

การวิเคราะห์ทางสถิติสำหรับตรวจความสัมพันธ์บิดา-มารดา-บุตรและการหาอัตราการกลายใน
ฐานข้อมูลไทย



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ศูนย์วิทยทรัพยากร
จุฬาลงกรณ์มหาวิทยาลัย

วิทยานิพนธ์นี้เป็นส่วนหนึ่งของการศึกษาตามหลักสูตรปริญญาวิทยาศาสตรมหาบัณฑิต


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คณะวิทยาศาสตร์ จุฬาลงกรณ์มหาวิทยาลัย

ปีการศึกษา 2553

ลิขสิทธิ์ของจุฬาลงกรณ์มหาวิทยาลัย

STATISTICAL ANALYSIS FOR PARENTAGE TEST AND MUTATION RATE
DETERMINATION IN THAI DATABASE



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ศูนย์วิทยทรัพยากร
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A Thesis Submitted in Partial Fulfillment of the Requirements

for the Degree of Master of Science Program in Genetics

Department of Botany

Faculty of Science

Chulalongkorn University

Academic Year 2010

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Thesis Title Statistical analysis for parentage test and mutation rate
determination in Thai database.
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การหาอัตราการกลายในฐานข้อมูลไทย. (STATISTICAL ANALYSIS FOR
PARENTAGE TEST AND MUTATION RATE DETERMINATION IN THAI
DATABASE) อ.ที่ปรึกษาวิทยานิพนธ์หลัก : รศ.ดร. วรุณี จุฬาลักษณ์านุกูล, อ.ที่ปรึกษา
วิทยานิพนธ์ร่วม : ดร. ศิราวุธ กลิ่นบุหงา, 72หน้า.

การใช้ลายพิมพ์ดีเอ็นเอเพื่อหาความสัมพันธ์บิดา มารดา และบุตร จากครอบครัวที่ไม่ได้
เป็นญาติกันจำนวน 1,011 ครอบครัว โดยใช้ชุดน้ำยาสำเร็จรูปจำนวน 9 ตำแหน่ง ในการตรวจ
ความสัมพันธ์บิดา มารดา และบุตร จำนวน 324 ครอบครัว สำหรับชุดน้ำยาสำเร็จรูปจำนวน 15
ตำแหน่ง ใช้ตรวจความสัมพันธ์ระหว่างบิดา-บุตรและมารดา-บุตร จำนวน 305 ครอบครัวและ 382
ครอบครัวตามลำดับ เพื่อคำนวณหาค่า combined paternity index (CPI) หรือ combined
maternity index (CMI) พร้อมทั้งรวบรวมกรณีที่เกิดการกลายในบางครอบครัวด้วย ผลการศึกษา
พบว่าการตรวจความสัมพันธ์บิดา มารดา และบุตร มีค่า CPI จำนวน 376 ค่า ซึ่งมีค่า CPI อยู่
ระหว่าง 420.07 ถึง 359,558,681.35 ส่วนการตรวจความสัมพันธ์ระหว่างบิดา-บุตร มีค่า CPI
จำนวน 423 ค่า มีค่า CPI อยู่ระหว่าง 228.71 ถึง 38,900,000,000 และ การตรวจความสัมพันธ์
ระหว่างมารดา-บุตร มีค่า CPI จำนวน 543 ค่า มีค่า CPI อยู่ระหว่าง 70.45 ถึง 1,730,000,000 ใน
กรณีการเกิดการกลายพบทั้งหมด 35 กรณีด้วยกัน ซึ่งเป็นลักษณะการกลายในสองรูปแบบ คือการ
กลายในลักษณะรูปแบบที่มีการเพิ่มหรือลดของเบสลำดับซ้ำ จำนวน 34 กรณี และลักษณะรูปแบบ
ที่มีการเปลี่ยนแปลงของเบสเดี่ยว จำนวน 1 กรณี รายงานนี้ได้นำเสนอข้อมูลที่จะนำไปใช้เพื่อ
พิจารณาความเหมาะสมในการกำหนดค่า CPI หรือ CMI ขั้นต่ำเพื่อใช้ในการสรุปผลความเป็นบิดา
และ/หรือมารดาทางสายโลหิตของบุตรที่แท้จริง

ภาควิชา พุทธศาสนศาสตร์

สาขาวิชา พันธุศาสตร์

ปีการศึกษา 2553

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5072299623 : MAJOR GENETICS

KEYWORDS : PARENTAGE TEST / MUTATION RATE / COMBINED PATERNITY INDEX /
COMBINED MATERNITY INDEX

TAWAT RINTHACHAI : STATISTICAL ANALYSIS FOR PARENTAGE TEST
AND MUTATION RATE DETERMINATION IN THAI DATABASE. ADVISOR :
ASSOC. PROF. WARAWUT CHULALAKSANANUKUL Ph.D., CO-ADVISOR :
SIRAWUT KLINBUNGA Ph.D., 72 pp.

Using DNA fingerprinting to determine the relationship parents and children from families that are not relatives, each of 1,011 families. By the Profiler Plus on 9 STR loci to establish in relationship parents and children of 324 families. For the Identifiler on 15 STR loci used to detect relationships between fathers-children and mothers-children of 305 families and 382 families respectively. To calculate the combined paternity index (CPI) or the combined maternity index (CMI) and to collect the event of a mutation in some families. The results showed that in the examination of parent and child relationship with the CPI of 376 values which were the CPI values between 420.07 to 359,558,681.35. Examination of the relationship between the father – child with the CPI of 423 values were between 228.71 to 38,900,000,000 and monitoring the relationship between the mother - child of 543 values were between 70.45 to 1,730,000,000. In the case of the mutation was found for 35 cases with a characteristic mutation in two forms. Is to turn the feature on the increase or decrease of the base sequence repeat of 34 cases and feature a single base change in one case. This report presents data that will be used to determine the appropriateness of the CPI or the CMI to a minimum at the conclusion of a father and / or mother of child's true blood.

Department : Botany.....
Field of Study : Genetics.....
Academic Year :2010.....

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ACKNOWLEDGEMENTS

I really would like to express my appreciation to my supervisory committees for their encouragement for this thesis and commented on the manuscript. First of all, I am deeply indebted to my advisor, Assoc. Prof. Dr. Warawut Chulalaksananukul and my co-advisor, Dr. Sirawut Klinbunga for their help and suggest all the time I have work on this thesis. I also thanks to other committee members, Assist. Prof. Dr. Manit Kidyoo and Dr. Rachaneekorn Tammachote for their helpful suggestion and corrections during my study. And I wish to thank Assoc. Prof. Dr. Budsaba Rerkamnuaychoke, the external examiner of this thesis defense, allowed me to use the facility of Human Genetics Unit and advised me throughout this study.

My thesis has been supported by Faculty of Medicine Ramathibodi Hospital, Mahidol University. I hope to use my knowledge that I receive from this thesis there. And I would like to thank my friends at Department of Botany for their kind support.

I am so grateful to my colleagues of Human Genetics Unit for their help, advice, guidance, suggestions, cheerfulness and kind support.

Finally, I would like to thank my family for their love. The usefulness of this thesis, I dedicate to my father, my mother and all teachers who have taught me since my childhood.

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LIST OF ABBREVIATIONS

PI	=	Paternity Index
MI	=	Maternity Index
CPI	=	Combined Paternity Index
CMI	=	Combined Maternity Index
PCR	=	Polymerase Chain Reaction
DHPLC	=	Denaturing High-Performance Liquid Chromatography



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CHAPTER I

INTRODUCTION

1.1 Background and rationale

Since Alec Jeffreys established DNA fingerprint technique, human DNA sequence has been used in paternity testing and forensic casework investigation (Buckleton, Triggs, and Walsh, 2005). DNA testing becomes highly accurate analysis of the genetic profiles between parent-offspring pairs according to the Mendel's laws of inheritance (Ayadi et al., 2007, Mixich, Ioana, and Mixich, 2004). The method of choice in paternity and forensic laboratories is based on the interpretation of similarities or differences at genetic marker loci of biochemically in vitro amplified small regions of genomic DNA, known as short tandem repeat (STR) loci or microsatellites to generate population STR databases all over the world (Halos et al., 1999, Lee et al., 2001, Thomson et al., 1999). The STR typing technique allows DNA discrimination and association between biological evidence and its source. Also this technique plays an important role in human identification and paternity testing which involves the statistic parameters such as the power of discrimination, probability of exclusion and likelihood ratio or paternity index. The paternity index (PI) (maternity index, MI, in a case of the alleged mother) is a special parameter used for paternity testing to describe the likelihood ratio (LR) as defined by contrasting hypotheses (Ayres and Balding, 2005, Gjertson et al., 2008). Paternity testing is standard practice in DNA laboratory to exclude the fatherhood only when a minimum of three mismatches occurs between alleged parent-offspring pairs but the possibility of mutations must be taken into account for cases where one or two mismatches are observed as inconclusive (Balloch et al., 2008). Therefore, additional tests will be essential to confirm the results with hypervariable regions (HV1 and HV2) of mitochondrial DNA, X and/or Y-STR (Narkuti et al., 2007). Nowadays, many laboratories have been focusing to the statistic tools for paternity testing and human identification to support the laboratory results. It was reported that the paternity index and the probability of paternity in routine service paternity cases

were calculated and used for approximately 73% and 78% in 2000 and 2001 from a total of 33 and 36 laboratories, respectively (Hallenberg and Morling, 2002). In common paternity testing scenario, the statistic parameters such as paternity index (PI) is important to increase the confidence not only for forensic scientist but also in the court.

