

- ♦ Institute of Phytopathology

Examination questionnaire for EM8

Functional genomics of plant pathogens and plant animal pests

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- 1 . What are major features and differences between bacterial and fungal genomes?
- 2 . What is a representative genomic library?
- 3 . Why do we need a genomic library?
- 4 . Which cloning vectors are often used for the construction of a genomic library?
- 5 . What is a BAC clone and a BAC library?
- 6 . Explain the major features of a BAC-vector.
- 7 . What does the “next generation sequencing” mean?
- 8 . What is a genome “re-sequencing”?
- 9 . Tell the importance/applications of genome re-sequencing.
- 10 . Describe the principle of Sanger sequencing technique.
- 11 . What is a “pyrosequencing” and which next-generation sequencing technology is based on the pyrosequencing?
- 12 . Please tell the advantages/disadvantages of three different next-generation sequencing technologies in comparison.
- 13 . Describe a representative DNA/protein-based database,
- 14 . What does “BLAST” mean?
- 15 . Please explain two different alignment types.
- 16 . What is an E-value?
- 17 . Brief explain the program used for multiple sequence alignment analysis
- 18 . What is a phylogeny tree? and tell a program for its generation.
- 19 . Explain different types of phylogeny tree and their difference?
- 20 . What is a sequence “motif” and its importance in the sequence/genome analysis?
- 21 . Tell how to develop pathogen species-specific primers on the basis of genome analysis.