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Research paper

STRSeq: A catalog of sequence diversity at human identification Short Tandem Repeat loci

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ABSTRACT

The STR Sequencing Project (STRSeq) was initiated to facilitate the description of sequence-based alleles at the Short Tandem Repeat (STR) loci targeted in human identification assays. This international collaborative effort, which has been endorsed by the ISFG DNA Commission, provides a framework for communication among laboratories. The initial data used to populate the project are the aggregate alleles observed in targeted sequencing studies across four laboratories: National Institute of Standards and Technology (N = 1786), Kings College London (N = 1043), University of North Texas Health Sciences Center (N = 839), and University of Santiago de Compostela (N = 944), for a total of 4612 individuals. STRSeq data are maintained as GenBank records at the U.S. National Center for Biotechnology Information (NCBI), which participates in a daily data exchange with the DNA DataBank of Japan (DDBJ) and the European Nucleotide Archive (ENA). Each GenBank record contains the observed sequence of a STR region, annotation ("bracketing") of the repeat region and flanking region polymorphisms, information regarding the sequencing assay and data quality, and backward compatible length-based allele designation. STRSeq GenBank records are organized within a BioProject at NCBI (https://www.ncbi.nlm.nih.gov/bioproject/380127), which is sub-divided into: commonly used autosomal STRs, alternate autosomal STRs, Y-chromosomal STRs, and X-chromosomal STRs. Each of these categories is further divided into locus-specific BioProjects. The BioProject hierarchy facilitates access to the GenBank records by browsing, BLAST searching, or ftp download. Future plans include user interface tools at strseq.nist.gov, a pathway for submission of additional allele records by laboratories performing population sample sequencing and interaction with the STRidER web portal for quality control (http://strider.online).

1. Introduction

As the forensic DNA community evaluates the potential of sequencing applications for Short Tandem Repeat (STR) loci, it is imperative to define the allelic diversity in these regions of the human genome. Large-scale sequencing projects within the broader genomics community may use shorter read chemistries (e.g. 100 bp) and may not describe repetitive regions due to their complexity and non-conformity to typical alignment parameters [1]. Additionally, knowledge of the forensic literature is needed to report STR sequences in the same manner established by the forensic community.

Even within forensic sequencing studies, there are differences in the reporting of sequence-based STR alleles. Names of convenience such as **20(a)** [2] or **FL1X20** [3] have not been standardized and may create confusion about the specific allele being reported. There may be differences in format for the compression or "bracketing" of STR sequences, such as **ATAG[9]** [4,5] or **[ATAG]$_9$** [6] or **[ATAG]9** [7]. More importantly, there may be differences in strand reporting where choice of the forward strand will match the reference sequence direction, and choice of the reverse strand aligns the sequence in the opposite direction. The DNA Commission of the ISFG on minimal nomenclature requirements in 2016 recommended reporting all sequences

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in the forward strand orientation [8]. However, some loci were historically reported on the reverse strand [9]. In particular, STRs for which the reported strand has changed over time may differ in reporting where the repeat region begins. This can result in shifted (different) allele number designations for the same sequence [8]. Lastly, the recovery and reporting of varying lengths of flanking regions (and hence flanking region variants) is inherent to differences in kit designs and bioinformatic pipelines.

The international forensic DNA community continues to develop guidance on STR sequence nomenclature, and additional resources for quality control of STR sequence data are being developed [10]. However, the need for standardization is immediate. A 2016 survey was recently published by the European Network of Forensic Science Institutes (ENFSI) DNA Working Group [11], in which over half of the 33 responding laboratories have already purchased at least one sequencing instrument. The respondents (primarily composed of government forensic laboratories across 25 countries) reported *lack of nomenclature and reporting standards* as the highest ranking scientific and legal challenge for the implementation of new sequencing technologies in forensic genetics. Also in 2016, the Applied Genetics Group of the U.S. National Institute of Standards and Technology (NIST) queried forensic laboratories to assess the utility of STR reference sequences for loci of forensic interest. The feedback received from 22 laboratories (representing 11 countries) mirrored the ENSFI survey with strong support for the development of STR sequence nomenclature resources.