1.2 Research questions

1. How much each paternity index from statistical analysis for parentage testing in Thai DNA database.
2. How much each locus mutation rate in Thai DNA database.

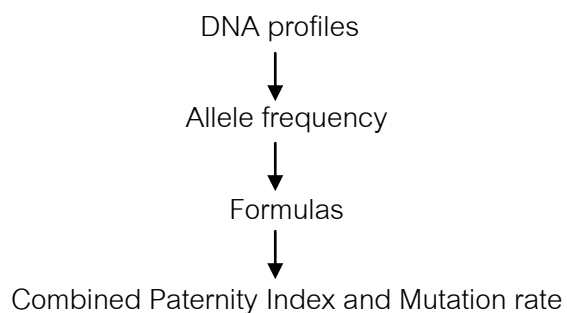
1.3 Objectives

1. To conduct statistical analysis for parentage testing in Thai population.
2. To determine the mutation rate in Thai DNA database.
3. To compare the calculation reliability of the statistic parameter between manual calculation and commercial analysis software.

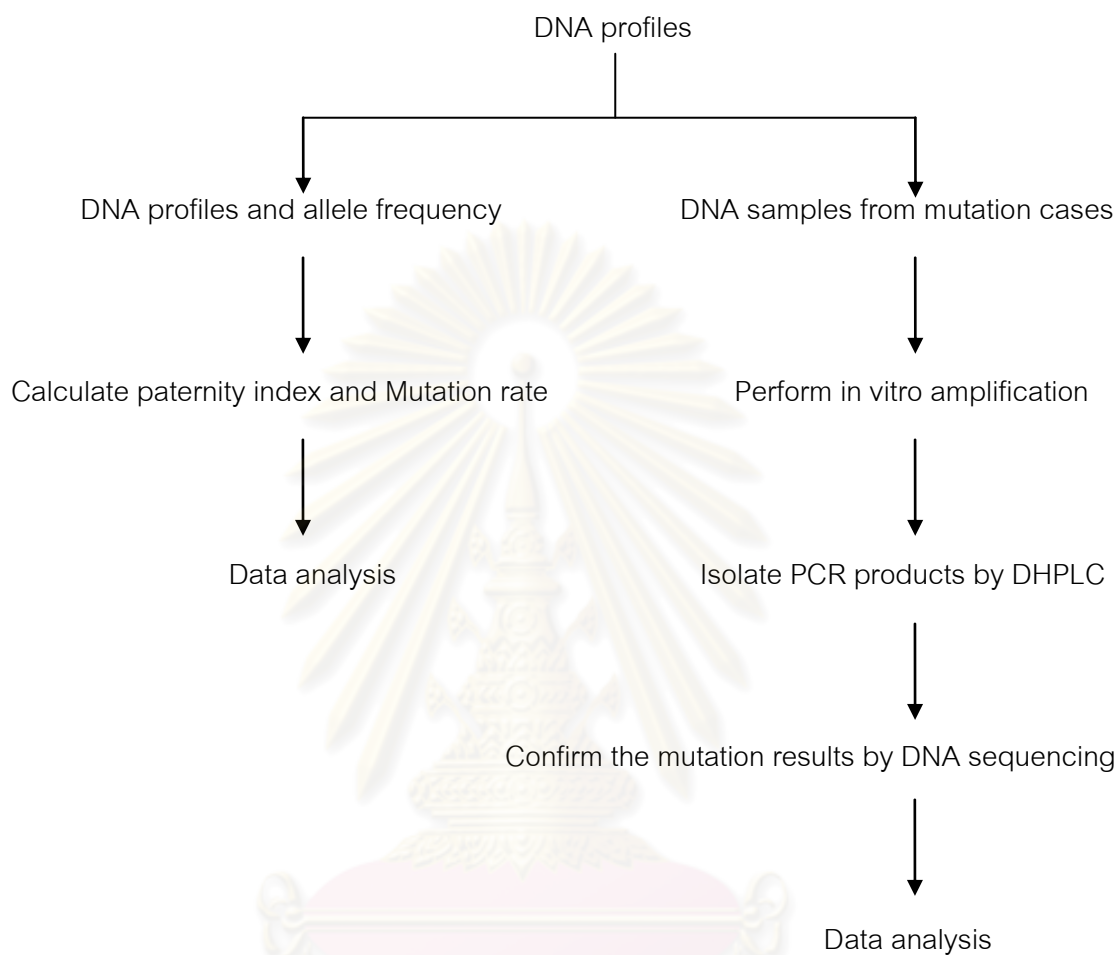
1.4 Hypothesis

1. Paternity index is a great value to identify parentage test in Thai DNA database.

1.5 Conceptual framework



1.6 Methodologies



1.7 Expected Benefit

Firstly, this study will generate the paternity index and the probability of paternity of Thai population for application in routine paternity testing. Secondly, the mutation rate of 9 STR loci in trios and 15 STR loci in duos will be calculated and applied to evaluate the real paternity cases with the incidence of mutation. Finally, results of this study will be used to compare the calculation reliability of these statistic parameters between manual calculation and one commercial analysis software.

1.8 Research Methodology

1. Collect of DNA profiles from parentage tests
2. Prepare of DNA profiles and allele frequency of Thai population in to database
3. Calculate paternity index by commercial analysis software
4. Data analysis
4. Collect of DNA samples from mutation case
5. PCR product
6. Isolate PCR products by DHPLC
7. DNA sequencing
8. Data analysis
9. Conclusion



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CHAPTER II

REVIEW OF THE RELATED LITERATURES

Paternity testing is being increasingly requested with the purpose of dispute presumptive fatherhood. The ability to constitute the biological father is analyzed, using the short tandem repeat (STR) profiling in alleged father, mother and child (Ayadi et al., 2007, Iwamura et al., 2008). Generally, the parentage testing is performed by commercial DNA paternity testing kit to investigate whether the alleged parent is the true parent of the child based on the DNA profiles of the individuals involved (Balloch et al., 2008, Ayres, 2000). Moreover, the evaluation of DNA evidence for parentage testing, the battery of potentially applicable genetic polymorphisms has never been so great, and parentage testing laboratories are experiencing increasing economic competition (Lee et al., 2001, Henke et al., 1999). According to that DNA polymorphism is very useful in paternity analysis, genetic marker analysis is a powerful tool for paternity testing. The most polymorphic genetic markers in the human genome are belonged to the tandem repeated mini- and micro-satellites (Cifuentes et al., 2000). Microsatellites are short tandem repeated DNA sequences widespread throughout the human genome which exhibit individual genetic differences exploited extensively in several fields including genetic mapping, linkage analysis, population studies, personal identification, and paternity testing Turchi et al., 2004). Short Tandem Repeat (STR) loci are polymorphic loci found throughout all eukaryotic genomes. They characteristically consist of tandem arrays of short repeated sequences of 2–6 base pairs in length. Polymorphism occurs when the number of copies of the repeat sequence present at a given STR locus varies between individual chromosomes. DNA profiling by analysis of STR loci has been widely used in forensic casework since 1993. These benefits are as pertinent in parentage testing as in a forensic casework. Greater sensitivity will allow the use of more convenient sample types. The continuing development and validation of STR systems for use in identity testing have now resulted in twenty or more suitable STR systems being available either commercially or via published primer sequences. An abundant event to the paternity tester provided that these systems can be shown to satisfy the

basic requirements of Mendelian inheritance, independence and sufficiently low mutation rates, then a battery of such tests can be applied (Thomson, Pilotti et al., 1999). The usefulness of STR loci in relatedness testing has been the subject of many recent studies. Multiplexes have a high power of discrimination for paternity testing Thomson, Ayres et al., 2001. The Combined DNA Index System (CODIS), originally established by the FBI in 1998, is composed of 13 autosomal short tandem repeat (STR) loci in addition to a sexual identity test. STR DNA typing is the “gold standard” of human identification but evidential value of a genetic match can be easily misinterpreted. Therefore, careful use of statistical methods is essential for the proper evaluation of laboratory results (Biruš et al., 2003).

