

Submission of Population Samples to the National Database

We invite all forensic laboratories and institutions to contribute to the US Y-STR Database. The resulting increase in the database size and the inclusion of geographically and ethnically varied population groups will increase the scientific and forensic efficacy of the database. Data contribution involves only three steps: successfully completing a 5-sample quality control exercise, typing samples from any specific population group with any commercial kit, and submission of data via email using the downloadable Excel file template, adhering to our rules of nomenclature below. Please [contact](#) us to participate.

1. Successfully complete the quality control exercise using challenge samples.

The US Y-STR haplotype reference database is intended to serve the forensic community. Demonstration of basic competency by the submitting lab is a mandatory requirement for any institution wishing to submit Y-STR population data for incorporation into the database.

For competency testing, we provide to a potential participating laboratory 5 challenge samples to be typed. These samples are dried human bloodstains that have previously been typed at the 17 Y-STR loci used in the National Database. There is no deadline for the quality control testing to be completed. The QC results can be emailed or faxed for evaluation at the National Center for Forensic Science in Orlando, FL. A "Certificate of Participation" will be issued to all laboratory participants that successfully complete the quality control exercise. Upon successful completion, the laboratory's Y-STR haplotype data can be submitted for upload into the database.

2. Type the samples for one or more representative regional male population using any commercial kit.

To be accepted into the database, typed samples must include a minimum of the 11 core SWGDAM loci and must have never been previously submitted to any commercial database, NCFS, or the University of Arizona. We are currently accepting samples from any geographical and/or ancestral group. We also invite any autosomal data pertaining to these samples, as it will help to ensure that each sample in the National Database is from a unique individual.

3. Submit data via email using the downloadable Excel file template, adhering to the US Y-STR rules of nomenclature.

- Once the QC challenge has been successfully completed and the Certificate of Participation has been issued, download the Data-Submission Template [here](#). Please follow the instructions on the first worksheet and only fill in the cells for which you have information, leaving everything else blank. Enter any of the following value types:
- Standard ladder allele such as "14"
- Off-ladder allele value such as "17.2"
- Off-ladder-low or off-ladder-high values such as "<15" or ">17"
- Chromosomal segmental duplications in numerical order separated by commas, such as "12,13,14"
- Null allele: enter "0" as the allele designation when the sample is believed to contain a legitimate null allele type (due to mutation)

Email your data to lfatolit@mail.ucf.edu. The submitted data will be uploaded to the database during our next update (normally semi-annually).

Please Note: All donors are anonymous and electropherograms do not exist in a curated fashion. All submitting entities are solely responsible for their own data. NCFS will deal with legal requests for general information about the database, including its compilation and management. In the event that precise details of a certain population sample are formally requested via the judicial process (via Court order), the request will be redirected to the collaborating scientists and their institutions.