In response to this need, NIST partnered with the U.S. National Center for Biotechnology Information (NCBI), leveraging NIST's over 20-year history supporting the forensic STR typing community [12] and NCBI's extensive infrastructure for accepting, maintaining and serving DNA sequence data. Through this partnership, the STR Sequencing Project (STRSeq) has been initiated to facilitate the description of sequence-based alleles at the STRs targeted in human identification assays. This resource consists of a curated catalog of sequence diversity at forensic STR loci, along with the key elements of nomenclature conforming to current guidelines [8], and will serve as the data backbone during this time of transition, as well as a stable resource for the future.

2. Samples and submission strategy

The initial data used to populate STRSeq are the aggregate alleles observed in targeted sequencing studies of single source samples across four laboratories: NIST, Kings College London (KCL), University of North Texas Health Science Center (UNT), and University of Santiago de Compostela (USC), for a total of 4612 individuals. The number of alleles aggregated differs by locus due to variable multiplex performance and quality requirements described in Section 3. As only aggregate alleles are displayed, the source of the alleles is anonymized. The targeted sequence data used in STRSeq either have been, or are expected to be published by the submitting laboratory ([6,13], additional manuscripts in preparation). Records will be added to the STRSeq BioProject in sets, largely coinciding with associated publications, as follows:

NIST: N = 1786 samples from multiple sources: 1) N = 665 liquid blood samples purchased from Interstate Blood Bank (Memphis, TN) and Millennium Biotech, Inc. (Ft. Lauderdale, FL) with self-declared ancestries from three U.S. population groups: Caucasian, African American, and Hispanic; 2) N = 781 buccal swabs provided by DNA Diagnostics Center (Fairfield, OH) from paternity testing samples with self-declared ancestries from four U.S. population groups: Caucasian, African American, Asian and Hispanic; 3) N = 297 buccal swabs collected from anonymous volunteers of self-reported, diverse ancestries, provided by the George Washington University; and 4) N = 43 control samples and reference materials. All samples have been sequenced with the ForenSeq system (Illumina) and a subset (> 600 samples) has overlapping sequence data from the PowerSeq Auto-Y assay (Promega). In addition, for the majority of these samples, capillary electrophoresis (CE) STR data is available at all ForenSeq and PowerSeq Auto-Y loci ([14,15] and unpublished data).

KCL: N = 1043 samples were obtained from consenting adult volunteers resident in the U.K. The samples relate to six U.K. population groups with self-declared ancestries of: White British, West African, North East African, South Asian, Chinese and Middle Eastern. All samples have been sequenced with the ForenSeq system and additionally genotyped with at least two commonly available CE kits.

UNT: N = 839 samples which have been described in associated sequence-based allele frequency publications and were sequenced with the ForenSeq system [6,13].

USC: N = 944 samples from the HGDP-CEPH diversity panel cell-line DNAs from 51 diverse populations were sequenced with the ForenSeq system.

Initially, STRSeq records will be created for the STR loci targeted in the aforementioned assays; additional records will be created as samples are sequenced with other available commercial assays, e.g. Precision ID GlobalFiler NGS STR Panel (Thermo Fisher Scientific). If new STR loci (see [16]) are targeted in commercially available assays launched in the future, additional records will be created.

A single laboratory will be indicated as having submitted each record. The association of a *submitting laboratory* with a record does not imply "discovery" of a sequence variant; rather the designation is simply the organization that initially provided the sequence and maintains the supporting data. For the initial data set, NIST will be the *submitting laboratory* of all sequences generated at NIST and the other laboratories will be the *submitting laboratory* of those sequences generated at that specific laboratory for which records do not already exist in the database. Duplicate records will not be created, which will generally result in a decreasing number of new sequence records as successive sample sets are added. Fig. 1 outlines an example submission strategy of non-duplicate allele records that might be expected from a typical highly polymorphic STR such as D12S391.

