



Explanation of Changes

The Specify Project has updated Specify's database schema changes to more effectively handle information associated with tissue preparations, extracts ("material samples"), and Sanger method DNA sequences, DNA sequencing runs, and DNA primers. The changes were made in collaboration with the GGBN Project to comply with the GGBN DarwinCore Material Sample extension. Specify 6.6.06 and 7.3.0 also add support for Next Generation Sequencing data lodged with NIH, Dryad, and other community data archives and aggregators. The appropriate NIH SRA identifiers have been added to the schema for linkouts to those repositories.

Prior to the Specify 6.6.06 and 7.3.0, v2.3 of the database schema related Collection Object as 1-to-Many with DNA Sequence. With the increased in tissue collecting for DNA extraction and sequencing, the Specify schema needed to accommodate additional cataloging and usage scenarios. Within each table shown here, a few sample data fields are shown. Complete table and field descriptions are available. In this updated v2.4 schema, a tissue sample would be a Preparation (of a Collection Object), with a count, description, and a PreparationType of "Tissue" (from a look-up table of Prep Type names, not shown). Detailed metadata about the tissue itself would be described in the Preparation Attribute table (not shown). A DNA extract sample derived from a tissue would be recorded in the Material Sample table, using GGBN Material Sample Vocabulary data elements.

Any Specify collection using the DNA Sequence table in its current relationship to Collection Object in schema v2.3 and earlier that wishes to use the new relationship with the Material Sample table will need to have their sequence records moved by the Specify Project after the schema update. Also Specify installations that use Preparation for cataloging tissues and which wish to use the Material Sample table for DNA or other extracts, will need their Preparation data form schemas updated in order for Material Sample data fields to be visible. Sites installing Specify for the first time with release 6.6.06 or 7.3.0 will have the updated forms.

Changes apply to both Specify 6 and 7 databases; the two platforms will continue to use the same database schema. Sites using both Specify 6 and 7 with the same database, will need to update both Sp6 thick clients on workstations, and Sp7 server software, concurrently, in order to continue to use both platforms after the update.

An alternate method for cataloging tissue samples as Collection Objects is available for collections comprised exclusively of tissues or extracts. The tables and relationships described here would still apply. Material Sample would be used for extract information. Please contact the Specify Software Project with any questions about the update.