The current situation in DNA testimony has arisen from a path that began in 1985 (Jeffreys, Wilson, and Thein, 1985). The model in Sir Alec’s work was not a population genetic model. However, DNA probabilities became based on the standard population genetic assumptions of Hardy-Weinberg and linkage equilibrium (Curran, Walsh, and Buckleton, 2007). Samples from 121 cases of disputed paternity, routinely submitted to this laboratory, were analyzed using the two multiplex STR systems. The data was then analyzed to give information on expected paternity indices and exclusion rates for these STR systems. In addition, population frequency databases have been constructed for the three major ethnic groups in the UK; British Caucasians, Afro-Caribbeans and Asians. These databases were analyzed for consistency with Hardy-Weinberg (HW) proportions and were subsequently used in the calculation of paternity indices and in other analysis carried out on the data [6]. A sample of 100 Finnish trios and duos with three sets of commonly used STR markers (containing 15, 10 and 9 markers) and 14 population databases, representing different marker allele frequencies (Moroni et al., 2008). To facilitate the introduction of DNA typing in the Philippines, a population database from the National Capital Region (NCR), the largest urban center in the country, was constructed (Halos et al., 1999). The validity of 15 STR loci included in the identifiler system for the use in paternity testing in Poland (Jacewicz et al., 2004). There is now widespread acceptance that the power of independence testing to find realistic

disequilibrium in DNA datasets of modest size (200-1000 samples) is very restricted (Triggs and Buckleton, 2002).

The laboratory that carried out the initial paternity test did not address the possibility of mutational events in a report despite existing literature on methods for analyzing and interpreting the effects of apparent mutations on paternity testing conclusions (Balloch et al., 2008). Step mutations are characterized by one or two repeat additions or diminutions creating an incompatibility that is impossible to distinguish as a mutation or exclusion (Phillips et al., 2008). The stepwise mutation model has been proposed to explain conversion between alleles at STR loci (Dawid, Mortera, and Pascali, 2001). Paternity test protocols are based on microsatellite polymorphisms (short tandem repeats, STRs), a class of loci affected by non-sporadic gametic mutation. The most plausible genetic mechanism involved in STR mutations is two mechanisms may be responsible for mutation: DNA slippage during replication, and recombination between DNA strands which both depends on repeated motif, allele size, chromosome position, GC content in flanking DNA, cell division, sex and genotype (Turchi et al., 2004). In paternity testing, one or two mismatches between alleged parent-offspring pairs are usually still regarded as representing true paternity because they might be due to one-step mutations or null alleles. The criteria concerning exclusions and consequences of mutations have been evaluated in 131 presumed parent-child combinations with mismatches from immigration families using 22 STR loci (Kersbergen et al., 2008). A model for the probability q_{ij} that allele i mutates to allele j in the pre-meiotic stage. The paternal and maternal mutation rates to be equal but the model can equally be applied with different mutation rates in the maternal and paternal germ lines (Dawid et al., 2001). All 15 loci provided by the multiplex kit were determined and the non-matching locus is regarded as being a mutation. Using the before mentioned statistical program, the mutation can be handled as a negative factor for paternity calculation. A sufficient paternity probability is achieved after the mutation calculation. Therefore, it is important to have a statistical methodology for making inferences about mutation rates from paternity casework. An object-oriented Bayesian

network is used to facilitate computation of the likelihood function for the mutation parameters (Vicard et al., 2008). Paternity index (PI) shall be modified for possible mutation patterns between tested individuals when isolated mismatches among tested systems which normally lead to an opinion of non-relationship, may be the result of mutant DNA causing false conclusions. The method for modifying PI shall be documented (Gjertson et al., 2008). Paternity index ($PI=X/Y$) is even to $\mu/4P(Q)$, where μ represents mutation rate for mutated locus and $P(Q)$ is the frequency of the Q mutated allele in the population (Turchi et al., 2004).

In paternity testing, it is interested in calculating the probability that the tested man (alleged father) is the biological father (or the ratio of that probability to the probability that a random man is the biological father) given data on genotypes or haplotypes of some DNA markers. If the weight of the evidence is calculated, it shall be based on likelihood ratio principles (Buckleton, Triggs, and Walsh, 2005). In paternity cases, the likelihood ratio (LR) is called the paternity index which is the posterior probability of paternity called the probability of paternity (W). If other values on likelihood ratio principle are presented, e.g., Wahrscheinlichkeit (W), the premises and assumptions shall be clearly specified. The W-value (Wahrscheinlichkeit = probability of paternity) was devised by Essen-Möller for the alleged father-mother-child trios which enabled hemogenetic results to be expressed numerically as a Bayesian a posteriori probability of paternity (Essen-Möller, 1938). Again, highest/lowest values observed in a series were denoted as maximum/minimum W values (Henke et al., 1999). In much the analyses have made use of the likelihood ratio which is a standard statistical procedure in parentage testing. Combined with a prior odds equally in favour of the putative parent and an unrelated individual, the Essen-Möller probability of parentage that is $PI/(1+PI)$, can be calculated (Essen-Möller, 1938). In simple cases, this statistics is the conditional probability that a second individual would have the same DNA profile as the one under consideration termed the match probability, or its reciprocal which is mathematically equivalent to the likelihood ratio (Curran et al., 2007). The likelihood ratio (LR), that is the ratio of the probability of observing the given DNA profiles under two different

relationship scenarios, is a useful tool for answering the question of interest (Decker et al., 2008). The paternity index is the special case of the likelihood ratio that commonly arises in paternity testing (Ayres and Balding, 2005). In 1956, Gürtler proposed the ratio $PI = X/Y$ as a basic index to report the likelihood of paternity with large values suggesting the fatherhood (Essen- Möller, 1938). Additionally, for international comparisons, the combined paternity index (CPI) is given when possible (Vicard et al., 2008).

Laboratories are responsible for establishing and admitting their exclusion criteria. Preference shall be given to criteria stated in terms of a PI threshold. Laboratory procedures shall document assumptions and validate frequencies used to compute PI. The reference database shall be selected so that it can be used for estimation of the probability of obtaining the genetic results under the assumption of the relevant hypotheses. If a threshold PI exists for issuing test reports, the values shall be documented. In addition to the combined PI, test reports shall also contain the individual PI's for each genetic system reported and the racial/ethnic backgrounds used for calculations. If the probability of paternity (W) is reported, then the prior probability assumption used to calculate W shall be stated. Test reports shall include statements of assumptions, validation and computational techniques whenever alternative biostatistical methods to PI are used (Gjertson et al., 2008).