3. BioProject hierarchy and record format

The BioProject hierarchy serves to organize the GenBank records (Table 1). The highest-level STRSeq umbrella project contains four sub-umbrella projects: (a) **Commonly Used Autosomal STR Loci**, (b) **Alternate Autosomal STR Loci**, (c) **Y-Chromosomal STR Loci**, and (d) **X-Chromosomal STR Loci**. These sub-umbrella projects are divided further into locus-specific data-level projects which contain the GenBank sequence record data. Each umbrella and data-level project has a corresponding accession number, e.g. PRJNA380127 is the STRSeq umbrella project, PRJNA380345 is the **Commonly Used Autosomal STR Loci** sub-umbrella project, and PRJNA380554 is the **TPOX Sequence-Based Alleles** project (the common PRJNA prefix identifies the six-digit number as a BioProject). Entering one of these accession numbers at https://www.ncbi.nlm.nih.gov/bioproject allows direct access to the umbrella or data-level project of interest. Each BioProject page contains additional links for up, down, and cross navigation. Table 1 contains direct links to STRSeq umbrella and data-level projects.

The sequence records in GenBank are flat files of specified format that can be downloaded and parsed en masse (see Fig. 2 for an example record for the TPOX locus). Starting from the bottom of the record, in a section labeled **ORIGIN**, users will find the full sequence that was reported by the submitting laboratory. The length of reported sequence is dependent upon the assay and the quality of the flanking sequence data, but generally will be consistent with the assay-specific configuration files published in [17]. Above the sequence is the **FEATURES** table, which includes the position of the repeat region within the sequence, the position and dbSNP rs number of variations in the flanking regions (when applicable), and the subset of sequence that was observed with different commercial assays (when applicable). Each feature can be selected in order to highlight the appropriate region in the sequence

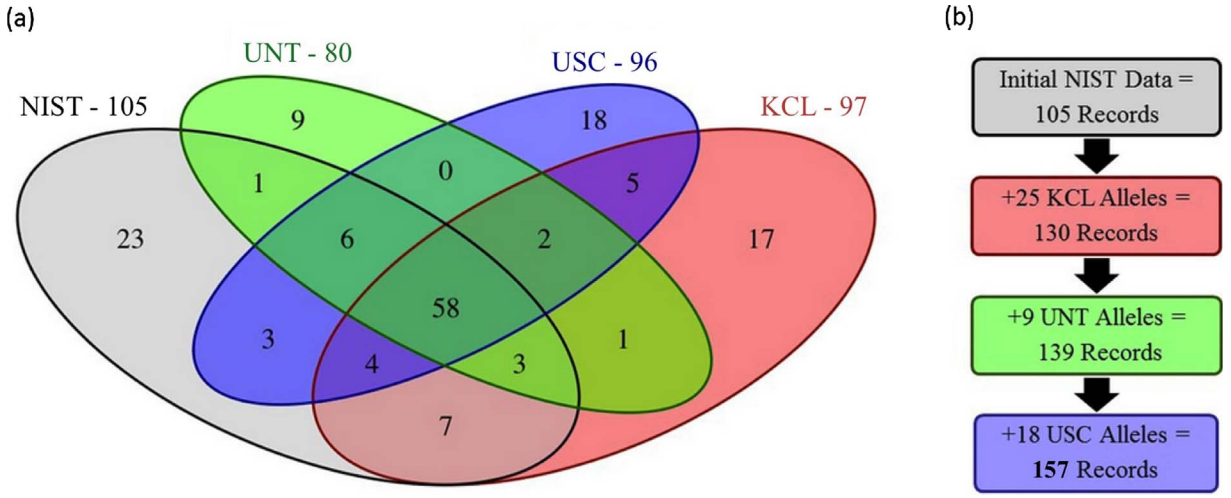

Fig. 1. (a) Venn diagram demonstrating the overlap of D12S391 sequence-based alleles observed among the four laboratories, and the total number of unique sequence-based alleles observed within each laboratory. (b) Submission strategy for 157 unique sequence-based alleles observed at the D12S391 locus. The 105 unique alleles generated at NIST form the basis of STRSeq records. Subsequent submissions from KCL, UNT, and USC will add records for sequences generated at each laboratory for which records do not already exist (25, 9, and 18 records, respectively).

string. SNP rs numbers are hyperlinked to dbSNP, allowing users to navigate and access frequency information quickly. If the polymorphism has not been assigned a dbSNP reference number, the GRCh38 coordinate is given, and the field will be updated if an rs number is assigned later or if the assembly is updated.

