Method for DNA fingerprinting using handheld DNA sequencers

Technology #cu16211

This technology is an algorithm that enables reliable DNA sampling to be performed using existing handheld DNA sequencers for forensics analysis in the field.

Unmet Need: Rapid, reliable DNA sequence matching in the field

Forensic DNA analysis requires specialized lab equipment and a long turnaround time, with no viable means of performing this analysis quickly and reliably in the field. While handheld DNA sequencers are available, these devices are limited by large average error rates and low throughput compared to large, laboratory-stationed equipment. Moreover, DNA forensics techniques rely on the comparison of short tandem repeats, which are challenging to amplify using portable sequencing equipment. Thus, there remains an unfulfilled need for a portable DNA sequencing solution.

The Technology: DNA sampling algorithm compatible with existing handheld DNA sequencers

In this technology, single nucleotide polymorphisms are identified and compared to a reference database, and the likelihood of an identity match is determined. The algorithm accounts for error rate and allele frequency in determining the probability of a match. Moreover, this algorithm is compatible with low coverage reference databases, enabling a cost-effective method of reliable DNA sampling in the field.

Preliminary results obtained using this technology demonstrated identification of a person with 100% accuracy and a false non-match rate of 0-2%.

Applications:

- Forensic DNA analysis in the field, for law enforcement and security applications
- Identification and monitoring of infectious disease
- Rapid identification of hazardous species
- Epidemiology, especially in low-resource areas
- Commercial personal genomics products
Advantages:

• Compatible with existing commercial handheld DNA sequencers
• Cost-effective
• Uses randomly sampled genomic DNA fragments, as opposed to predetermined short tandem repeat loci that are difficult to amplify, for better accuracy and more precise inferring of familial networks
• Accurate sample identification with low input and low coverage reference database
• Quick sample identification (scale of minutes)

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Patent Information:

Patent Pending

Related Publications:


Tech Ventures Reference:

• IR CU16211
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