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CHAPTER III

MATERIALS AND METHODS

3.1 Materials

A. Instruments and laboratory supplies for amplification

1. Automated pipette, P2/P10/P20/P100/P200/P1000 μ l: Gilson, France
2. GeneAmp PCR System 9700: Applied Biosystems, USA
3. Veriti 96 Well Fast Thermal Cycler: Applied Biosystems, USA
4. Freezer (-80°C): Sanyo, Japan
5. Freezer (-20 °C): Sanyo, Japan
6. Refrigerator (4 °C): Sanyo, Japan
7. Microcentrifuge tube (1.5 ml and 0.5 ml in sizes): Treff, Switzerland
8. Top-bench microcentrifuge: JOUAN, France
9. Water bath: MEMMERT, Germany
10. Vortex: FINEVORTEX, Korea
11. Pipette tip 2-10 μ l: Gilson (white), 20-200 μ l: Corning Incorporated (yellow), Mexico
12. 1-200 μ l Universal Fit Pipette Tips Yellow: Corning Incorporated (yellow), Mexico
13. 1-10 μ l Universal Fit Pipette Tips Yellow: Corning Incorporated (yellow), Mexico

B. Reagents for amplification

1. Deionized water, PCR grade: Gibco, USA
2. 10X PCR buffer II (100mM Tris-HCl, pH 8.3, 500mM KCl): Applied Biosystems, USA
3. 25mM MgCl₂: Applied Biosystems, USA
4. Deoxynucleotide triphosphate (1.25mM each of dATP, dTTP, dGTP, dCTP): Applied Biosystems, USA
5. Primer (5 pmole/μl): Applied Biosystems, USA
6. 250 units AmpliTaq Gold DNA polymerase: Applied Biosystems, USA

C. Reagents and instrument for PCR purification

1. High Pure PCR Product purification Kit: Roche Diagnostics, Germany
2. Top-bench microcentrifuge: JOUAN, France
3. Water bath: MEMMERT, Germany

D. Reagent and instrument for Gel Electrophoresis

1. 0.5X TBE buffer (0.089 M Tris-borate, 0.089 M Boric acid, and 0.002 M EDTA): CARLO ERBA, France
2. Gel loading dye solution: Promega, USA
3. DNA molecular weight marker (contained linear double strand DNA fragments of 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000 and 2650 base pairs): BioExcellence, USA
4. 2% agarose gels:FMC, USA

5. Horizontal gel electrophoresis: Mupid, Japan
6. UV-transluminator with camera and computer processing:
Stratagene, Egle Eye II Still video, USA
7. Ethidium Bromide: Sigma, USA

E. Reagents and instrument for DHPLC

1. WAVE System 4500 HT-HS : Transgenomic, USA
2. WAVE Optimized Buffer A : Transgenomic, USA
3. WAVE Optimized Buffer B : Transgenomic, USA
4. WAVE Optimized Buffer D : Transgenomic, USA
5. Water HPLC Grade : Transgenomic, USA

F. Reagents for DNA sequencing

1. BigDye Terminator v1.1 cycle sequencing kit: Applied Biosystems,
USA
2. Primer (1.6 pmole/ μ l): Applied Biosystems, USA
3. Deionized water, PCR grade: Gibco, USA

G. Reagent and instrument for cycle sequencing purification

1. 3 M Sodium acetate (NaOAc), pH 4.6: CARLO ERBA, France
2. Absolute ethanol: CARLO ERBA, France
3. Top-bench microcentrifuge: JOUAN, France
4. DNA 120 SpeedVac Concentrator: ThermoFisher scientific, USA

H. Instruments and laboratory supplies for DNA sequencing

1. ABI Prism 3130 Genetic Analyzer: PE Applied Biosystems, USA
2. Performance Optimized Polymer 4: Applied Biosystems, USA
3. 3130 Capillaries, 36 cm: Applied Biosystems, USA
4. MicroAmp Optical 96-well reaction plate: Applied Biosystems, USA
5. 96-Well plate septa (20/pkg.): Applied Biosystems, USA
6. MicroAmp Reaction Tube with CAPs: Perkin Elmer Cetus, USA

Table 1 Primers for single STR amplification

Primers	Nucleotide Sequence (5'-3')
D21S11 Forward primer	ATATGTGAGTCAATTCCCCAAG
D21S11 Reverse primer	TGTATTAGTCAATGTTCTCCAG
FGA Forward primer	GCCCCATAGGTTTTGAACTCA
FGA Reverse primer	TGATTTGTCTGTAATTGCCAGC
vWA Forward primer	CCCTAGTGGATAAGAATAATC
vWA Reverse primer	GGACAGATGATAAATACATAGGATGGATGG
CSF1PO Forward primer	AACCTGAGTCTGCCAAGGACTAGC
CSF1PO Reverse primer	TTCCACACACCACTGGCCATCTTC
D8S1179 Forward primer	TTTTTGTATTCATGTGTACATTCCG
D8S1179 Reverse primer	CGTAGCTATAATTAGTTCATTTTCA
D13S317 Forward primer	ACAGAAGTCTGGGATGTGGA
D13S317 Reverse primer	GCCCCAAAAGACAGACAGAA
D2S1338 Forward primer	CCAGTGGATTTGGAAACAGA
D2S1338 Reverse primer	ACCTAGCATGGTACCTGCAG
D7S820 Forward primer	TGTCATAGTTTAGAACGAACTAACG
D7S820 Reverse primer	CTGAGGTATCAAAAACCTCAGAGG

Table 1 Primers for single STR amplification (continued)

Primers	Nucleotide Sequence (5'-3')
TH01 Forward primer	GTGATTCCCATTGGCCTGTTCCTC
TH01 Reverse primer	ATTCCTGTGGGCTGAAAAGCTC
D3S1358 Forward primer	ACTGCAGTCCAATCTGGGT
D3S1358 Reverse primer	ATGAAATCAACAGAGGCTTG
D5S818 Forward primer	GGGTGATTTTCCTCTTTGGT
D5S818 Reverse primer	TGATTCCAATCATAGCCACA
D18S51 Forward primer	GAGCCATGTTTCATGCCACTG
D18S51 Reverse primer	CAAACCCGACTACCAGCAAC
D19S433 Forward primer	CCTGGGCAACAGAATAAGAT
D19S433 Reverse primer	TAGGTTTTTAAGGAACAGGTGG
D16S539 Forward primer	GATCCCAAGCTCTTCCTCTT
D16S539 Reverse primer	ACGTTTGTGTGTGCATCTGT
TPOX Forward primer	CACTAGCACCCAGAACCGTC
TPOX Reverse primer	CCTTGTCAGCGTTTATTTGCC

3.2 Procedure

1. DNA profiles

DNA profiles from 1,011 unrelated Thai families are recorded. All samples were the left-over materials of parentage routine service who submitted the DNA samples at Human Genetics Unit, Department of Pathology, Faculty of Medicine, Ramathibodi Hospital, Mahidol University. The document for sample collection was submitted to Ramathibodi Hospital Ethic Committee.

2. Allele frequencies in a Thai population database

Population studies indicate that microsatellite alleles can be applied to Hardy-Weinberg criteria and these alleles segregate in a Mendelian fashion in families and are therefore, ideal candidates for personal identification systems in parentage test. DNA profile frequencies are calculated by first considering the genotype frequency for each

locus and then multiplying the frequencies across all loci. The DNA profile frequencies for fifteen short tandem repeat (STR) loci are determined using allele frequencies from a Thai population data of 420 alleles (210 unrelated Thai individuals) using the commercially available AmpF/STR Identifiler kit (Rerkamnuaychoke et al., 2006).

3. Calculation of paternity/maternity index

The statistic values in DNA profiling analysis will be calculated for the paternity/maternity index and the probability of parentage by using a commercially available computer program and manual calculation. A likelihood ratio is a ratio of two probabilities of the same evidence under different hypotheses. The weight of the evidence is calculated, and it shall be based on likelihood ratio principles. Therefore, the paternity index, PI, is a likelihood ratio. The two hypotheses are as following (Buckleton, Triggs, and Walsh, 2005)

$$LR = PI = H_p / H_d$$

Paternity trios: mother, child, and alleged father could be:

H_p : The alleged father is the true father (and the mother is the true mother).

H_d : A random person who is not related to the alleged father is not the true father (and the mother is the true mother).

Suppose that an STR locus has n alleles, a, b, c, \dots , with allele frequencies P_a, P_b, \dots , respectively. For paternity trios, PI can then take one of the values if the alleged father is excluded. A compilation of formulae appears in $1/P_a, 1/2P_a, 1/(P_a+P_b), 1/2(P_a+P_b)$, or 0.

Paternity duos: child and alleged father could be:

H_p : The alleged father is the true father (and the true mother's genotype is unknown).

H_d : A random person who is not related to the alleged father is not the true father (and the true mother's genotype is unknown).

A compilation of formulae appears in $1/P_a, 1/2P_a, (P_a+P_b)/4P_aP_b, 1/4P_a$, or 0.

Maternity duos: child and alleged mother could be:

H_p : The alleged mother is the true mother (and the true father's genotype is unknown).

H_d : A random person who is not related to the alleged mother is not the true mother (and the true father's genotype is unknown).

A compilation of formulae appears in $1/P_a$, $1/2P_a$, $(P_a+P_b)/4$, $P_a P_b$, $1/4P_a$, or 0.

Profile matching is the ultimate step in forensic DNA analysis. The FEDDS-Profile Management software (ESR, Institute of Environmental Science & Research Limited, New Zealand) has various matching functions depending on the configuration.

Procedure

1. Load the profiles under a single case number.
2. From the Match menu, select Run Paternity Match. The Run Paternity Match window opens, as shown below.
3. Select one of the Match radio buttons. If a Paternity Profile is selected, enter the profile's barcode in the Profile Barcode field.

