

Molecular Marker Multiplex Study

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Introduction

The project described in this report could not have happened without the hard work and support of some people at GeneTrace Systems, Inc. First (and most importantly), Jia Li did some of the early (easy book/basic reading) design and STR work to (show or prove) that STRs could be effectively carefully studied by mass (measuring light colors). Jia taught us a lot about PCR and was always encouraging of our work. Also, Tom Shaler was important in the early phases of this research with his expert (opinions about what could or should be done about a situation) in mass (measuring light colors) and data processing [1]. The first GeneTrace STR mass spectra were carefully collected by Tom, and so he and Jia deserve credit for helping get the money available for this study. Dan Pollart made/created many cleavable easy books/basic reading books for this project, especially in the first year of our work. David Joo and Wendy Lam also prepared PCR and SNP easy books/basic reading books for the later part of this work. Some people helped in robotic sample preparation and sample cleanup, including Mike Abbott, Jon Marlowe, David Wexler, and Rebecca Turincio. Joanna Hunter, Vera Delgado, and Can Nhan ran many of the STR samples on the automated mass light-color meters. Their hard work made it possible to focus on experimental design and data analysis rather than (something commonly done) sample handling. It was a great blessing to have talented and supportive coworkers throughout the course of this project. [2] useful discussions on some issues and helped develop test-related limits/guidelines and tackle automation issues, among other things. Nathan Hunt was especially important to the success of this project because he developed the STR genotyping set of computer instructions and CallSSR software as well as the (movie theater building with many screens) SNP (easy book/basic reading) design software. Kevin Coopman developed the SNP genotyping set of computer instructions and calling software and was always eager to carefully study our (movie theater building with many screens) SNP samples. Joe Monforte and Roger Walker served as our supervisors for the first year and second year of this project, (match up each pair of items in order), which allowed us the opportunity to give/reserve (good) enough time to doing the work described in this project. Last but not least, Debbie Krantz served as an able manager of these two NIJ grants and took care of the

(related to managing money) aspects. We also were supported with samples and sequence information from some scientific work partners [3]. Steve Lee and John Tonkyn from the California Department of Justice DNA Laboratory gave/given (related to the study of tiny chemical instructions within cells) DNA samples and STR allelic ladders. Debang Liu from Northwestern University gave/given the sequence used for improved (easy book/basic reading) design purposes. Peter Oefner and Peter Underhill from the Department of (the study of tiny chemical assembly instructions inside of living things) at Stanford University gave/given male population samples and Y-(genetic information storage area) SNP sequences. The encouragement and support of Lisa Forman and Richard Rau from the Office of Justice Programs at the National Institute of Justice pushed this work from an idea to a working product. Also, Dennis Reeder from the National Institute of Standards and Technology was always a constant source of encouragement at scientific meetings.

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