SEARCHES IN TUBERCULOSIS GENOTYPING INFORMATION MANAGEMENT SYSTEM (TB GIMS)

National Centers for HIV/AIDS, Viral Hepatitis, STD, & TB Prevention
Centers for Disease Control and Prevention

During this presentation we will review the different search options in the Tuberculosis Genotyping Information Management System, or TB GIMS. The target audiences for this course are TB GIMS Super and Standard Users.
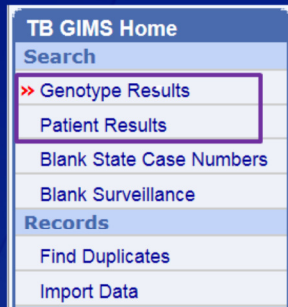
Objectives

At the end of the presentation, participants will be able to

☐ **Describe how to use search functions in TB GIMS**

☐ **Explain the difference between**
 - Genotype Results and
 - Patient Results

☐ **Search for data, create and export line lists of Genotype and Patient Results for your jurisdiction**
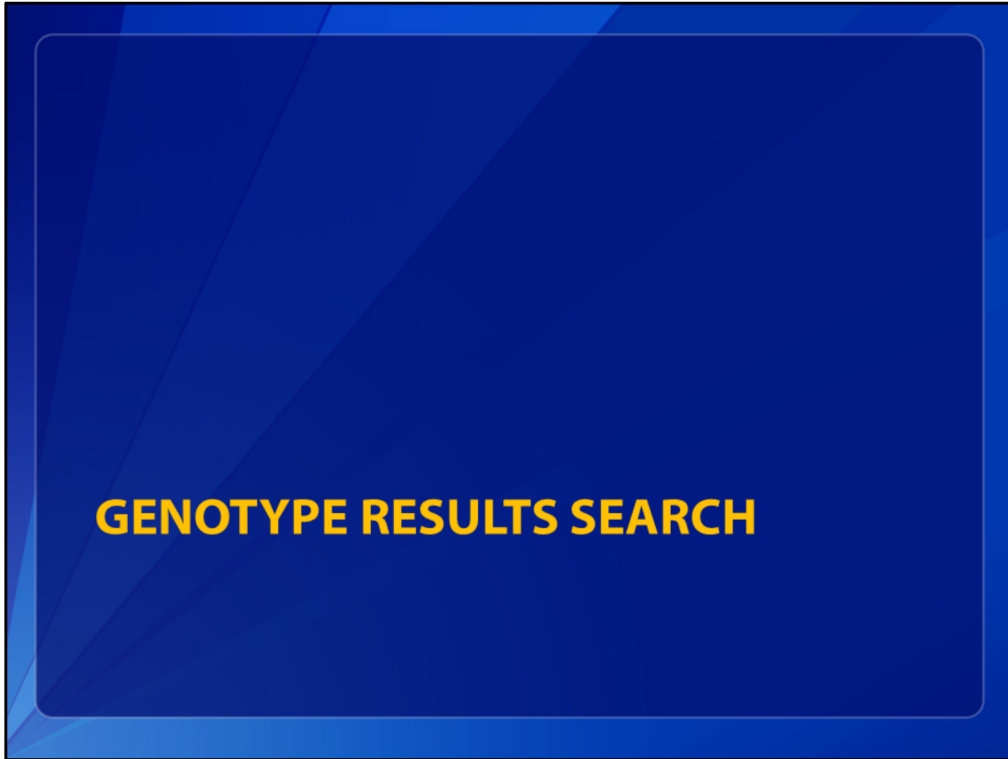
By the end of this presentation, you will be able to describe the search options available in TB GIMS and how they can be used. You will be able to explain how data in Genotype Results and Patient Results differ. And you'll be able to perform various searches for information in each of these applications and create lists of isolates and patients in your jurisdiction. You can also query on Genotype and Patient Results in TB GIMS to view a single record or to view genotype clusters in your jurisdiction. Then you can export the data for further analysis.

Most TB GIMS users are typically TB program managers, TB controllers, nurse case managers, nurse consultants, public health advisors, epidemiologists, and other public health staff who use genotype data in routine TB control activities. Access to TB GIMS is limited to registered users and is coordinated by a designated State TB GIMS Administrator. Standard Program Users are not able to edit data in the system; however, they do have access to both Genotype Results that have been entered into GIMS, and Patient Results that have been linked to genotype records for your jurisdiction. The small purple box on the left shows where you can find Genotype and Patient Results Search Options on the homepage of TB GIMS.