4. Calculation of mutation rate

In the case that one or two mismatches from several loci are observed in parentage testing, it is often assumed to be due to a mutation event rather than a genuine exclusion. In a family which the maternal and paternal STR loci cause allelic mismatch in the children, it is confirmed by performing additional tests under issues using hypervariable regions (HV1 and HV2) of mitochondrial DNA, X chromosome and Y chromosome STR analysis [10]. Mutation rates for the STR markers used in paternity tests are approximately 5×10^{-4} to 7×10^{-3} per generation (von Wurmb-Schwark et al., 2006). Such a rate is commonly estimated by the observed frequency, $\mu = s/n$, of inferred mutation (μ = locus-specific rate of one-step parental mutations) at that marker in a casework, where n is the total number of meioses, and s , the number of these seemed to be mutations (Vicard et al., 2008). The mutation rate will be calculated and applied to evaluate the real paternity cases with the incidence of mutation at the locus established to DNA sequencing.

5. Amplification and Sequencing

All amplified alleles of mutation cases are excised from DHPLC, extracted by using of High Pure PCR Product Purification kit (Roche, Mannheim, Germany) and subsequently reamplified. The nucleotide sequence of the PCR products is used for direct sequencing using the BigDye Terminator v1.1 Cycle Sequencing kit (Applied Biosystems, Foster City, CA, USA) with the purified alleles as templates. DNA sequences were

analyzed by the Applied Biosystems DNA Sequencing Analysis Software v5.1 and were compared with BioEdit v7.0.9.

6. Data analysis

The statistical analysis for parentage test is performed on the FEDDS-Profile Management software (ESR, Institute of Environmental Science & Research Limited, New Zealand) and manual calculation using the formula in part 3 calculation of paternity/maternity index.



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CHAPTER IV RESULTS

A total of 1,011 families were observed with at least one matching allele for parentage tests. For trio (Mother, Child and Alleged Father) for 324 families, 376 CPI values (Table 2), motherless duo (Child and Alleged Father) for 305 families, 423 CPI values (Table 5) and fatherless duo (Child and Alleged Mother) for 382 families, 543 CMI values (Table 8) have been calculated.

Table 2 Relative frequency of CPI range from trio parentage tests.

CPI range in trio	Relative frequency	Percentage of relative frequency (%)
1 to 100	0	0
101 to 1,000	1	0.27
1,001 to 10,000	80	21.28
10,001 to 100,000	170	45.21
100,001 to 1,000,000	81	21.54
1,000,001 to 10,000,000	35	9.31
>10,000,000	9	2.39
Total	376	100

Figure 1 Relative frequency of CPI range from trio parentage tests

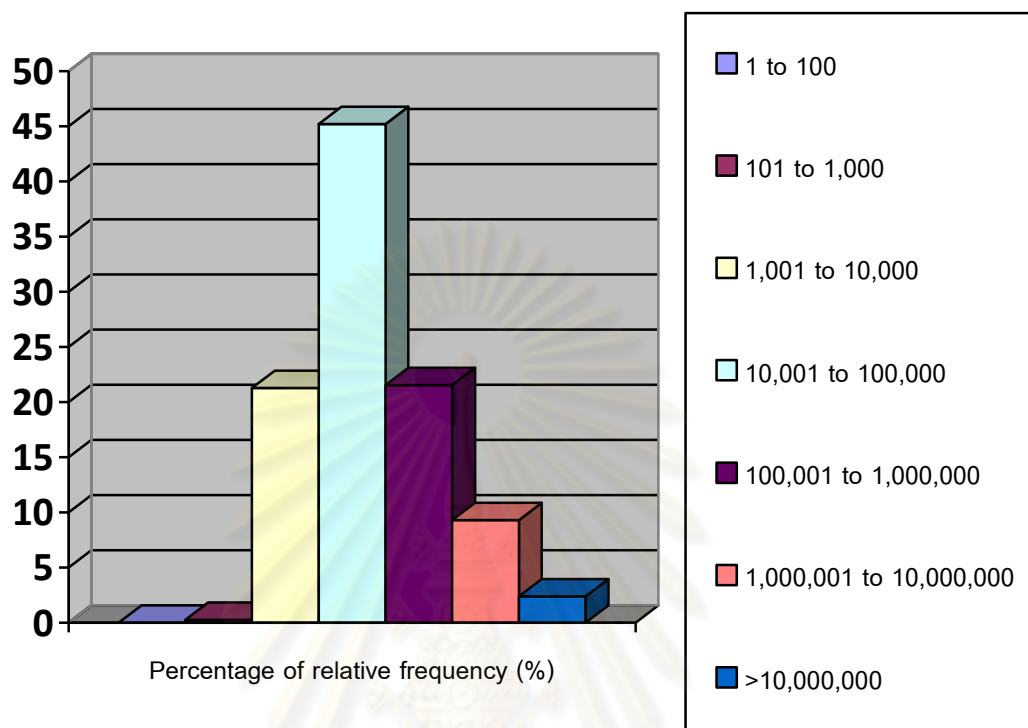


Table 3 The minimum CPI value resulted from trio parentage test.

Locus	Mother	Child	Alleged Father	Formula	PI
D3S1358	(15, 16)	(15, 17)	(15, 17)	$1/(2*P[17])$	2.30
vWA	(14, 18)	(14, 14)	(14, 16)	$1/(2*P[14])$	1.95
FGA	(22, 24)	(21, 22)	(21, 22)	$1/(2*P[21])$	3.88
D8S1179	(10, 12)	(10, 12)	(10, 16)	$1/(2*(P[10]+P[12]))$	1.82
D21S11	(29, 30)	(29, 30)	(29, 33.2)	$1/(2*(P[29]+P[30]))$	1.00
D18S51	(12, 17)	(15, 17)	(13, 15)	$1/(2*P[15])$	2.23
D5S818	(12, 13)	(11, 13)	(9, 11)	$1/(2*P[11])$	1.85
D13S317	(11, 12)	(11, 11)	(9, 11)	$1/(2*P[11])$	2.18
D7S820	(11, 12)	(11, 11)	(8, 11)	$1/(2*P[11])$	1.48
Minimum CPI					420.07

Table 4 The maximum CPI value resulted from trio parentage test.

Locus	Mother	Child	Alleged Father	Formula	PI
D3S1358	(15, 17)	(15, 17)	(15, 17)	$1/(P[15]+P[17])$	1.99
vWA	(16, 16)	(16, 19)	(14, 19)	$1/(2*P[19])$	4.39
FGA	(23, 25)	(23, 24.2)	(19, 24.2)	$1/(2*P[24.2])$	100.00
D8S1179	(10, 12)	(10, 10)	(10, 14)	$1/(2*P[10])$	3.38
D21S11	(29, 31.2)	(29, 30)	(30, 30)	$1/P[30]$	3.97
D18S51	(15, 16)	(16, 21)	(17, 21)	$1/(2*P[21])$	23.81
D5S818	(10, 11)	(10, 12)	(10, 12)	$1/(2*P[12])$	2.12
D13S317	(8, 11)	(7, 8)	(7, 11)	$1/(2*P[7])$	250.00
D7S820	(10, 11)	(11, 12)	(10, 12)	$1/(2*P[12])$	2.44
Maximum CPI					359,558,681.35

Using the 9 STR loci for trio parentage test with very low CPI value (420.07) in Table 3 and very high CPI value (359,558,681.35) in Table 4 were observed.

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Table 5 Relative frequency of CPI range from motherless duo parentage tests.

