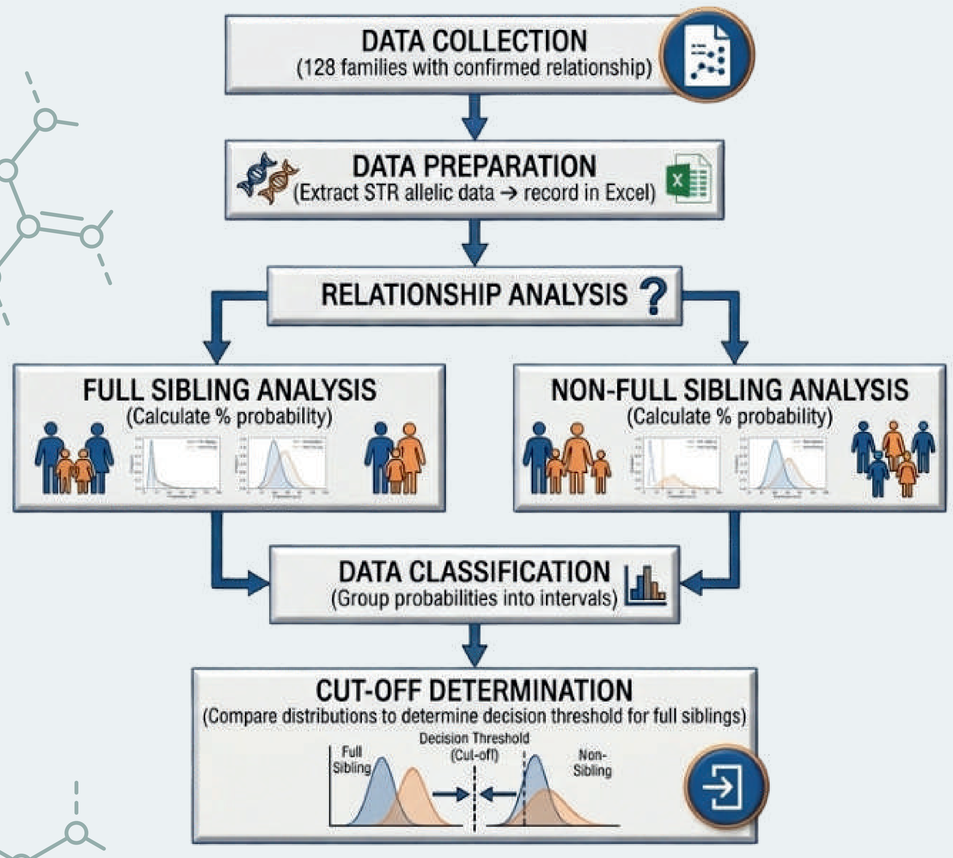
ESTABLISHING A CONFIDENCE PROBABILITY THRESHOLD FOR FULL-SIBSHIP ANALYSIS BASED ON AUTOSOMAL SHORT TANDEM REPEAT (STR) MARKERS

Haruesipat Chuederm[1], Supakit Khacha-ananda[2], Pattanapong Thangsunan[1]
Phatcharin Mahawong[2], Nitaya Khamkomkai[2], Pimpinan Punyathi[2]
[1]Division of Biochemistry and Biochemical Innovation, Department of Chemistry, Faculty of Science. Chiang Mai University
[2]Department of Forensic Medicine, Faculty of Medicine, Chiang Mai University
Email address: haruesipat_c@cmu.ac.th

