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Introduction to Genotyping

Course Objectives

By the end of the seminar, participants will be able to:

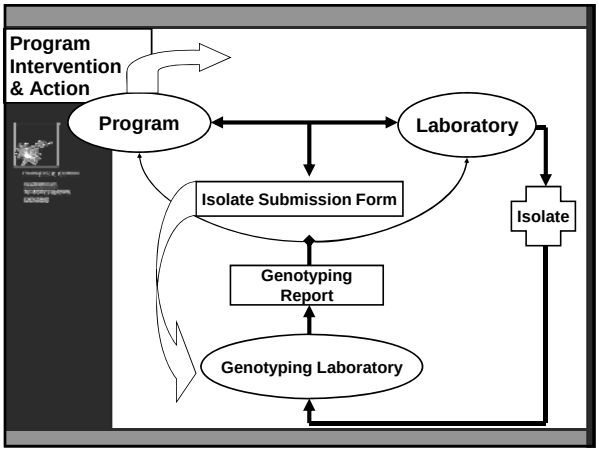
- describe the national tuberculosis (TB) genotyping program
- describe the use of genotyping data in TB control
- describe how to use genotyping data for outbreak surveillance
- describe how to apply genotyping data to ongoing contact investigations

Agenda

Time	Session	Speaker
11:00-11:05	Course Overview	Kelly Smith
11:05-11:10	Introduction to Genotyping	Lisa Pascopella
11:10-11:20	National Genotyping Program	Patrick Moonan
11:20-11:50	Practical Applications of Genotyping	James Watt
11:50-12:05	Case Presentation: Medium Incidence Setting	Wendy Cronin
12:05-12:15	Case Presentation: Low Incidence Setting	Christine Hahn
12:15-12:25	Question & Answer Period	Faculty Panel
12:25-12:30	Course Wrap-up	Kelly Smith

Genotyping May Be Used For:

- Surveillance
  - Detect potential outbreaks
  - Detect false-positive cultures
  - Rule out suspected outbreaks
- Understanding transmission patterns in your jurisdiction
- Program evaluation and improvement



Genotyping Requires Communication Between Laboratory and Program

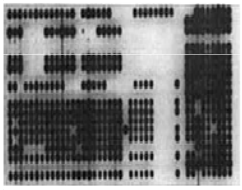
- Laboratory component
  - Specimen submission to genotyping laboratory
  - Genotyping methods performed in genotyping laboratory
  - Genotyping reports to programs
- Program component
  - Share patient information with laboratory
  - Receive and interpret genotyping reports
  - Decision to act on genotyping results

Genotyping Methods

- Two PCR-based methods: Spoligotyping and MIRU-VNTR
- Converted to numeric code that designates fingerprint pattern
- If a PCR-genotyping match is found, RFLP IS6110 typing may be requested

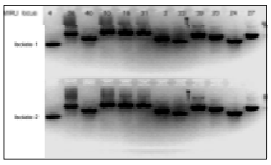
Spoligotyping
(Spacer Oligonucleotide Typing)

Identifies strains based on the presence or absence of 43 spacer sequences found in the Direct Repeat (DR) region of the *M. tuberculosis* genome



MIRU-VNTR
(Mycobacterial Interspersed Repetitive Units-Variable Number of Tandem Repeats)

Identifies strains by the difference in the number of copies of tandem repeats at 12 different regions of the genome



Fingerprint Designation

Spoligotype:

Original banding pattern	■	■	■	■			■	■			■	■	■	■	■ …
Binary code	1	1	1	1	0	0	1	1	0	0	1	1	1	1	1 …
14+1 grouping	111			100			110			011			111		…
Octal designation (15 digit)	7			4			6			3			7		…

MIRU type:

MIRU locus name	02	04	10	16	20	23	24	26	27	31	39	40
No. of repeats	2	3	2	2	3	4	2	5	3	3	2	2
MIRU designation	232234253322											