CPI range in duo	Relative Frequency	Percentage of relative frequency (%)
1 to 100	0	0
101 to 1,000	13	3.07
1,001 to 10,000	81	19.15
10,001 to 100,000	128	30.26
100,001 to 1,000,000	125	29.55
1,000,001 to 10,000,000	46	10.88
>10,000,000	30	7.09
Total	423	100

Figure 2 Relative frequency of CPI range from motherless duo parentage tests

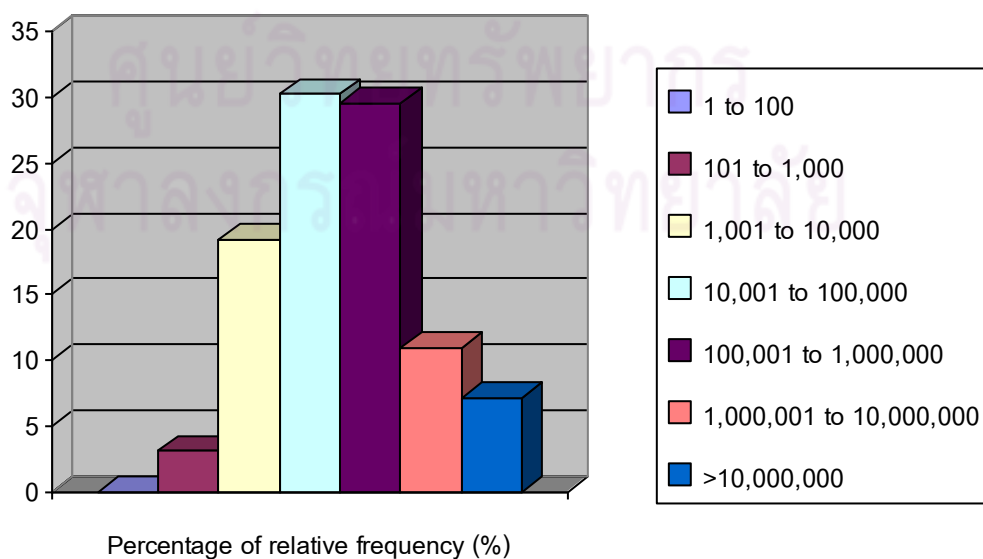


Table 6 The minimum CPI value resulted from motherless duo parentage test.

Locus	Child	Alleged Father	Formula	PI
D8S1179	(13, 13)	(12, 13)	$1/(2*P[13])$	2.99
D21S11	(29, 30)	(29, 30)	$(P[29]+P[30])/(4*P[29]*P[30])$	1.99
D7S820	(9, 11)	(8, 9)	$1/(4*P[9])$	4.55
CSF1PO	(7, 12)	(11, 12)	$1/(4*P[12])$	0.66
D3S1358	(15, 17)	(16, 17)	$1/(4*P[17])$	1.15
TH01	(8, 9)	(7, 9)	$1/(4*P[9])$	0.70
D13S317	(8, 11)	(8, 8)	$1/(2*P[8])$	1.71
D16S539	(11, 12)	(10, 11)	$1/(4*P[11])$	0.84
D2S1338	(17, 23)	(19, 23)	$1/(4*P[23])$	1.52
D19S433	(13, 15.2)	(13, 14.2)	$1/(4*P[13])$	0.89
vWA	(17, 20)	(14, 17)	$1/(4*P[17])$	1.04
TPOX	(8, 9)	(9, 10)	$1/(4*P[9])$	1.91
D18S51	(14, 21)	(12, 14)	$1/(4*P[14])$	1.40
D5S818	(12, 13)	(9, 13)	$1/(4*P[13])$	1.50
FGA	(21, 23)	(21, 24)	$1/(4*P[21])$	1.94
Minimum CPI				228.71

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Table 7 The maximum CPI value resulted from motherless duo parentage test.

Locus	Child	Alleged Father	Formula	PI
D8S1179	(15, 15)	(11, 15)	$1/(2 * P[15])$	2.99
D21S11	(31.2, 32.2)	(30, 31.2)	$1/(4 * P[31.2])$	3.52
D7S820	(12, 12)	(11, 12)	$1/(2 * P[12])$	2.44
CSF1PO	(9, 11)	(9, 12)	$1/(4 * P[9])$	13.16
D3S1358	(17, 18)	(16, 17)	$1/(4 * P[17])$	1.15
TH01	(9, 12)	(7, 12)	$1/(4 * P[12])$	53.00
D13S317	(8, 9)	(9, 12)	$1/(4 * P[9])$	1.50
D16S539	(13, 14)	(12, 13)	$1/(4 * P[13])$	2.38
D2S1338	(18, 23)	(18, 19)	$1/(4 * P[18])$	3.62
D19S433	(13.2, 15.2)	(13.2, 15.2)	$(P[13.2]+P[15.2])/(4 * P[13.2] * P[15.2])$	8.38
vWA	(14, 15)	(15, 18)	$1/(4 * P[15])$	9.62
TPOX	(9, 10)	(9, 10)	$(P[9]+P[10])/(4 * P[9] * P[10])$	9.97
D18S51	(13, 16)	(16, 20)	$1/(4 * P[16])$	1.28
D5S818	(10, 14)	(12, 14)	$1/(4 * P[14])$	14.71
FGA	(18, 24)	(18, 19)	$1/(4 * P[18])$	9.62
Maximum CPI				3.89×10^{10}

Using the 15 STR loci for motherless duo parentage test with very low CPI value (228.71) in Table 6 and very high CPI value (3.89×10^{10}) in Table 7 were observed.

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Table 8 Relative frequency of CMI range from fatherless duo parentage tests.

Range of CMI in duo	Relative Frequency	Percentage of relative frequency (%)
1 to 100	1	0.18
101 to 1,000	21	3.87
1,001 to 10,000	89	16.39
10,001 to 100,000	162	29.83
100,001 to 1,000,000	153	28.18
1,000,001 to 10,000,000	86	15.84
>10,000,000	31	5.71
Total	543	100

Figure 3 Relative frequency of CMI range from fatherless duo parentage tests

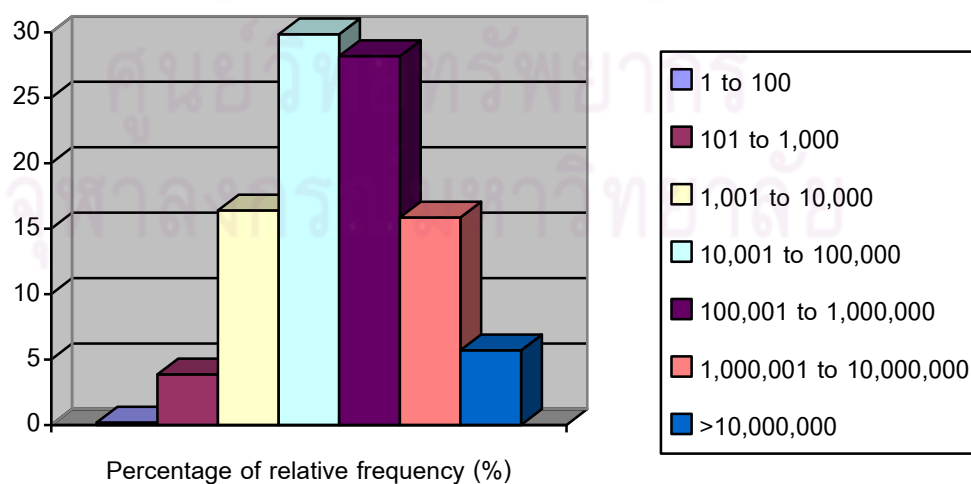


Table 9 The minimum CMI value resulted from fatherless duo parentage test.

Locus	Alleged Mother	Child	Formula	PI
D8S1179	(11, 13)	(10, 13)	$1/(4*P[13])$	1.50
D21S11	(30, 32.2)	(30, 32)	$1/(4*P[30])$	0.99
D7S820	(11, 12)	(11, 11)	$1/(2*P[11])$	1.48
CSF1PO	(10, 11)	(9, 10)	$1/(4*P[10])$	1.17
D3S1358	(15, 16)	(15, 17)	$1/(4*P[15])$	0.87
TH01	(7, 10)	(7, 9)	$1/(4*P[7])$	0.81
D13S317	(8, 11)	(8, 8)	$1/(2*P[8])$	1.71
D16S539	(11, 12)	(11, 11)	$1/(2*P[11])$	1.68
D2S1338	(19, 23)	(23, 23)	$1/(2*P[23])$	3.05
D19S433	(13, 14)	(13, 16.2)	$1/(4*P[13])$	0.89
vWA	(16, 18)	(14, 16)	$1/(4*P[16])$	1.72
TPOX	(8, 8)	(8, 8)	$1/P[8]$	1.77
D18S51	(13, 16)	(15, 16)	$1/(4*P[16])$	1.28
D5S818	(10, 12)	(7, 12)	$1/(4*P[12])$	1.06
FGA	(22, 23)	(22, 25)	$1/(4*P[22])$	1.21
minimum CMI				70.45