Above the **FEATURES** table is the *structured comments* section (offset with ##humanSTR-START## and ##humanSTR-END##), which contains field-based information relevant to STRSeq records. The given **Bracketed repeat** is intended to be consistent with the guidance of the ISFG nomenclature commission [8]. Specific to STRSeq records is the lower-case formatting of selected bases within the **Bracketed repeat**, which highlights sequence tracts that are not counted toward the length-based allele designation (when applicable, e.g. D19S433 14 allele will be presented as: [AAGG] aaag [AAGG] tagg [AAGG]12). The **Sequencing technology** field lists the commercial assay(s) and instrument(s) used to generate the sequence data. The **Coverage** field lists the minimum threshold of reads observed for the reported sequence. The current threshold for STRSeq record creation is > 30X. This is consistent with the default minimum "interpretation threshold" implemented in one commercial software, corresponding to the only relevant commercial assay with a published developmental validation [18] at the time of writing. This threshold will continue to be evaluated in the future as additional developmental validations are published. The **Length-based tech.** field lists the assay and instrument used to generate the **Length-based allele** given. Often a sequence will have been observed in multiple samples. The length-based information in each record indicates that, for at least one sample, the specified length-based allele was generated with the given length-based technology. This approach is not meant to be comprehensive; variation in the length-based allele among individuals or assays can result from indels in flanking regions. In some instances, length-based allele confirmation may not be possible, such as the lack of a CE assay for STRs targeted by commercial sequencing assays but not previously in common use. When a length-based allele confirmation has not been performed, the **Length-based allele** field will indicate e.g. "7 (Inferred from sequence)" and the **Length-based tech.** field will contain "Not reported". The remaining information in the *structured comments* section orients the sequence on the chromosome and will be updated along with the reference sequence assembly.

Above the *structured comments* section is the **COMMENT** block, which is identical across records and recapitulates this paper. Above the **COMMENT** block are references. **REFERENCE 1** will be this paper and **REFERENCE 2** identifies the submitting laboratory. The remaining topmost fields contain information for GenBank record organization. The **ACCESSION** and **VERSION** number is the GenBank sequence identifier (e.g. MF044256.1 in Fig. 2). If future commercial assay typing provides additional flanking sequence, the updated sequence will become e.g. MF044256.2 (coexisting with MF044256.1). If the additional flanking sequence reveals a polymorphism, the additional sequence consistent with the reference sequence becomes e.g. MF044256.2 and a new record is created for the additional sequence which differs from the reference sequence.

The **DEFINITION** line near the top of the record is the descriptor present in a list of sequences (see https://www.ncbi.nlm.nih.gov/nuccore/?term=strseq+tpox), and will uniquely identify each allele with components of the record itself. In addition, the top of each record contains hyperlinks to the **FASTA** sequence, which can be downloaded, and a **Graphics** view (Fig. 3). This graphical display presents an interactive version of the sequence (displaying forward and reverse strands) and the features identified in the GenBank record: the repeat region, the region(s) reported from each available sequencing technology, and any associated flanking region polymorphisms. The information shown in **Graphics** view is dependent on the **Tracks** selected in the viewer. All available information for the record is displayed simultaneously by selecting both the **Sequence** and **Aggregate features Track**. More information and tutorials on the NCBI Sequence Viewer can be found at https://www.ncbi.nlm.nih.gov/tools/sviewer.

4. Typical use cases

Several use cases for STRSeq have been identified based on feedback from the forensic community:

I. As a teaching tool to explore STR sequences. The STRSeq BioProject is expected to be useful to forensic operational, academic, and commercial laboratories interested in sequencing STRs as it allows the viewing and downloading of repeat region motifs, flanking region polymorphisms, and commercial assay overlap.
II. As the data backbone for software development. This catalog of sequences with associated forensic formatting and stable links to GenBank records facilitates development of STR sequencing methods and bioinformatic pipelines that conform to agreed variant data frameworks.
III. To provide a quality control function for the evaluation of rare sequences. When a sequence is observed in forensic casework that was not observed in initial validation studies or in the implemented

Table 1
STRSeq BioProject hierarchy, accession numbers, and direct links to all levels. The highest-level of organization is the STRSeq umbrella project (PRJNA380127, ncbi.nlm.nih.gov/bioproject/380127), containing four sub-umbrella projects: (a) Commonly Used Autosomal STR Loci, (b) Alternate Autosomal STR Loci, (c), Y-Chromosomal STR Loci and (d) X-Chromosomal STR Loci. Each of these contains locus-specific sub-projects, which are the data-level projects containing GenBank sequence records.

