

Projects at SVA bacteriology, Bo Segerman

Project1:

Whole genome sequencing and characterization of *Clostridium botulinum* isolates from avian botulism outbreaks in sweden:

Clostridium botulinum produces a botulinum neurotoxin (BoNT). The BoNT is one of the most toxic proteins known. The avian form, type C causes paralyzation and leads to massive and painful death in Swedish poultry. The toxin gene is carried by a bacteriophage and the variability in the chromosomal genome sequences can be large. In this project we are sequencing the whole genome from a selected set of clinical isolates. The project involves DNA preparation for high throughput sequencing, closing gaps in the draft whole genome sequence, annotating the genomes and comparing them to each other and to related genomes. Projects can involve DNA preparation, PCR, sequencing and various forms of computer work.

Project2:

Whole genome sequencing and characterization of *Brachyspira intermedia*.

Brachyspira causes intestinal disease in pigs and birds. *Brachyspira intermedia* is closely related to *Brachyspira hyodysenteriae*, which has been sequenced by our collaborators in USA. The project involves similar steps as Project1 but the comparison between *Brachyspira hyodysenteriae* and *Brachyspira intermedia* is central. Other Spirochetes are also in pipeline for sequencing.

Comparative genomics projects:

For students with a high level of computer skills, more advanced projects in comparative microbial genomics (e.g. for human forms of *Clostridium botulinum*, *Bacillus anthracis*, *Yersinia pestis*, EHEC etc.) , genetic biomarker discovery and analysis of metagenomics sequencing can be formulated.

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