

Research article

New autosomal STR loci[☆]

J.M. Butler^{*}, C.R. Hill, A.E. Decker,
M.C. Kline, P.M. Vallone

National Institute of Standards and Technology, Biochemical Science Division, Gaithersburg, MD 20899-8311, USA

Received 12 September 2007; received in revised form 11 October 2007; accepted 12 October 2007

Abstract

Additional STR loci can be beneficial for a number of human identity, forensic casework, and DNA database applications. The marker selection and characterization process applied at NIST in developing these new loci and assays are described along with concordance testing results from non-overlapping PCR primers. A 23plex for simultaneous amplification of 22 autosomal STR loci and an amelogenin sex-typing assay is also demonstrated.

© 2008 Published by Elsevier Ireland Ltd.

Keywords: STR; Short tandem repeat; NIST; D10S1248; D2S441; D22S1045; Multiplex assays; MiniSTRs; Degraded DNA; Forensic DNA typing

1. Introduction

At the U.S. National Institute of Standards and Technology (NIST), we are characterizing additional autosomal and Y-chromosome STR loci that have a number of potential uses. In casework, additional information can be obtained from degraded DNA samples using miniSTR systems [1,2]. For identity testing work, kinship analysis, missing persons/mass disaster sample testing, and complex paternity testing can benefit by additional genetic markers [3]. More loci can help resolve relatives in growing national DNA databases to avoid adventitious matches. For example, although the U.K. National DNA Database started with 6 STR loci (SGM loci), it quickly expanded to 10 STRs (SGM Plus kit), and a future pan-

European database is expected to include more than 10 STRs [4].

2. Materials and methods

This work represents an extension of initial studies begun by Coble and Butler [2] and continued by Hill et al. [5].

3. Results and Discussion

We have set about finding loci with narrow allele ranges, moderate to high heterozygosities, and clean flanking sequences that can be used in miniSTR assays [2,5]. The selected loci were characterized by examining the variation in ~660 U.S. population samples coming from African American, Caucasian, and Hispanic groups. Chromosomal positions were precisely defined, allelic ladders constructed, and standard samples were sequenced and genotyped to provide reference repeat calibration [6].

With the defined allele ranges characterized, a multiplex assay was developed that is capable of amplifying 22 of the 26 autosomal STRs and small amelogenin X–Y products for sex-typing purposes. This 23plex, dubbed the “Autoplex”, uses five-dye chemistry to keep all PCR products under 400 bp in size (Fig. 1). Comparison of allele calls between the miniSTR assays and the Autoplex found full concordance in 99.80% of the 14,058 genotypes evaluated. This is similar to the 99.74%

[☆] Contribution of the U.S. National Institute of Standards and Technology. Not subject to copyright. Points of view in this document are those of the authors and do not necessarily represent the official position or policies of the US Department of Justice. Certain commercial equipment, instruments and materials are identified in order to specify experimental procedures as completely as possible. In no case does such identification imply a recommendation or endorsement by the National Institute of Standards and Technology nor does it imply that any of the materials, instruments or equipment identified are necessarily the best available for the purpose. This work was funded in part by the National Institute of Justice through interagency agreement 2003-IJ-R-029 with the NIST Office of Law Enforcement Standards.

^{*} Corresponding author at: 100 Bureau Dr., M/S 8311, Gaithersburg, MD 20899-8311, USA. Tel.: +1 301 975 4049; fax: +1 301 975 8505.

E-mail address: john.butler@nist.gov (J.M. Butler).

