BIRLA INSTITUTE OF TECHNOLOGY & SCIENCE, PILANI
FIRST SEMESTER 2016-17
Advances in Recombinant DNA Technology (BIOG561)
Comprehensive Exam

Duration: 3 Hrs   **M. Marks: 60**   **Date: 14. 12. 2016**

Close book   **M. Marks: 40**

[Q.1] Explain how Polymorphic DNA can be detected in the absence of sequence information mentioning the process involved and the advantages associated.   [7]

[Q.2] Describe the principle and process of SAGE method of expression profiling distinguishing clearly its salient features.   [7]

[Q.3] Tabulate the differences between spotted glass microarrays and spotted nylon macroarrays in terms of target features, substrate, probe, and hybridization conditions.   [7]

[Q.4] How can one establish gene order in a pathway by epistasis? Illustrate with a hypothetical example.   [7]

[Q.5] What is being talked about in each of the following statements?   [4 x 3= 12]

(a) From amongst spotted DNA arrays and oligonucleotide chips, one method requires pre-existing sequence information.
(b) Tentative functions can be assigned to proteins based on crude structural features
(c) Protein modifications can also be determined by mass spectrometry.
(d) Gaps in sequences occur with all genome sequence methodologies and need to be closed.

Open book   **M. Marks: 20**

[Q.1]. Mutation is a random process and happens continually in all parts of the genome. However, when protein coding sequences are compared between species (e.g., between *Arabidopsis* and *Brassica* and between rice and sorghum), they are often very similar and are described as being "conserved". How can sequences be mutating all the time and yet still appear to be conserved?   [4]

[Q.2]. An artificial chromosome could be a useful tool for plant breeding because it could be introduced and removed by crossing. If you were going to build an artificial chromosome: [4]
(a) What components would you need to include to insure faithful transmission of the chromosome from one generation to the next?
(b) What challenges might you run in to constructing those components?
(c) To what extent could you rely on components from other species, and how would you address any problems that might arise? For example, what data, sequence or proteins from *Arabidopsis* chromosome structure would be helpful in creating an artificial chromosome in maize?

[Q.3]. It is easy to find examples in which transposon insertions are detrimental to the host, but occasionally they are beneficial. Provide at least one situation in which the insertion of a transposon might result in a favorable mutation.   [4]

[Q.4]. Justify the following two related statements: (a) The hybridization experiments are a sort of competition, just like musical chair. (b) The microarray analysis is similar to northern blot process in the above aspect except that there are more than enough chairs to grab.   [4]

[Q.5]. A SNP is a position in the genome at which two or more different bases occur in the population, each with a frequency greater than 1%. In general, a SNP can be found by first aligning a set of overlapping DNA sequences and then identifying positions in the alignment at which the same base does not occur in any sequence. For example, the following five sequences appear to have a SNP at position 8.

GCATGCAaGCATGCAT
GCATGCAcGCATGCAT
GCATGCAaGCATGCAT
GCATGCAaGCATGCAT
GCATGCAaGCATGCAT

Do you think this evidence is enough to conclude that position 8 is a SNP? State all possibilities justifying your answer in each case.   [4]