a		
Commonly Used Autosomal STR Loci – PRJNA380345		
ncbi.nlm.nih.gov/bioproject/380345		
D1S1656	PRJNA380553	ncbi.nlm.nih.gov/bioproject/380553
TPOX	PRJNA380554	ncbi.nlm.nih.gov/bioproject/380554
D2S441	PRJNA380555	ncbi.nlm.nih.gov/bioproject/380555
D2S1338	PRJNA380556	ncbi.nlm.nih.gov/bioproject/380556
D3S1358	PRJNA380558	ncbi.nlm.nih.gov/bioproject/380558
FGA	PRJNA380559	ncbi.nlm.nih.gov/bioproject/380559
D5S818	PRJNA380560	ncbi.nlm.nih.gov/bioproject/380560
CSF1PO	PRJNA380561	ncbi.nlm.nih.gov/bioproject/380561
SE33	PRJNA380562	ncbi.nlm.nih.gov/bioproject/380562
D6S1043	PRJNA380563	ncbi.nlm.nih.gov/bioproject/380563
D7S820	PRJNA380564	ncbi.nlm.nih.gov/bioproject/380564
D8S1179	PRJNA380565	ncbi.nlm.nih.gov/bioproject/380565
D10S1248	PRJNA380566	ncbi.nlm.nih.gov/bioproject/380566
TH01	PRJNA380567	ncbi.nlm.nih.gov/bioproject/380567
vWA	PRJNA380568	ncbi.nlm.nih.gov/bioproject/380568
D12S391	PRJNA380569	ncbi.nlm.nih.gov/bioproject/380569
D13S317	PRJNA380570	ncbi.nlm.nih.gov/bioproject/380570
Penta E	PRJNA380571	ncbi.nlm.nih.gov/bioproject/380571
D16S539	PRJNA380572	ncbi.nlm.nih.gov/bioproject/380572
D18S51	PRJNA380573	ncbi.nlm.nih.gov/bioproject/380573
D19S433	PRJNA380574	ncbi.nlm.nih.gov/bioproject/380574
D21S11	PRJNA380575	ncbi.nlm.nih.gov/bioproject/380575
Penta D	PRJNA380576	ncbi.nlm.nih.gov/bioproject/380576
D22S1045	PRJNA380577	ncbi.nlm.nih.gov/bioproject/380577
b		
Alternate Autosomal STR Loci – PRJNA380346		
ncbi.nlm.nih.gov/bioproject/380346		
D1S1677	PRJNA396107	ncbi.nlm.nih.gov/bioproject/396107
D2S1776	PRJNA396108	ncbi.nlm.nih.gov/bioproject/396108
D3S4529	PRJNA396109	ncbi.nlm.nih.gov/bioproject/396109
D4S2408	PRJNA396110	ncbi.nlm.nih.gov/bioproject/396110
D5S2800	PRJNA396111	ncbi.nlm.nih.gov/bioproject/396111
D6S474	PRJNA396112	ncbi.nlm.nih.gov/bioproject/396112
D9S1122	PRJNA396113	ncbi.nlm.nih.gov/bioproject/396113
D12ATA63	PRJNA396114	ncbi.nlm.nih.gov/bioproject/396114
D14S1434	PRJNA396115	ncbi.nlm.nih.gov/bioproject/396115
D17S1301	PRJNA396116	ncbi.nlm.nih.gov/bioproject/396116
D20S482	PRJNA396117	ncbi.nlm.nih.gov/bioproject/396117
c		
Y-Chromosomal STR Loci – PRJNA380347		
ncbi.nlm.nih.gov/bioproject/380347		
DYF387S1	PRJNA396118	ncbi.nlm.nih.gov/bioproject/396118
DYS19	PRJNA396119	ncbi.nlm.nih.gov/bioproject/396119
DYS385 a/b	PRJNA396120	ncbi.nlm.nih.gov/bioproject/396120
DYS389 I/II	PRJNA396122	ncbi.nlm.nih.gov/bioproject/396122
DYS390	PRJNA396123	ncbi.nlm.nih.gov/bioproject/396123
DYS391	PRJNA396124	ncbi.nlm.nih.gov/bioproject/396124
DYS392	PRJNA396125	ncbi.nlm.nih.gov/bioproject/396125
DYS393	PRJNA396126	ncbi.nlm.nih.gov/bioproject/396126
DYS437	PRJNA396127	ncbi.nlm.nih.gov/bioproject/396127
DYS438	PRJNA396128	ncbi.nlm.nih.gov/bioproject/396128
DYS439	PRJNA396129	ncbi.nlm.nih.gov/bioproject/396129
DYS448	PRJNA396130	ncbi.nlm.nih.gov/bioproject/396130
DYS456	PRJNA396131	ncbi.nlm.nih.gov/bioproject/396131
DYS458	PRJNA396132	ncbi.nlm.nih.gov/bioproject/396132
DYS460	PRJNA396134	ncbi.nlm.nih.gov/bioproject/396134

