CALIFORNIA STATE SCIENCE FAIR
2009 PROJECT SUMMARY

Name(s)
Jennifer S. Chen

Project Number
S0406

Project Title
Exploring a Sequencing-based Human Identification Method as a Replacement for Current Fragment Sizing Technology

Abstract

Objectives/Goals
There is currently an enormous forensic DNA backlog, meaning a large number of DNA samples from criminals have not been analyzed to create DNA profiles and entered into the FBI Combined DNA Index System (CODIS) database. Consequently, not all potential DNA profiles are in the database for comparison with DNA samples collected in the future. These DNA samples are used to provide evidence to determine the guilt or innocence of those accused of serious crimes, making this database critically important. The purpose of my project is to explore an innovative way to reduce the backlog of DNA samples by proposing a more accurate, more efficient, and less costly method of human identification--ultra-high throughput (UHT) DNA sequencing.

Methods/Materials
I amplifed the miniSTR D7S820 locus of three individual samples with polymerase chain reaction (PCR) on a thermal cycler. I then sized the PCR products by two methods: 1) agarose gel electrophoresis to represent the current fragment sizing technology and 2) Sanger DNA sequencing, a conventional sequencing method, to simulate UHT DNA sequencing. I also compared the cost and time required to finish processing a DNA backlog of variable size by both methods.

Results
Gel electrophoresis yielded blurred bands that were very difficult to size, while the Sanger method produced clear sequences from which size and allele were easy to determine. In addition, comparing fragment sizing with UHT DNA sequencing showed that the latter is both more efficient and less costly when dealing with a large number of DNA samples, such as those of the backlog.

Conclusions/Discussion
UHT DNA sequencing holds great promise as a more accurate, more efficient, and less expensive human identification method than what is currently used.

Summary Statement
My project explores a human identification method based on ultra-high throughput DNA sequencing as a more accurate, more efficient, and less costly replacement for the current method based on fragment sizing.

Help Received
Used lab equipment at the San Jose BioCenter under the supervision of Dr. Chun-Nan Chen.