VFAR Activity Summary

January-April 2003

Mobile Genetic Elements as VFARs

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Plenary Session

May 13, 2003

VFAR Conference Call

April 23, 2003

- Continue nucleic acid and protein sequence searches of plasmids and pathogenicity islands
- Pilot: MSU database to contain genetic sequences, outbreak data, and organism data
- Pilot: Dr. Wassanaar's project is beginning with whole DNA sequence comparisons of viruses
- Potency/prevalence data – how to use:
  - ✓ ID, MID, ID_{50} or MLD?
  - ✓ Normal hosts, sensitive subpopulations?

Mobile Genetic Elements

- Regions of DNA copy themselves and can be shared between bacteria
- Pathogenicity islands (PAIs) and plasmids mediate virulence mechanisms
- PAIs may be responsible for the emergence of new virulent organisms
- Search underway for PAI genes that are shared among virulent organisms

Mobile Genetic Elements Update

- Plasmids
  - low sensitivity
  - conserved regions found in genes not directly related to virulence
- Pathogenicity Islands
  - single genes and proteins offer promise
  - results are supported by the literature
  - single genes not likely to define virulence

Bottom Line…

- Several pilot projects are in progress and we should have data from them soon.
- Have looked at two possibilities for VFARs: “islands” of genes looks promising as a VFAR candidate.

Next steps

- White paper on VFAR potential, potential of using genomics
- Universe Definition coming along; attributes discussion in detail
- How to incorporate VFARS in attributes
- 1 pm May 23, 1 pm June 16; maybe June