GENType: New Genotyping Terminology to Integrate 24-locus MIRU-VNTR

Since the start of the National Tuberculosis (TB) Genotyping Service (NTGS) in 2004, TB genotypes have been defined as a unique combination of spoligotype and 12-locus MIRU-VNTR results. Each result combination has been assigned a PCRType. PCRType is designated as "PCR" followed by give digits. PCRTypes are assigned sequentially to every genotype identified in the United States. For example, the spoligotype result 000000000003771 with the 12-locus MIRU-VNTR result 223325173533 was the second genotype seen in the United States and was designated as PCR00002.

In April 2009, MIRU-VNTR analysis was expanded from 12 loci to 24 loci. The complete set of 24 loci is referred to as '24-locus MIRU-VNTR.' The additional 12 loci (reported in TB GIMS as "MIRU2") increase our ability to distinguish between strains of *M. tuberculosis* and better identify chains of transmission. In order to fully integrate 24-locus MIRU-VNTR into routine use, a new national naming system, **GENType**, has been developed.

What is a GENType and how is it assigned?

- Each unique combination of spoligotype and 24-locus MIRU-VNTR results has been assigned a GENType, formatted as "G" followed by five digits. For example, G00010 refers to the unique combination of spoligotype: 000000000003771 and 24 locus MIRU-VNTR: 223325173533 444534423428.

- Unique combinations of spoligotype and 24-locus MIRU-VNTR results will be routinely and sequentially assigned GENTypes as they are identified.

- GENTypes are not assigned to isolates without 24-locus MIRU-VNTR results. (This includes most isolates that were genotyped before April 2009.)

- A single PCRType may have multiple GENTypes assigned, since a single PCRType can include multiple 24-locus MIRU-VNTR patterns. However, each GENType has only one PCRType. (See Table below.) For example, Line #1 and Line #3 are both PCR00002, but represent two different GENTypes (G00010 and G00012) due to different 24-locus MIRU-VNTR results.

Comparative Examples for GENType and PCRType

Line#	GENType[†]	PCRType	Spoligotype	24-locus MIRU-VNTR	
1	G00010	PCR00002	000000000003771	223325173533	444534423428
2	G00011	PCR00015	777776777760601	224325153323	444234423337
3	G00012	PCR00002	000000000003771	223325173533	445644423328
4	G00013	PCR00016	700036777760731	222325143223	434534412334
5	G00014	PCR00051	776037777760771	223125163324	242434223525

† Unique combination of spoligotype and 24-locus MIRU-VNTR

How is GENType pronounced?

- GENType is pronounced like the woman's name 'Jen' followed by the word 'type.'

What is a meant by a percent sign (%) or a dash (-) in a MIRU-VNTR result?

- A percent sign (%) at a particular locus means that the result could be one of two possible results (e.g., a laboratory testing identifies an isolate with two possible MIRU2 results: 443324232614 or 443324232514; therefore the result will be shown as 443324232%14). This type of mixed result used to be represented by an asterisk (*).

- A dash (-) at a particular locus means that the result is unknown or cannot be determined (e.g., the MIRU-VNTR result would be: 44332-423261).

CS232896

What happens to GENType when MIRU-VNTR results include a percent sign (%) or a dash (-)?

- GENTypes are assigned for all isolates with 24-locus MIRU-VNTR results, even if they contain a percent sign or dash.

How is a "genotype cluster" defined using GENType?

- A genotype cluster should be defined on the basis of GENType.
- All patients with a single GENType are part of the same genotype cluster.
- Patients with the same PCRType, but multiple GENTypes, should not be considered part of the same genotype cluster; they are not likely to represent a single chain of transmission.

Is PCRType still available?

- PCRTypes will continue to be assigned to Spoligotype and 12-locus MIRU-VNTR patterns until the use of GENType becomes routine practice.
- Both GENType and PCRType are available in TB GIMS for searches, reports, and maps.
- A table is available in TB GIMS to cross-reference GENTypes and PCRTypes; the format is similar to the example table above.

How do I find out the GENTypes for the clusters in my jurisdiction?

- There are several ways in TB GIMS that you can find the GENType for a specific cluster or generate a list of all the GENTypes in your jurisdiction.
- Go to the Genotype or Patient Results searches and search by a PCRType or Cluster Name. The GENType is shown in the line list in the column right before PCRType.
- Go to "Training Resources" and scroll down to "Additional Resources." The Excel file "GENType Reference Table" includes all GENTypes and their corresponding PCRTypes. Of note, this file will only be updated with each new TB GIMS release; thus, it may not be completely up to date.
- Go to "Generate Reports" and select "State List of GENTypes." This report shows all the GENTypes in the state and their corresponding PCRType and Cluster Name2.

Additional information

- For general information on TB genotyping, please see the TB genotyping fact sheet: http://www.cdc.gov/tb/publications/factsheets/statistics/genotyping.htm
- For information on TB GIMS, please see the TB GIMS fact sheet: http://www.cdc.gov/tb/publications/factsheets/statistics/gims.htm
- For more information on TB genotyping, please contact tbgenotyping@cdc.gov