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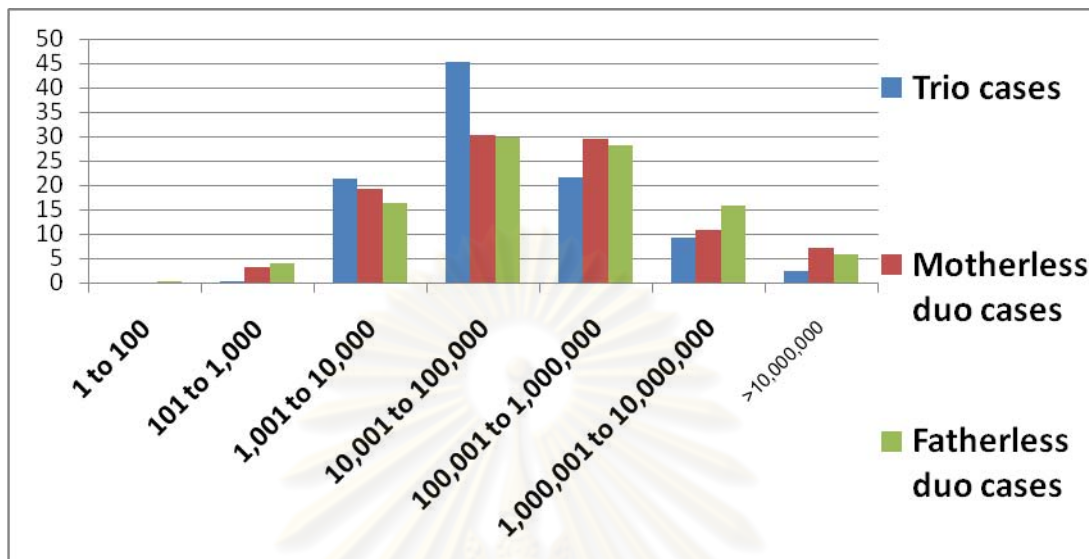
Table 10 The maximum CMI value resulted from fatherless parentage test.

Locus	Alleged Mother	Child	Formula	MI
D8S1179	(11, 14)	(11, 15)	$1/(4*P[11])$	2.14
D21S11	(31.2, 32)	(30, 32)	$1/(4*P[32])$	9.62
D7S820	(9, 14)	(11, 14)	$1/(4*P[14])$	125.00
CSF1PO	(11, 12)	(11, 12)	$(P[11]+P[12])/(4*P[11]*P[12])$	1.50
D3S1358	(15, 18)	(15, 18)	$(P[15]+P[18])/(4*P[15]*P[18])$	4.04
TH01	(7, 9)	(7, 7)	$1/(2*P[7])$	1.61
D13S317	(8, 8)	(8, 11)	$1/(2*P[8])$	1.71
D16S539	(9, 12)	(9, 11)	$1/(4*P[9])$	1.15
D2S1338	(17, 18)	(18, 23)	$1/(4*P[18])$	3.62
D19S433	(14, 14.2)	(14.2, 15.2)	$1/(4*P[14.2])$	2.69
vWA	(16, 17)	(16, 18)	$1/(4*P[16])$	1.72
TPOX	(10, 11)	(8, 10)	$1/(4*P[10])$	8.06
D18S51	(11, 14)	(11, 14)	$(P[11]+P[14])/(4*P[11]*P[14])$	22.23
D5S818	(11, 13)	(13, 13)	$1/(2*P[13])$	2.99
FGA	(21, 21)	(21, 25)	$1/(2*P[21])$	3.88
Maximum CMI				1.73×10^9

Using the 16 STR loci for fatherless duo parentage test with very low CMI value (70.45) in Table 9 and very high CMI value (1.73×10^9) in Table 10 were observed.

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Figure 4 Relative frequency of CPI and CMI range from parentage tests



Validation software for calculating the combined paternity index for parentage tests between the FEDDS-ProfileManagement and MS Excel Manual calculation.

To test basic functions, data with all possible allelic paternity situations were input into software. Then, the results of MS Excel manual and FEDDS-ProfileManagement software were compared. In trio parentage tests of 16 family cases (Table 11) the differences between results obtained are not statistically significant. Among motherless parentage tests of 17 family cases (Table 12) the results acquired are not changed.

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Table 11 The CPI for FEDDS and MS Excel manual resulted from trio parentage tests.

Family cases	CPI for FEDDS	CPI for MS Excel
1.089-51	2,957.97	2,957.97
2.0013-50	6,264.65	6,264.65
3.0010-50	7,163.83	7,163.83
4.0071-50	9,098.27	9,098.27
5.0115-50	19,117.61	19,117.61
6.0376-51	19,335.91	19,335.91
7.0114-50	22,530.90	22,530.90
8.0032-50	23,680.14	23,680.14
9.0089-50	53,376.58	53,376.58
10.0039-50	55,253.47	55,253.47
11.0033-50	56,886.57	56,886.57
12.0397-51	59,460.85	59,460.85
13.0041-50	101,146.40	101,146.40
14.0030-50	177,064.00	177,064.00
15.0107-50	230,555.70	230,555.70
16.0396-51	73,435,050.00	73,435,050.00

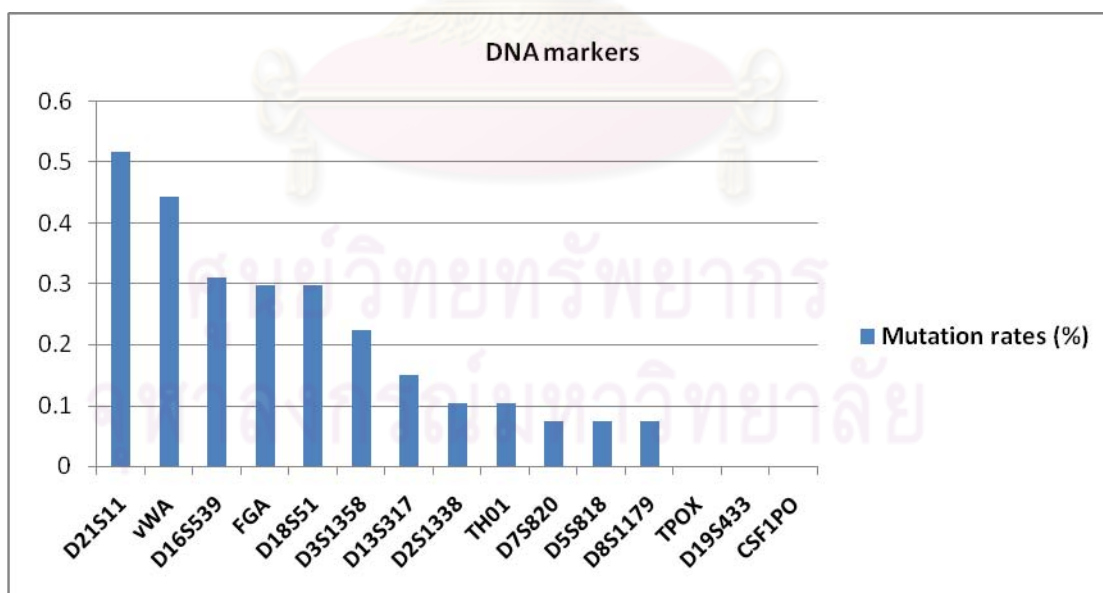
Table 12 The CPI for FEDDS and MS Excel manual resulted from duo parentage tests.

Family cases	CPI for FEDDS	CPI for MS Excel
1.0181-51	228.71	228.71
2.0054-50	517.89	517.89
3.0106-50-1	4,828.39	4,828.39
4.0132-50	5,090.19	5,090.19
5.0106-50-2	5,613.74	5,613.74
6.0099-50-1	12,766.12	12,766.12
7.0380-51	13,352.27	13,352.27
8.0051-50	18,396.71	18,396.71
9.0376-51	19,335.91	19,335.91
10.0099-50-2	23,506.30	23,506.30
11.0160-50	65,694.06	65,694.06
12.0103-50	176,897.10	176,897.10
13.0068-50	212,290.30	212,290.30
14.0042-50	364,108.90	364,108.90
15.0079-50	987,903.60	987,903.60
16.0147-50-2	4,302,935.00	4,302,935.00
17.0147-50-1	13,538,910.00	13,538,910.00

Table 13 Mutation types and observed cases

Mutation types	Total observed cases
1-step mutation	29
1.2-step mutation	1
2-step mutation	1
3-step mutation	2
3.2-step mutation	1
Point mutation	1
Total	35

. Figure 5 Observed mutation rates for the 15 STR loci present in commercial kits



The type of the mutations observed in a total of 35 cases in Table 13 show that 1-step mutation : 29 cases, 1.2-step mutation : 1 case, 2-step mutation : 1 case, 3-step mutation : 2 cases, 3.2-step mutation : 1 case and single point mutation : 1 case. The

mutation rates at the individual STR loci were present at D21S11: 0.517%, vWA: 0.444%, D16S539: 0.31%, FGA: 0.297%, D18S51: 0.297%, D3S1358: 0.223%, D13S317: 0.149%, D2S1338: 0.103%, TH01: 0.103%, D7S820: 0.0745%, D5S818: 0.0744%, and D8S1179: 0.0744%, while all other loci (TPOX, D19S433, CSF1PO: <0.0744% (Figure 5).