GENOTYPE RESULTS SEARCH

Now, how to search in Genotype Results.

To search for isolates that have been processed and have results, click on Genotype Results (the small purple box in the top left corner). This screen shot shows the Basic search options in Genotype Results on top. Your state will automatically be selected. If you would like to list this information just for one county or region, you may choose that, as well. You can click on the County variable for an alphabetical list of counties in your state that have results of genotyped isolates. You can search any of these variables, including Date Type (we'll look at those in a moment), or any of the actual Genotype Results (Spoligotype, MIRU, MIRU2, Submitter Number or Accession Number). If you want to see all cases in your state that had a certain GENType or PCRType, you would enter that specific GENType or PCRType and click Find. And the Advanced Options are on the lower part of the screen. You may leave all search criteria blank to view all entered Genotype Results for your jurisdiction, or you may select any combination of the search criteria.

Search for a Genotype Result Using

❑ **Submitter Number**
- Unique identifier that the state public health laboratory assigns before submitting the isolate for genotyping (e.g., 4677886656)

❑ **Accession Number**
- Unique identifier that genotyping laboratories assign to each isolate as they are received from state laboratories (e.g., 15RF9999)

The Submitter Number is a unique identifier assigned to isolates by the submitting laboratory before sending it to the genotyping laboratories. The Accession Number is a unique identifier that the genotyping laboratories assign to each isolate as they are received from state laboratories. Accession Numbers will be available in TB GIMS after genotyping results are entered by the CDC laboratory. These searches would yield only one record.

In order to find a Genotype Result using Submitter Number or Accession Number you would enter that number in the corresponding field on the Basic Search page. This will show you the one record with that Submitter or Accession Number, whichever one you entered. Let's search for Accession Number 16RF2110. When you type the Accession Number in that variable, click Find, and this is what you would get.

The one record with that Accession Number is listed here (the Accession Number is in the small purple box). This are fake data for confidentiality reasons. After you click Export, you will get a message that says, 'You are creating a line-listed patient-level dataset. Ensure that you maintain strict confidentiality of this information as you would protect other patient-level records.' Please be sure to maintain confidentiality of these data at all times.
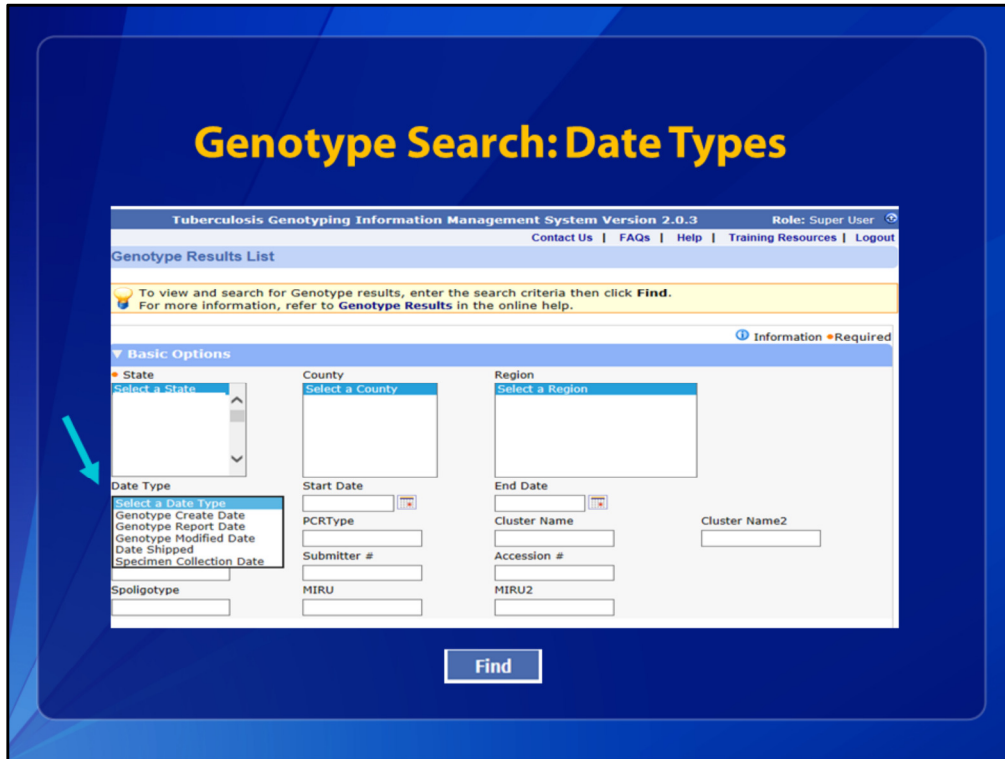
If you would like to see Genotype Results for a specific date, you would look at Date Type pointed out by the arrow. These are the Options: Genotype Create Date, Genotype Report Date, Genotype Modified Date, Date the Specimen was Shipped, and the Date the Specimen was Collected.

