Examrace

Biotechnology Question Bank, Molecular Evolution, Tissue Specific Genomes

14. What is molecular evolution? What are the observations regarding protein sequence variations Vis-a Vis evolution?

- Zucker Kandle and Pauling (1962) proposed a new approach of studying evolutionary relations using sequence variability. This initiated a new field called molecular evolution. The approach was based on the observation that functionality related homologous protein sequence were similar. It was observed that protein sequences undergo variation during evolution according to certain patterns such as:
    - Amino acids were not replaced at random but were altered with specific preferences e.g. amino acids of similar physicochemical characteristics were preferred one over another.
    - Some amino acids such as tryptophan, was generally not replaced by any other.
    - Based on several homologous sequences, a point accepted mutation (PAM) matrix could be developed.

15. What are the different areas which can be studied using microarray technologies?

This technique can be used to study the following areas:

- Tissue specific genomes.
- Regulatory defects in a disease.
- Cellular responses to environment.
- Cell cycle variations.
- Discovering drugs.

16. Write a short note on SNPs and their relevance as molecular tools?

- All human beings or Homo sapiens share 99.8% of their genomic sequence i.e. only 0.2% of the sequence varies between different individuals. One of the most important variations, particularly, because of its use as a molecular tool are point mutation called as SNPs or single nucleotide polymorphisms which occur both in the coding and non-coding regions of the genome. They occur in approximately, 1 in every 800 base pairs frequency.

- They occur when one base at a particular portion differs for different individual. These SNPs are proving to be excellent tools for DNA fingerprinting detecting susceptibility and predisposition to various diseases. Example: a single base difference in the ApoE gene is known to be associated with Alzheimer's disease.

17. What is meant by SNP map? How many SNPs occur in the whole genome?

- The position of SNPs on human DNA is depicted by SNP map. Around 1.6 to 3.2 million sites.

18. Give example of one disease, whose susceptibility has been located with the help of SNPs.

- Alzheimer's disease

19. In which direction is the DNA sequences always read?

5'--------3' directions

20. What does the C-value paradox indicates?

- The C-value paradox indicates that despite the increasing complexity in higher animals, the number of genes does not increase likewise.

Questions on Bioinformatics

1. What is bioinformatics?

- Bioinformatics is the management and analysis of biological information stored in data bases especially in late 1980's when researchers started to use computers as central sequence repository, from where the data could be accessed remotely.

2. What is Ref Seq?

- Ref Seq is a well verified database of mRNAs and proteins of human, mouse and rat. The data provided in Ref Seq has been used in many cases such as designing gene chips and describing the sequence features of the human genome.

3. What is the BLAST family of search tools?

- The "BLAST" acronym stands for Basic Local Alignment Search Tool. A given sequence in the database using matrices that specify scores to either "reward" a match or "penalize" a mismatch.
- Top scoring matches are ranked to distinguish between a similarity due to ancestral relationship or due to random chance. True matches are further examined thoroughly with other details accessible through Entrez and other tools available at NCBI.

4. What are the differences between directed and random sequencing?

- Directed Sequencing of BAC Contigs- BAC vectors are capable of carrying inserts as large as 80-100 Kb. The vectors are used to make Genomic Libraries. The overlapping regions are used to assemble the various insets into continuous contigs. The individual contigs are then sequenced by breaking the DNA and cloning into smaller vectors. Since this is a stepwise directed method it is also called as Directed sequencing.
- Random Shotgun Sequencing- In this method the genome is randomly broken up into sizes of 2-10 kb range and inserted into a vector (plasmids). These are then sequenced and ordered with respect to each other with the help of overlapping or common sequences.