Table 1 *(continued)*

c		
Y-Chromosomal STR Loci – PRJNA380347		
ncbi.nlm.nih.gov/bioproject/380347		
DYS481	PRJNA396135	ncbi.nlm.nih.gov/bioproject/396135
DYS505	PRJNA396136	ncbi.nlm.nih.gov/bioproject/396136
DYS522	PRJNA396137	ncbi.nlm.nih.gov/bioproject/396137
DYS533	PRJNA396138	ncbi.nlm.nih.gov/bioproject/396138
DYS549	PRJNA396139	ncbi.nlm.nih.gov/bioproject/396139
DYS570	PRJNA396140	ncbi.nlm.nih.gov/bioproject/396140
DYS576	PRJNA396141	ncbi.nlm.nih.gov/bioproject/396141
DYS612	PRJNA396142	ncbi.nlm.nih.gov/bioproject/396142
DYS635	PRJNA396143	ncbi.nlm.nih.gov/bioproject/396143
DYS643	PRJNA396144	ncbi.nlm.nih.gov/bioproject/396144
Y-GATA-H4	PRJNA396145	ncbi.nlm.nih.gov/bioproject/396145
d		
X-Chromosomal STR Loci – PRJNA380348		
ncbi.nlm.nih.gov/bioproject/380348		
DXS7132	PRJNA396146	ncbi.nlm.nih.gov/bioproject/396146
DXS7423	PRJNA396147	ncbi.nlm.nih.gov/bioproject/396147
DXS8378	PRJNA396148	ncbi.nlm.nih.gov/bioproject/396148
DXS10074	PRJNA396149	ncbi.nlm.nih.gov/bioproject/396149
DXS10103	PRJNA396150	ncbi.nlm.nih.gov/bioproject/396150
DXS10135	PRJNA396151	ncbi.nlm.nih.gov/bioproject/396151
HPRTB	PRJNA396152	ncbi.nlm.nih.gov/bioproject/396152

allele frequency database, a STRSeq BLAST search determines if a similar or identical sequence has been recorded. When a link to previous data is identified, STRSeq provides nomenclature information and leads the analyst to published allele frequency data (see Fig. 4).

5. Future directions for STRSeq

As previously described, sample sets and STRs will be added iteratively, allowing the BioProject to be built further and records to be released in phases. Once created, the GenBank records are expected to be stable but STRSeq should be viewed as a dynamic resource.

Some users will be familiar with NCBI interfaces and will quickly adapt their workflows to access, search, and download records contained in the STRSeq BioProject. While many tutorials exist to facilitate access to NCBI resources (see https://www.ncbi.nlm.nih.gov/guide/all/#howtos), it is likely that most users will prefer customized interface tools specific to this BioProject. Future plans include the development of such tools at strseq.nist.gov, in order to streamline BLAST searches and batch record downloads from the BioProject.

Additionally, we aim to provide a pathway for submission of new sequence records from laboratories performing population sample sequencing. We anticipate an integrated, seamless process whereby users upload population sample sequencing data to the STRidER web portal (http://strider.online) [10] for quality control, and STRidER queries STRSeq for a matching sequence accession number. In cases where the STRidER query finds no match in STRSeq, a process could be initiated to evaluate the sequence and then aim to create a new GenBank record. Such a process would strengthen the STRidER quality control function and expand STRSeq, while harmonizing nomenclature between both resources. This is particularly important for novel sequence variants likely to be encountered as population studies extend their geographic scope or sample numbers.