Date Types in Genotype Results

- **Genotype Create Date**
  - Date the genotype result was first completed (Spoligotype and MIRU)

- **Genotype Report Date**
  - Date that the genotype result was first reported to the state TB program (MIRU* and MIRU2)

- **Genotype Modified Date**
  - Date changes are made to any of the following: Spoligotype, MIRU, MIRU2, GENType, PCRType, or State Cluster Name fields

* Mycobacterial interspersed repetitive units

Here are three definitions for Genotype Dates that you can use for searching. The Genotype Create Date is the date the genotype result was first completed by the CDC lab. This is when the spoligotype result is added to the MIRU. If there is no Genotype Create Date, that means the results are pending. Genotype Report Date is the date that the genotype result was reported to the state TB program by the Michigan lab. This is when the two MIRU results are available. Because Report date is an RVCT variable (on the Report of Verified Case of Tuberculosis), isolate results must be successfully linked to patient surveillance records to be included in Genotype Results. When changes are made to any of the genotype result variables (Spoligotype, MIRU, MIRU2, GENType, etcetera), a date is assigned by TB GIMS, called the Genotype Modified Date.

Genotype Results and Information Icon

Another helpful function of TB GIMS is little light blue circled "i' for information. When you can hover the mouse over the "i" by each record for more information about that specific record, this yellow box will appear with detailed information about that isolate record. In Genotype Results, the data are the GIMS ID number, which is a unique identifier assigned to each isolate by TB GIMS upon creation of the record within TB GIMS. Also listed are The State, County, Specimen Collection Date, Submitter Number, Date Shipped, Accession Number, etc. You can also sort by any variable on this page by clicking on that variable. For example, if you click on County, you will get an alphabetical list of all Counties in your state with Genotype Results. This slide is mainly to show the value of the yellow information box.

When new Genotype Results are available, TB GIMS will send you this email, which says, 'New Genotyping Results' as of (a certain date, here it's April 2, 2016, 'are now available for review.' Let's see what is recommended when you receive this type of email.

To find those new results, use the Genotype Create Date under Basic Options. The Start Date defaults to 01/01/2005, but you could enter the date on the email, 4/2/2016. The End Date will be that day's date, this one is May, 2, 2016. Leave the End Date as it is. Then just click Find.

You can see there were three new genotype results all received on April 2, 2016. for this jurisdiction. Where it says Page 1 of 1 on the top line (where the arrow is), that means this is the only page of results. You'll see the first 15 records, and if there are more than 15, you use this arrow to go to the next page. You can also sort by any variable on this list by clicking on that variable name. You could export this information using the button at the bottom of the screen. Let's look for Pending results.

The Advanced Options, indicated by the purple box in the lower half of the screen, differ somewhat between Genotype Results and Patient Results. The advanced options here in Genotype Results are Linked, Linkable, Reason Not Linkable, and Pending results. Linked isolates means that the isolates have been linked to a patient surveillance record. Linkable indicates whether the isolate can and should be linked to a patient surveillance record or not. Linkable Unknown is when the isolate corresponds to a patient record that is not a TB case (e.g., false-positive culture result). If the isolate is Not Linkable, the choices are: Out of State, Out of Country, Not a Case, or Other. You can view a list of all Genotype Results by leaving all this search criteria blank and clicking Find.

To find Genotype Results that may be Pending, select Yes under Pending Results and click Find.

