Institute of Legal Medicine

Medical University of Innsbruck
Director: Prof. Richard Scheithauer, MD
Muellerstraße 44, A-6020 Innsbruck, Austria
Tel: +43/512/9003-70600, Fax: +43/512/9003-73600
e-mail: gmi@i-med.ac.at

Prof. Dr. Walther Parson
Head of High Throughput DNA Database Unit
Head of Forensic Genomics
walther.parson@ i-med.ac.at

Dr. Martin Bodner
Forensic Genomics
martin.bodner@i-med.ac.at

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STRidER QC Report –Datasets Caputo_ARG_STR000327

Dear submitter,

Thank you for providing autosomal STR data for quality control (QC) to STRidER. Please find the results in this report.

1. Submitted datasets

origin of samples:	Argentina admixed general population
submitter:	Mariela Caputo Universidad de Buenos Aires Facultad de Farmacia y Bioquímica Departamento de Microbiología, Inmunología y Biotecnología Cátedra de Genética Forense y Servicio de Huellas Digitales Genéticas caputomariela@yahoo.com.ar
no. of datasets:	7 (submitted), 6 (accepted)
autosomal STR loci:	26 loci, various kits used: Promega PowerPlex 16, Promega PowerPlex 18, Promega PowerPlex 21, Promega PowerPlex Fusion 6C, TFS AmpFLSTR Identifiler, TFS VeriFiler Express
format:	genotype table, CE length based alleles

accepted genotype numbers (combined from accepted datasets):

D3S1358, D18S51, CSF1PO, TH01, vWA, D21S11, D7S820, D5S818, TPOX, D8S1179, FGA: 6454 genotypes
D2S1338, D19S433: 3496 genotypes
PENTA E, PENTA D: 6253 genotypes
D1S1656, D13S317, D16S539, D12S39: 1606 genotypes
D2S441, D10S1248, D22S1045: 527 genotypes
D13S317, D16S539: 4848 genotypes
D6S1043: 1234 genotypes
SE33: 372 genotypes

2. General information on the QC process

The STR genotypes were scrutinized applying plausibility checks performed with the STRidER software suite and further manually scrutinized. Observations were made that included the invitation to send raw data. The reason for doing so is that we cannot know whether our observations indicate new variation or actual errors in the dataset. To clarify this, we invited contributors to check/confirm all observations.

3. Results of QC: corrections made to the datasets

Previous versions of all datasets were rejected after quality concerns. **Dataset ARG_694 was rejected** also in its resubmitted version after quality concerns.

QC results of the remaining six re-submitted datasets indicated several errors that were corrected after direct communication with the submitters.

(a) Dataset ARG_155:

- invalid alleles corrected
    - sample JN2019-077, locus D3S1358, 51|16 corrected to 15|16
    - sample JN2019-095, locus D22S1045, 15|5 corrected to 15|15
- erroneous alleles corrected
    - sample JN2019-090, locus D22S1045, 5|5 corrected to 15|15
    - sample JN2019-119, locus PENTA E, 14.3|16.4 corrected to 14.4|16.4

(b) Dataset ARG_1080:

- identical copy of sample SF2013-542 deleted (**remaining n= 1079**)
- erroneous alleles corrected
    - sample MIS2014-571, locus Penta E, 10|25.4 corrected to 10|26
    - sample FOR2014-316, locus D6S1043, 15.1|19 corrected to 16.1|19

(c) Dataset ARG_1690:

- deletion of sample RN20212-1072 (no raw data provided) (**remaining n= 1689**)
- erroneous allele corrected
  - sample RN2012-1033, locus D21S11, 30|32.3 corrected to 30|32.2

(d) Dataset ARG_2958:

- erroneous allele corrected
  - sample RN2009-658, locus TPOX, 8|8 corrected to 8|16

(e) Dataset ARG_372: no corrections

(f) Dataset ARG_201: no corrections

In their revised version, QC results indicated otherwise inconspicuous quality of the six re-submitted datasets, that seem to have been produced and analysed in high-quality DNA laboratories.

4. Summary

We thank the authors for providing autosomal STR population data for STRidER QC! The general quality of the data as determined by plausibility checks and inspection of raw data appears to meet forensic requirements.

Please find the **corrected datasets** and the **combined allele frequency table** calculated by STRidER attached. When publishing the data, please indicate **STRidER dataset reference STR000327** in the manuscript and provide these numbers to the editor during submission. If you encounter any inconsistencies in this dataset in the future, please let us know.

Please **cite STRidER** when publishing your research:

Bodner M., Bastisch I., Butler J.M., Fimmers R., Gill P., Gusmão L., Morling N., Phillips C., Prinz M., Schneider P.M., Parson W. (2016), 'Recommendations of the DNA Commission of the International Society for Forensic Genetics (ISFG) on quality control of autosomal Short Tandem Repeat allele frequency databasing (STRidER)', *Forensic Sci. Int. Genet. 24, 97-102*

For **more information** about **STRidER quality control results**, typical errors and how to avoid them, please refer to:

Bodner M., Parson W. (2020), 'The STRidER Report on Two Years of Quality Control of Autosomal STR Population Datasets', *Genes* 11(8), 901

The STRidER online platform is work in progress. Additional datasets and features will continuously become available. To receive periodic news and stay updated about

STRidER, please register for the **STRidER newsletter** [https://mailman.i-med.ac.at/mailman/listinfo/strider-l].

Kind regards,

Dr. Walther Parson   Dr. Martin Bodner

Disclaimer: The applied quality control cannot be regarded as comprehensive independent evaluation of all raw data of the submitted dataset, but constitutes an optimized procedure for the detection of common data idiosyncrasies. The signatories cannot be made liable for correctness, completeness and topicality of the contents.