Homo sapiens microsatellite TPOX 7 [AATG]7 rs115644759 sequence

GenBank: MF044247.1

FASTA Graphics

Go to:

```
LOCUS       MF044247                163 bp    DNA     linear   PRI 30-MAY-2017
DEFINITION  Homo sapiens microsatellite TPOX 7 [AATG]7 rs115644759 sequence.
ACCESSION   MF044247
VERSION     MF044247.1
DBLINK      BioProject: PRJNA380554
KEYWORDS    STRSeq, STR, TPOX.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 163)
  AUTHORS   Gettings,K.B., Borsuk,L.A. and Vallone,P.M.
  TITLE     The STR Sequencing Project [manuscript in preparation]
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 163)
  AUTHORS   NIST,A.G.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-MAY-2017) Applied Genetics Group, National Institute
            of Standards and Technology, 100 Bureau Drive, MS-8314,
            Gaithersburg, MD 20899, USA
COMMENT     Annotation ('bracketing') of the repeat region is consistent with
            the guidance of the ISFG (International Society of Forensic
            Genetics), PMID: 26844919.  Lower case letters in the 'Bracketed
            repeat' region below denote uncounted bases.   The given
            length-based allele value was determined using the designated
            length-based technology.  Variation in the length-based allele
            between individuals or assays can result from indels in flanking
            regions.  The length of reported sequence is dependent on the assay
            (see 'Sequencing technology') and the quality of the flanking
            sequence. This information is provided as part of the STR
            Sequencing Project (STRseq), a collaborative effort of the
            international forensic DNA community.  The purpose of this project
            is to facilitate the description of sequence-based STR alleles.
            Additional resources can be found at strseq.nist.gov.  For
            questions or feedback, please contact strseq@nist.gov.  Allele
            frequency data can be accessed in the strider.online database.

            ##HumanSTR-START##
            STR locus name        :: TPOX
            Length-based allele   :: 7
            Bracketed repeat      :: [AATG]7
            Sequencing technology :: ForenSeq, MiSeq FGx; PowerSeq Auto, MiSeq
            Coverage              :: >30X
            Length-based tech.    :: PowerPlex Fusion, ABI3500xl
            Assembly              :: GRCh38 (GCF_000001405)
            Chromosome            :: 2
            RefSeq Accession      :: NC_000002.12
            Chrom. Location       :: 1489532..1489698
            Repeat Location       :: 1489653..1489684
            Cytogenetic Location  :: 2p25.3
            ##HumanSTR-END##
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     misc_feature    1..163
                     /note="Promega PowerSeq Sequence"
     variation       25
                     /note="C/T SNP"
                     /db_xref="dbSNP:rs115644759"
     misc_feature    120..154
                     /note="Illumina ForenSeq Sequence"
     repeat_region   122..149
                     /rpt_type=tandem
                     /satellite="microsatellite:TPOX"
ORIGIN
        1 tggcctgtgg gtccccccat agattgtaag cccaggagga agggctgtgt ttcagggctg
       61 tgatcactag cacccagaac cgtcgactgg cacagaacag gcacttaggg aaccctcact
      121 gaatgaatga atgaatgaat gaatgaatgt ttgggcaaat aaa
//
```

Fig. 2. Example STRSeq GenBank record, available online at https://www.ncbi.nlm.nih.gov/nuccore/1197990967.