And you will get a screen that looks like this, with how ever many Genotype Results are pending in your state or in a certain county. This shows that there are two records with Pending Spoligotype results in this county. The Spoligotype fields are blank. Also later in the list if you scroll right, you will see the GenoStatus says, "Pending" for all of these records. That is because it takes a week after MIRU and MIRU2 results for Spoligotype results to be entered into the system.
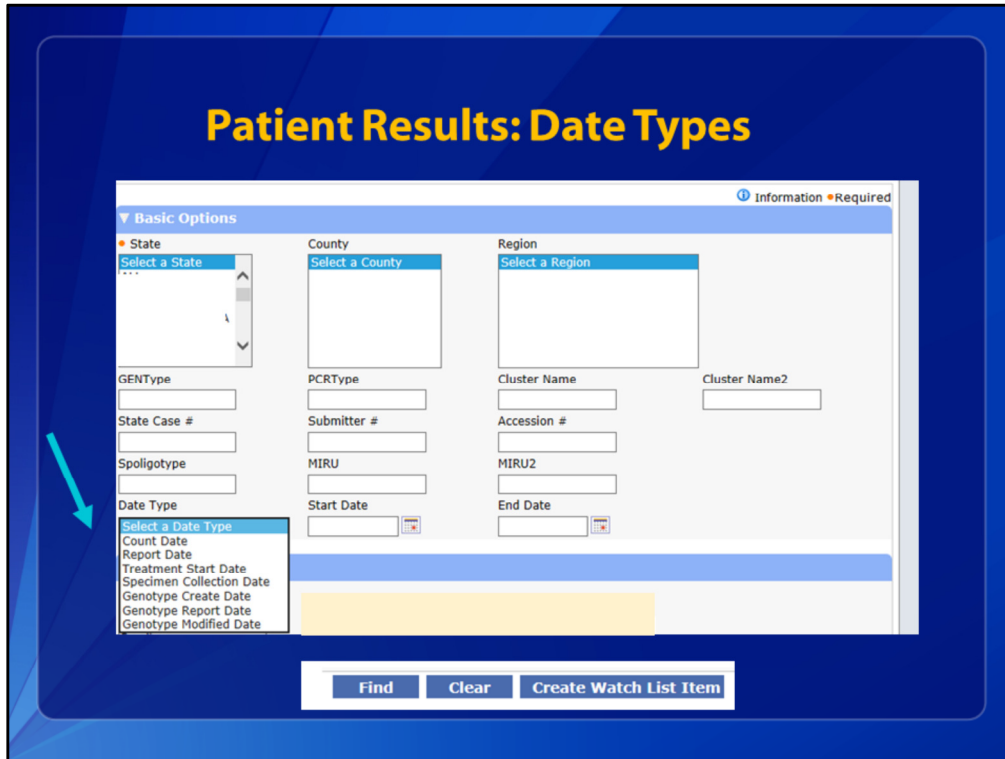
PATIENT RESULTS SEARCH
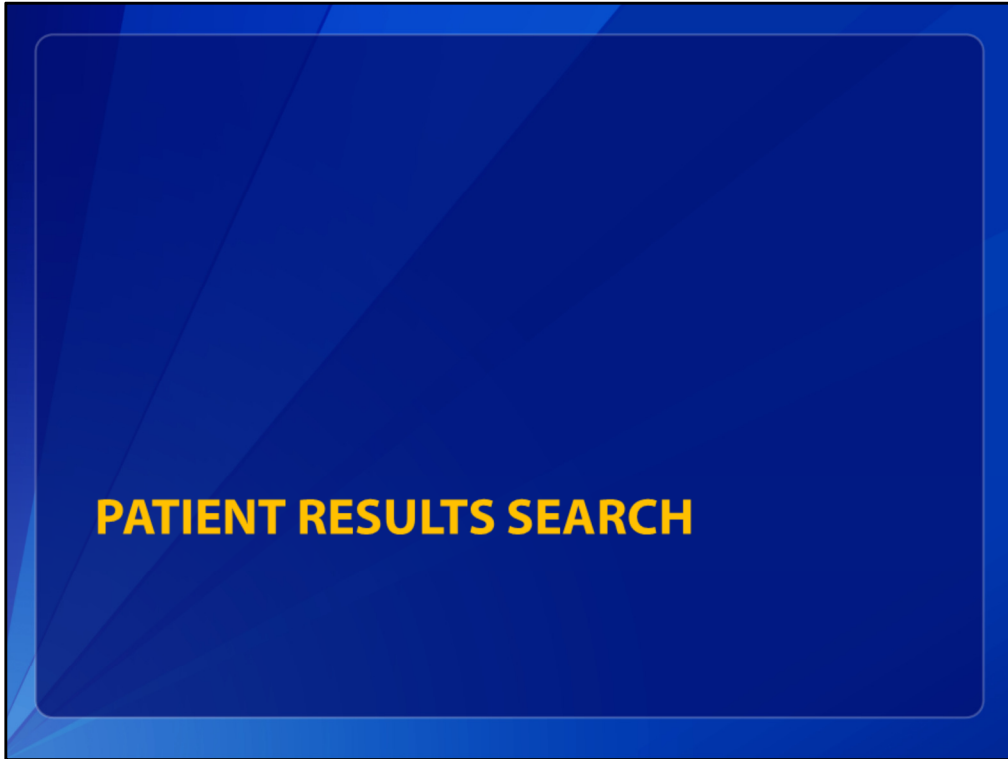
Now for searching in Patient Results.