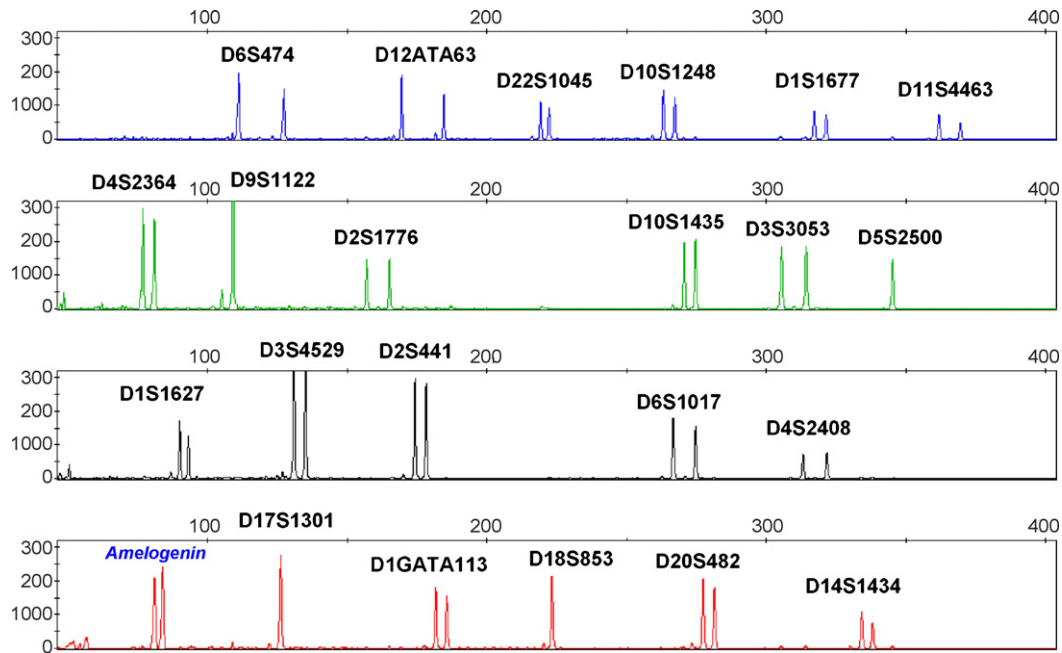


Fig. 1. Results from a 23plex amplification including 22 autosomal STRs and amelogenin for sex typing.

concordance rate found when evaluating the Identifiler kit versus MiniFiler kit allele calls [7].

Thus far, three of the 26 autosomal STR loci – D10S1248, D2S441, and D22S1045 – have been recommended for extending the core European loci [4]. We plan to continue to make information on these new loci available on the STRBase website at <http://www.cstl.nist.gov/biotech/strbase/newSTRs.htm>.

Acknowledgments

We thank Mike Coble for his initial work with the autosomal miniSTR loci and Jan Redman and Rich Schoske for early work in preparing the U.S. population samples.

Funding Source

U.S. National Institute of Justice – but without involvement in the development of this paper.

Conflict of interest

None.

References

- [1] J.M. Butler, Y. Shen, B.R. McCord, The development of reduced size STR amplicons as tools for analysis of degraded DNA, *J. Forensic Sci.* 48 (5) (2003) 1054–1064.
- [2] M.D. Coble, J.M. Butler, Characterization of new miniSTR loci to aid analysis of degraded DNA, *J. Forensic Sci.* 50 (1) (2005) 43–53.
- [3] J. Henke, L. Henke, Which short tandem repeat polymorphisms are required for identification? Lessons from complicated kinship cases, *Croat. Med. J.* 46 (4) (2005) 593–597.
- [4] P. Gill, L. Fereday, N. Morling, P.M. Schneider, The evolution of DNA databases—recommendations for new European loci, *Forensic Sci. Int.* 156 (2006) 242–244.
- [5] C.R. Hill, M.C. Kline, M.D. Coble, J.M. Butler, Characterization of 26 miniSTR loci for improved analysis of degraded DNA samples, *J. Forensic Sci.* 53 (1) (2008) 73–80.
- [6] Margaret Kline poster at 17th International Symposium on Human Identification (Nashville, TN), October 10–12, 2006, “NIST SRM Updates: Value-added to the Current Materials in SRM 2391b and SRM 2395”; available at http://www.cstl.nist.gov/biotech/strbase/pub_pres/Promega2006_Kline.pdf.
- [7] C.R. Hill, M.C. Kline, J.J. Mulero, R.E. Lagace, C.-W. Chang, L.K. Hennessy, J.M. Butler, Concordance study between the AmpFISTR MiniFiler PCR Amplification Kit and conventional STR typing kits, *J. Forensic Sci.* 52 (4) (2007) 870–873.