3. AIMS AND OBJECTIVES
For the comparative analysis of the genomes of the species the specific objectives of the study were stated as

1. Enlist and collecting the genomes of all the 12 strains of *Yersinia pestis*
2. Analysis of the genome properties and allocate differences among the enlisted species
3. Prediction Genome Islands by using Island viewer
4. Sequence based comparison of the among the species genome
5. Sequence based comparison within the strain
6. Prediction of Pathogenic Islands using GIST genomic island
7. Prediction of Functionally related PAI- Gene clusters using Cluster technology
8. Prediction of the functions of functionally related PAI-Islands using Domain prediction tool.