To be included in Patient Results, isolate results must be successfully linked to a patient surveillance record. This purple box outlines the Basic Search Options for patient results. You can view a list of all Patient Results by leaving the search criteria variables blank and clicking Find. You can see these options are very similar to those in Genotype Results. However a few of the Date Types differ and those in Patient Results are related to surveillance records and date fields from the RVCT, or Report of a Verified Case of Tuberculosis.

Patient Results: Date Types

There are three additional Date Types for Patient Results than in Genotype Results. The Count Date and Report Date are the first two date criteria listed. The others are Treatment Start Date, Specimen Collection Date, Genotype Create Date, Genotype Report Date, and Genotype Modified Date. Dates in Genotype Results had similar options, but also included Date the isolate was Shipped, rather than Treatment Start Date, which is here for patients. We'll see definitions for these dates on the next two slides.

Patient Results: Date Type Definitions

❑ **Count Date**
- Date the count authority verified the case as TB and included it in the official case count

❑ **Report Date**
- Date that a health department first suspected a person might have TB or the date the health department first received notification from a healthcare provider that a person had suspected TB

The Count Date represents the date that the count authority in a state verified the case as TB and included it in the official case count for that jurisdiction. The Report Date is the date that a health department first suspected that the person might have TB or the date the health department first received notification from a healthcare provider that a person had suspected TB.

Patient Results: Date Type Definitions

❑ **Treatment Start Date**
- Date the patient began therapy for TB disease or suspected TB disease

❑ **Specimen Collection Date**
- Date the clinical specimen was collected from a patient

Treatment Start Date is the date the patient began multidrug therapy for TB disease or suspected TB disease. The Specimen Collection Date is when the clinical specimen (which produced the submitted isolate) was collected from a patient.
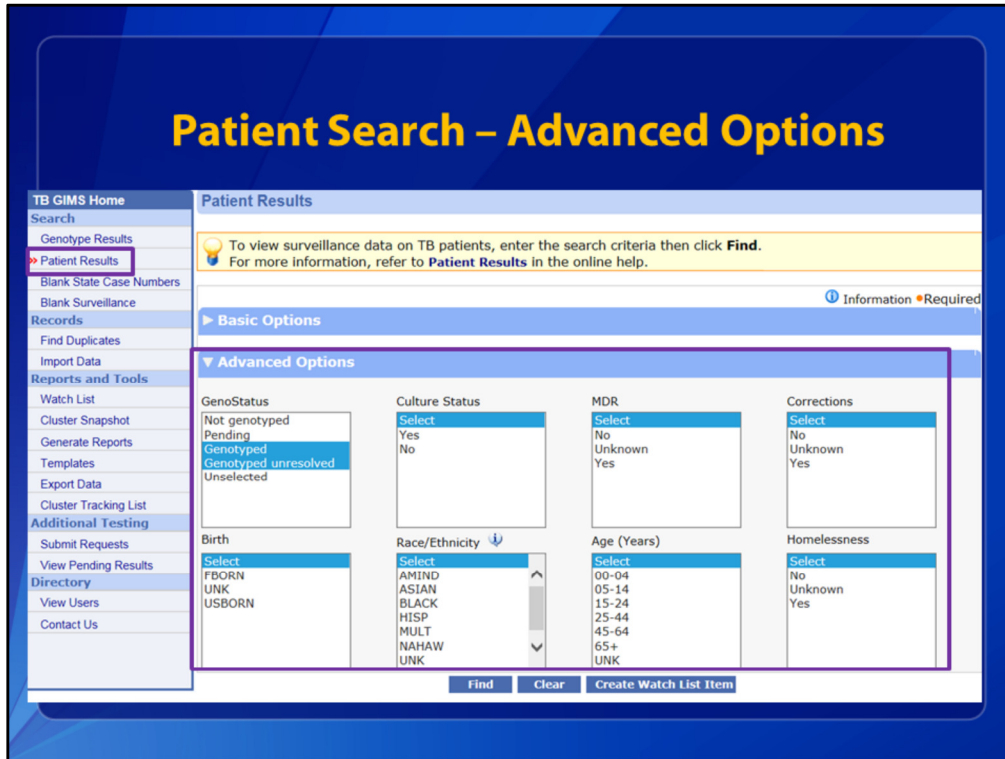
Advanced Options in Patient Results are different than the Advanced Options in Genotype Results. For one, there are several more options to use. With the GenoStatus variable in the middle left of the screen, you can see which patients do not have genotype data (Not Genotyped), which ones have Pending results, or whether the result is Genotyped Unresolved. We'll see that definition on the next slide. You can search to find patients who have multidrug-resistant, or MDR TB, those of a particular race/ethnicity or age group, those who were incarcerated at TB diagnosis (under the Corrections variable) or those who experienced Homelessness during the 12 months prior to TB diagnosis.