Abstract

Kinship testing plays a critical role in forensic science and legal medicine for human identification. A confidence threshold for full-sibship analysis at 90% is currently used by the Forensic Genetics and Evidence Laboratory, Department of Forensic Medicine, Faculty of Medicine, Chiang Mai University to cut-off between matches or non-matches for full-sibling relationships. However, it is imperative to reevaluate the suitability of this criterion due to the intrinsic complexity of inheritance patterns and the growing genetic diversity within Thai population. This study aims to establish an optimized confidence threshold for full-sibship testing based on 15 autosomal STR markers. The inclusion criteria for data collection was to sample from families with at least two children whose biological relationships to both parents. Also, random pairings between members of various families were created for the non-sibling group. The combined paternity index (CPI) and the probability of sibship were calculated using GenoProof 3 software. One hundred and twenty-eight pairs of sibling samples were collected. The 125 pairs of confirmed full siblings (97.65%) yielded a probability of sibship within the range of 95.00–99.99%, indicating an extremely high level of confidence. Only one pair was identified within each of the probability ranges of 75.00–79.99%, 85.00–89.99%, and 90.00–94.99%, corresponding to moderate to high confidence levels.. However, the non-sibling group predominantly fell into the low-probability ranges: 115 pairs in the 0.00–4.99% range, 4 pairs in the 5.00–9.99% range, and 5 pairs in the 10.00–14.99% range. Single pairs were also observed in the 15.00–19.99%, 30.00–34.99%, 35.00–39.99%, and 65.00–69.99% ranges. In conclusion, our study suggests that the confidence threshold for full-sibship relationships should be adjusted to the 95.00–99.99% range to ensure maximum accuracy and reliability in forensic interpretations.

Methodology



Conclusion

In the confirmed full-sibling group (128 pairs), 97.6% showed a relationship probability of ≥95%, with most cases exceeding 99%. These results demonstrate that analysis using 15 STR loci provides high reliability for full-sibship evaluation. Therefore, a probability threshold of 95.00–99.99% is recommended for reporting full-sibling relationships, offering greater interpretative confidence than the previously used 90% cutoff.

A probability threshold of 95.00–99.99% is recommended.

Introduction

Genetic variation among individuals forms the basis of forensic identification and kinship analysis. In forensic genetics, highly polymorphic Short Tandem Repeats (STRs) are widely used due to their high discriminatory power. Relationship inference is typically evaluated using statistical parameters such as the Combined Paternity Index (CPI) and probability values. While parent–child relationships can be interpreted with high confidence, full-sibling testing is more complex because allele sharing varies across STR loci and is influenced by the number of loci analyzed and population allele frequencies. Although a 90% probability threshold is commonly used in practice, its suitability for full-sibship interpretation remains unclear. Therefore, this study aims to determine an optimized confidence threshold for full-sibship testing using 15 autosomal STR markers

Results and Discussion

Table 1. Summary of CPI and %Probability calculated from 15 autosomal STR loci

Sample Group	CPI Range	%Probability Range	Interpretation
Full siblings	$3.79 - 2.62 \times 10^{21}$	79.13% – 99.99%	Most samples showed %Probability > 99.9%, strongly supporting the hypothesis of a full sibling relationship
Unrelated individuals	$9.74 \times 10^{-8} - 2.0592$	< 1% – 67.31%	Most samples showed probabilities lower than 1%, indicating no support for a full sibling relationship

The combined paternity index (CPI) and the percentage of probability were calculated based on genotyping of 15 autosomal STR loci using GenoProof 3. The results clearly distinguished full siblings from unrelated pairs. The calculation was based on population allele frequencies and the product rule, combining the Paternity Index (PI) values across multiple STR loci. In the confirmed full sibling group (128 pairs), CPI values ranged from 3.79×10^{21} to 2.62×10^{21}, with the percentage of probability between 79.13% and 99.99%. Most samples showed probabilities higher than 99.9%, demonstrating the high discriminatory power of the 15 STR loci. The cases with relatively lower CPI values were explained by the presence of common alleles in the population, resulting in moderate PI values and consequently lower combined CPI. In the unrelated group (128 pairs), most CPI values were below 1 (9.74×10^{-8} to 2.0592), with the percentage of probability below 1, indicating no support for the full-sibling hypothesis. A small number of cases showed CPI slightly greater than 1, likely due to coincidental allele sharing, as expected under population genetics principles.

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