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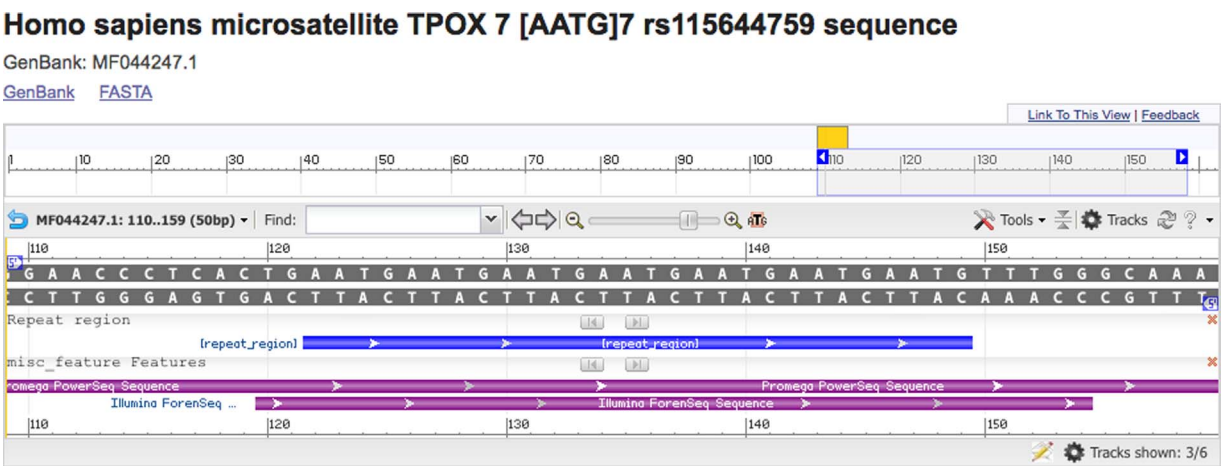

Fig. 3. Example Graphics view of STRSeq Genbank record, available and interactive online at https://www.ncbi.nlm.nih.gov/nuccore/1197990967?report=graph.

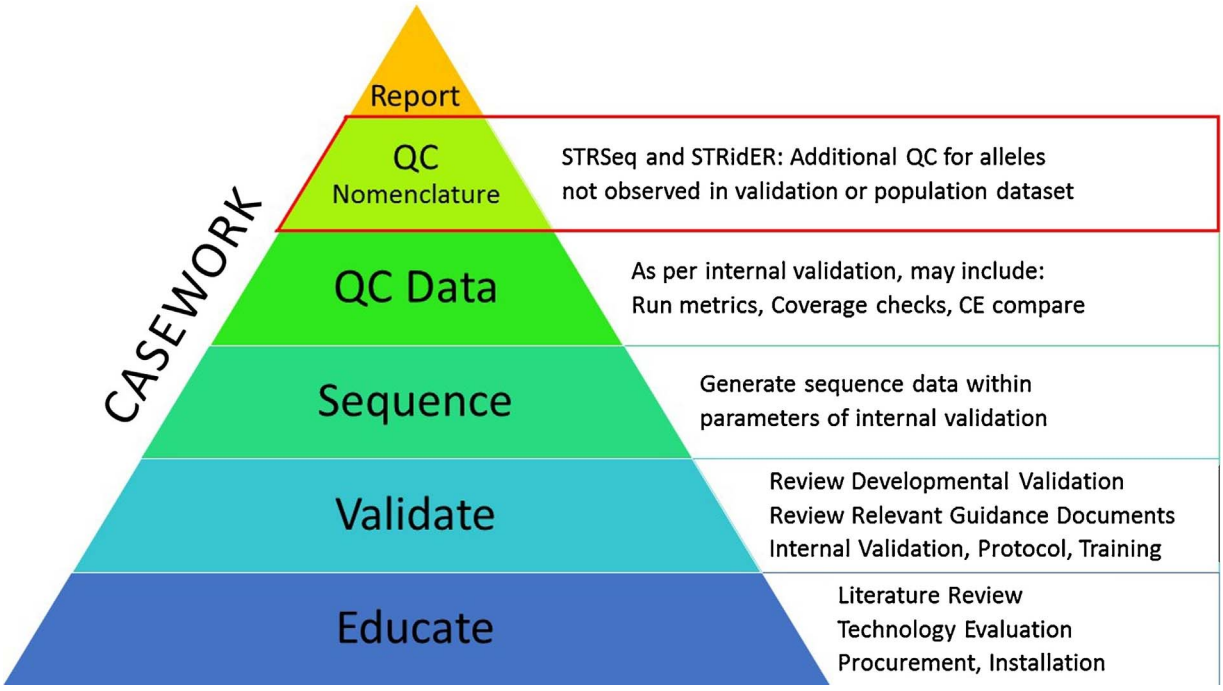

Fig. 4. Outline of the anticipated STRSeq use cases for evaluation of rare alleles in forensic casework, integrated into an overall quality assurance system.

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