For GenoStatus, options include: Not Genotyped, Pending, Genotyped, and Genotype Unresolved. It defaults to the last two options, both Genotyped and Genotyped Unresolved. Unresolved means that more than one isolate was submitted for this patient, and the record has been reviewed by the Program Super User, but they have not made a final determination about which genotype result should be associated with that specific patient record.

Find the Number of US-born Children with TB in Your Jurisdiction

❑ **In Patient Results/Advanced Options**
1. Choose USBORN under Birth
2. Choose the first two Age ranges (00–04 and 05–14)
3. Click Find
4. Then Export

In order to determine the number of US-born children with TB in your jurisdiction, you would look under Patient Results (because this is about a case patient, not an isolate). In the Advanced Options click USBORN under the Birth variable. And under the Age variable, click the age ranges of 00–04 and 05–14 years.

These are the Advanced Options for Patient Results. So again, under the Birth variable, choose USBORN, and choose the first two Age variables for children aged 0 to 14. Hold down the Shift key to choose multiple options. When you click Find, you will see something like this.

You can see there are 34 records in this search (three screens of results). That is, there are 38 US-born children with TB in that jurisdiction. The City, County and Zip Code will not be blanked out for your search, but they are blanked out here for confidentiality purposes. When you click Export, it makes an Excel file of all the records in your search.

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Excel List of US-born Children with TB

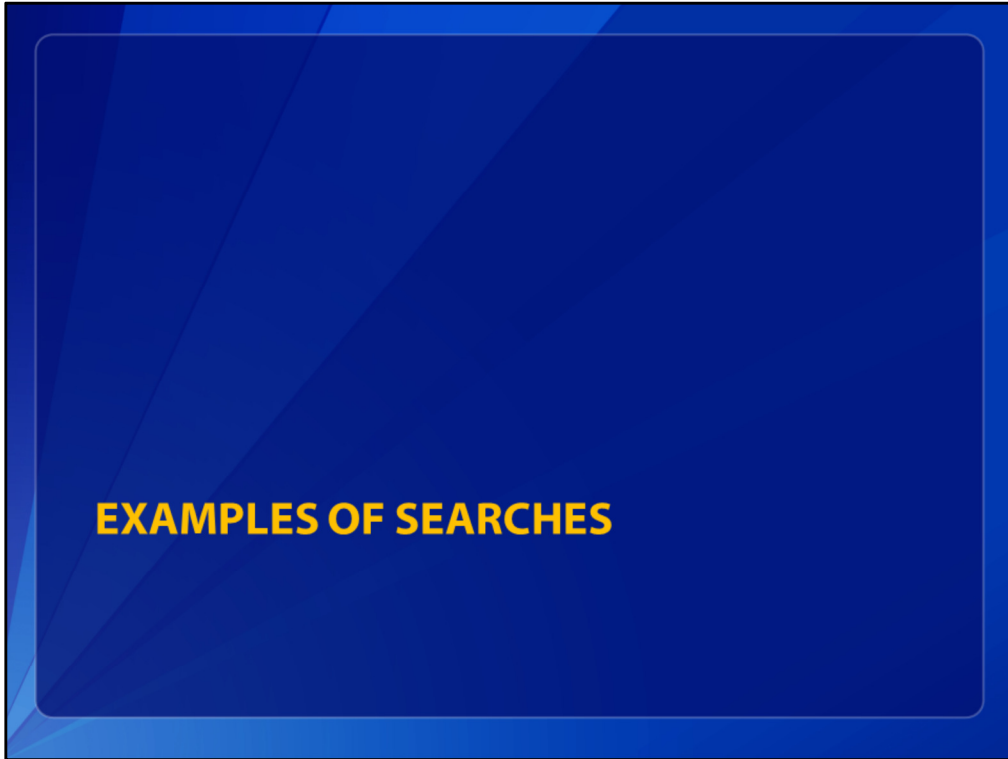|	DJ	DK	DL	DM	DN
1	MOVED	THERREAS	ORIGIN	RACEHISP	AGE3
2			USBORN	HISP	00-04
3			USBORN	BLACK	05-14
4	N	COMPLETED	USBORN	BLACK	00-04
5	N	COMPLETED	USBORN	BLACK	00-04
6	N	COMPLETED	USBORN	BLACK	05-14
7	N	COMPLETED	USBORN	HISP	00-04
8	N	COMPLETED	USBORN	BLACK	05-14
9	N	COMPLETED	USBORN	BLACK	05-14
10	N	COMPLETED	USBORN	BLACK	00-04
11		COMPLETED	USBORN	WHITE	00-04
12	N	COMPLETED	USBORN	HISP	00-04
13	N	COMPLETED	USBORN	BLACK	05-14
14	Y	COMPLETED	USBORN	BLACK	05-14
15	N	COMPLETED	USBORN	WHITE	00-04

