential has been identified in a plant species. The protein need to be produced on a large scale in a bacterial culture. Design a suitable gene cloning strategy for the production of target protein in a bacterium.
- Q. 2. Whole genome sequence of a fungal species is given to you. How would you develop a molecular map based on SSR markers and what would be potential applications of SSRs?
- Q. 3. Why several cDNA libraries are constructed for a particular organism? What potential applications of cDNA libraries can be in biotechnology and bioinformatics fields? (4.0)
- Q. 4. A new genetic disorder is recorded in a particular part of India. How would you ensure whether it is due to genetic factors? What genomic strategy would you suggest to develop a DNA diagnostic for early detection of genetic disorder? (5.0)
- Q. 5. Why SNPs are considered to be precise markers? Which SNPs either from genic or nongenic regions are desigable and why? (3.0)
- O. 6. Differentiate the following:
  - i) Genetic/Physical distance
  - ii DNA probe/ Protein probe
  - ni) mRNA/tRNA
  - (v) Gene/ Operon
  - Western blot/RT-PCR
  - vi) Genomic clone/ cDNA clone
  - vii) YAC/ Cosmid
  - viii) E. coli genome/ Human genome
  - ix) Kinase/ Phosphatase
  - x) 3'-5' exonuclease/ 5'-3' nuclease

(10x 0.5 = 5.0)