Stanford HIV Drug Resistance Database

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Outline

- Uses
- Types and sources of data
- Sequence analysis programs
- Access policies

Uses

- Surveillance:
  - Which mutations should be used to track transmitted drug resistance?
  - What are the most common mutations associated with virological failure on different regimens?
- Research:
  - How does resistance data in one study correlate with data from other studies (different populations, different treatments)
  - Identify gaps in the published literature or publicly available sequences
- Clinical:
  - Interpreting genotypic resistance tests

Types of Data

- Genotype-Rx:
  - Sequences linked to the treatment of the person from whom the sequenced virus was obtained.
  - Mutation percentages by treatment and genotype
- Genotype-phenotype:
  - In vitro susceptibility data on sequenced isolates: site-directed mutants and clinical isolates
- Genotype-clinical outcome:
  - Virological response to a new treatment regimen in patients with a known baseline genotype, virus level, and past treatment history

Sources of Data

- GenBank sequences:
  - Annotated with data from accompanying publications primarily: Country, year of isolation, source of sample, sequence type, treatment history
- PubMed:
  - Request sequences as well as relevant annotation directly from authors. Occasionally assist with GenBank submission
- Collaborative meta-analysis:
  - May include additional studies that are not in GenBank or PubMed

Sequence Analysis Programs

- Genotypic resistance interpretation:
  - Input: Web page, Automated web service
  - Output: Web page, spreadsheet, XML
- Additional programs:
  - CPR, HIVSeq, HIVAlg

Access Policy

- Free access to pages with frequently updated data summaries and to pages with user-defined queries.
- Access to additional types of data as part of a collaboration or if the effort involved is not too large.
- Software: migrating to open-access platform for distribution of several of the sequence analysis programs