And this is what the list Excel list looks like. Many of the previous columns are hidden (again, for confidentiality purposes)his is to show the first 15 of the 34 cases of children with TB in your state. All Genotype Results will have the GIMS ID, the State, the Report Date, the State Case Number, and many other variables. You would scroll across this list to view all of the data.

Patient Results and Information Icon

And here is an example of the Information icon for Patient Results. When you hover your mouse over this small blue icon with an "i" for information, this yellow box appears. These data are somewhat different from Information in the yellow box in Genotype Results, because these results are for patients, not isolates. You have the case patients' demographics in this information box (as opposed to Linked and Linkable isolates and those with Pending results). The last variable listed is Status to indicate if the patient was alive or dead at diagnosis. Again, you can click on any of the variable names to sort the rows.

EXAMPLES OF SEARCHES

Now we'll see some examples of searches in both Genotype and Patient Results.

Wildcards

Wildcard	Function	Example
*	Matches any number of characters.	Enter *235 to list all MIRU results with 235 in the sequence of digits.
Blank	Same as asterisk. Matches any number of characters. It can be used as the first or last character in the character string.	Enter "(blank space)2015" in State Case Number for all cases reported in 2015.
%	Matches any number of characters. You can use the percent sign anywhere in a character string.	Enter "%235"to list all MIRU/MIRU2 results with %235 in the sequence of digits.

TB GIMS has a feature called "Wildcards." A Wildcard is a special symbol that stands for one or more characters in a string of results, and they can help to narrow your search. These are the three Wildcard characters: An asterisk, a blank space, and a percentage sign. You can search for results using an asterisk (*) in place of any combination of characters in the State Case Number, Spoligotype, and MIRU fields. Leaving a field blank acts the same as an asterisk. A blank matches any number of characters. It can be used as the first or last character in the character string. The percent sign can be used to search for a string of characters in MIRU/MIRU2 results to show all isolates that have the same or similar character string.

To search for any MIRU result that contains the string of a certain character and then 322 at the end, you would type "22422515*(asterisk)322" into the MIRU field (upper left screen shot in Basic Options you can see the asterisk before 322). The screen shot on the lower right shows the results of both "224225153322" and "224225154322" (shown in the purple box). This search would also show any other MIRU results that have these characters (some character and then 322) at the end of the string.

To find all patients diagnosed in 2015, in State Case Number search variable, enter a blank space (just hit the space key), then type 2015. It's not easy to tell here, but there is a blank space in front of 2015 in the State Case Number variable. There were five patients diagnosed in 2015 for this small (fake) state (with very few cases).

To determine if your state has any isolates with Pending results you would go to Patient Results under Advanced Options. Choose Pending under the variable, GenoStatus. Then click Find.

And you will get a screen that looks like this, with how ever many Genotype Results that are pending in your state or in a certain County. This shows that there are seven records in this County with Pending Genotype Results. The GenoStatus says Pending, so the MIRU and MIRU2 results may be there, but GENType, PCRType, and Spoligotype results further to the right in this line list would be blank.

To find the number of isolates that were Not Linked in your jurisdiction, you go to Genotype Results, Advanced Options. You would choose No under the Linked variable and click Find. This will give you a list of all isolates that are Not Linked to patient surveillance records in your state or county.

It would look like this. See all of the records have an N for No, Not Linked.

To search for all homeless TB patients in your state (or a county), you would go to Patient Results under Advanced Options. For the "Homelessness" variable, select Yes. Then click Find. No other variables are needed for this search. If no dates are specified in Basic Options, you will get all of the records that are in the database for your jurisdiction.

It would look like this. Here you can see all of these patients who have Y for Yes, they were homeless within 12 months prior to TB diagnosis. This state has 91 homeless TB patients (that is in red). There are seven pages of results (as you can see in the top right corner).
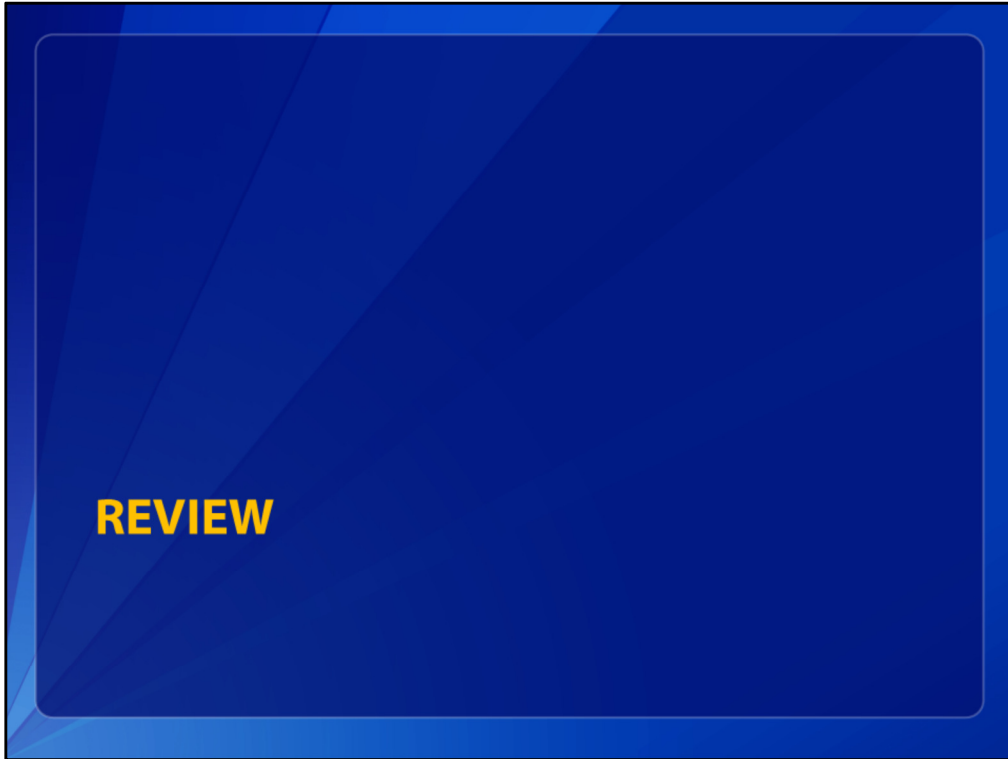
REVIEW

Now let's review some of the main points of Searching in TB GIMS.

Number of Records in Genotype Results Versus Patient Results

❑ **Genotype Results** search provides a line list of isolates with genotype results

❑ **Patient Results** search provides a line list of patient records with genotype results that have been linked with their surveillance record
- Because TB patients may have multiple results and multiple isolates may be submitted, Genotype Results will always have more records than Patient Results

First, every isolate in TB GIMS that has a genotype result can be found in Genotype Results. Patient Results search provides a line list of patient records with genotype results that are selected to be linked with its surveillance record based on the criteria entered on the search screen. Because TB cases may be transferred from other jurisdictions, or TB patients may have multiple results for multiple isolates, which may have been submitted inadvertently, Genotype Results will always have more records than Patient Results.

Take Home Points

❑ **Standard TB GIMS Users can access, search, and manage, and export data using**
   ▪ Genotype Results to list all isolates
   ▪ Patient Results to list a single genotype result linked to one patient surveillance record

❑ **Searching is easy in TB GIMS**

We are almost finished. These are the Take Home points for this training. Standard TB GIMS users can search for information in Patient Results or Genotype Results. In Patient Results, only one genotype result is linked to a patient surveillance record. You learned how to find and export data and what to do when you receive an email indicating that your state has new Genotype Results. And I hope you will agree that Searching in TB GIMS is easy.

Finally, we would like to announce a training developed in early 2016 that is now available for public use, called, Introduction to TB Genotyping. This is a 28-slide Powerpoint presentation, with an accompanying Facilitator Guide with notes for the instructor. The course is available from either of these websites to those who want to learn the basics of TB genotyping, how genotyping results are obtained, and how TB genotyping can be useful in TB control. Find TB Resources is a searchable database of national and international TB education and training resources.

And that concludes the presentation. If you have a question about TB GIMS after this session, please either email the DTBE support mailbox or the genotyping mailbox, or call this phone number. If you send an email, please put the words, TB GIMS in the subject line for a quicker response. Thank you.