Figure 6 Case 0316/48 sample fragment collection by DHPLC of the TH01 locus.

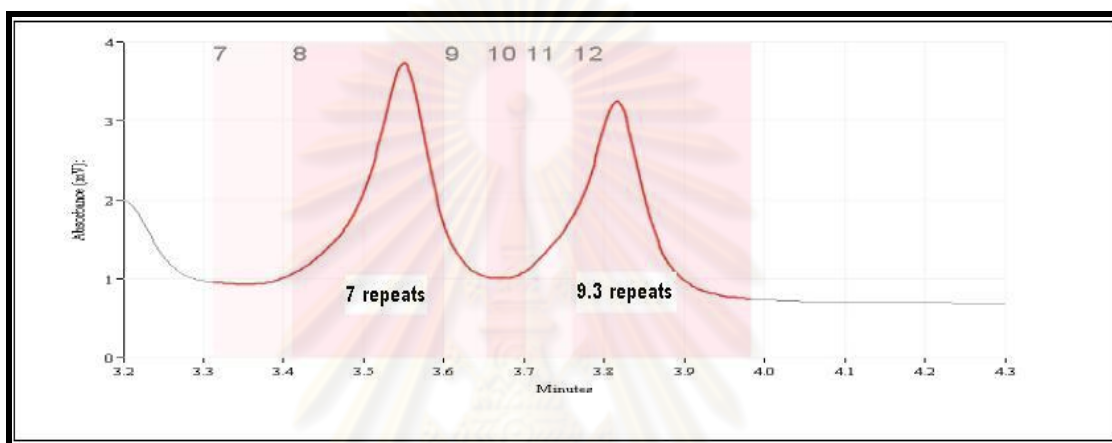
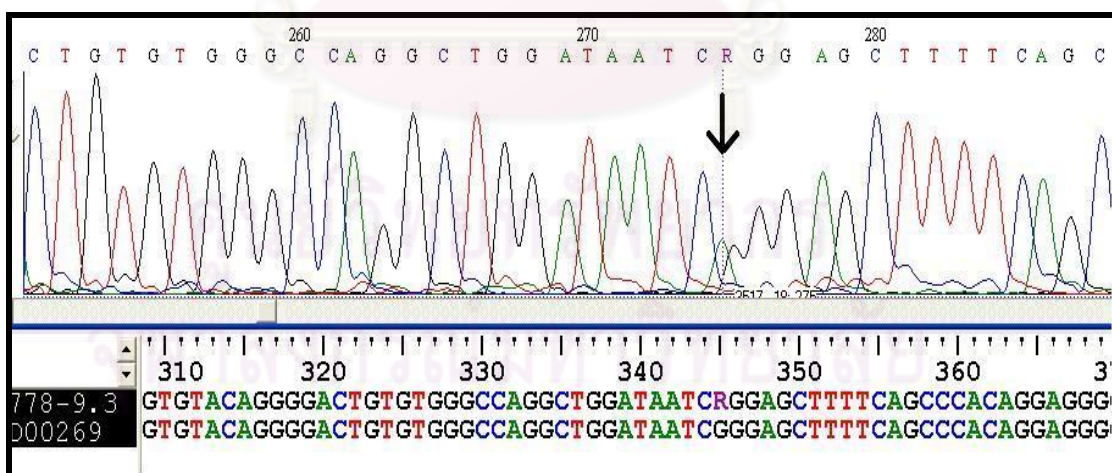


Figure 7 Case 0316/48 sample sequence electropherograms of the TH01 locus (A insertion is indicated by an arrow).



Two peaks of small and large sizes were detected on DHPLC of the PCR products obtained using the new primer set. These peaks considered to represent 7 and 9.3 repeats of TCAT, respectively (Figure 6). A single point mutation was found in the sequence of allele 9.3, while no mutation was found in the sequence of allele 7.

Sequencing analysis revealed an A insertion (Figure 7) at position 1287 (GenBank Accession No. D00269) located 82 bases downstream of the last TCAT motif of the repeat region. This single point mutation was located at the reverse primers of the Identifiler kit.



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CHAPTER V

DISCUSSION

The determination of parentage testing is made based on whether or not alleles are shared between the child and the alleged father when a number of genetic markers are examined. Thus, the outcome of parentage testing is simply inclusion or exclusion. If the man tested cannot be excluded as the biological father of the child in question, then statistical calculations are performed to aid in understanding the strength of the match. The most commonly applied test in this regard is the paternity index. The paternity index (PI) is the ratio of two conditional probabilities where the numerator assumes paternity and the denominator assumes a random man of similar ethnic background was the father. The numerator is the probability of observed genotypes, given the tested man is the father, while the denominator is the probability of the observed genotypes, given that a random man is the father. The paternity index then is a likelihood ratio of two probabilities conditional upon different competing hypotheses. This likelihood ratio reflects how many times more likely it is to see the evidence under the first hypothesis compared to the second hypothesis. The paternity index is generally represented in the formula X/Y , where X is the chance that the alleged father could transmit the obligate allele and Y is the chance that other man of the same race could have transmitted the allele. Typically, X is assigned the value of 1 if the alleged father is homozygous for the allele of interest and 0.5 if the alleged father is heterozygous. A population database containing frequency distributions for the various alleles at the tested genetic markers is used to calculate the potential of a randomly selected man passing the obligate allele to the child. The combined paternity index is calculated for each locus and then individual PI values are multiplied together to obtain the paternity index for the entire set of genetic loci examined. We calculate the combined paternity index or the combined maternity index and to gather the event of a mutation in some families. The results showed that in the examination of the parents and child relationship of 376 CPI values that were the CPI values which minimum value as 420.07 and the highest CPI value as 359,558,681.35. Most of these CPI values in the range of 1000 to 10,000,000 up to 88.03% with only

0.27% which is less than 1,000, while the more than 10,000,000 as 2.39% (Figure 1). To examine the relationship between father and child are all the CPI values of 423 by the smallest is 228.71 and the most is 38,900,000,000. The majority of the CPI value in the period 1,001 to 10,000,000 up to 89.84%, but only the 3.07% which is less than 1,000, while more than 10,000,000 is 7.09% (Figure 2). Check the connection between the mother and child all 543 CPI values. CMI is the minimum value 70.45 and the maximum is 1,730,000,000. Most of the CMI value from 1,001 to 10,000,000 available to 90.24%. CMI values of less than 1000 are 4.05% while the values of more than 10,000,000 are only 5.71% (Figure 3). The CPI or the CMI which is less than the 1,000 average was 2.46% which is relatively very small. It can be used as the minimum in order to determine the results correlated to parents and children. Meanwhile, more than the 10,000,000 average value was 5.06%, which is not very common characteristics of families in those populations (Figure 4). We suggested that they should use the lowest CPI value at 1000 is probably the best value from the data acquired. Report the requirements from the past several laboratories for issuing a report with a weight of positive paternity have defined the difference between the CPI most are in the range from 100 to 100,000 (Hallenberg and Morling, 2002). There is no theoretical requirement of a lower limit for reporting, and the decision to have a limit is based on pragmatic reasons such as avoiding court cases in which the biological evidence is evaluated under the limit. Many of the reports show that it is not the minimum of the CPI or CMI which contains information reported by various reports that will be discussed further. From the American Association of Blood Banks (AABB) surveyed data, a cutoff point of a minimum CPI value of 100 was used 23 in 34 laboratories (Pu and Linacre, 2007). A minimum CPI value requirement or cutoff point is employed, on top of that there is a high degree of confidence that the samples tested are genetically linked as first degree relatives and which a false inclusion are going to be prevented (Pu and Linacre, 2007). In real paternity duo cases with very low CPI values and coincidental kinship-matched pair with very high CPI values were observed. The ideal method to resolve duo cases with greater confidence would be adding more autosomal STR loci to increase the CPI

value and if possible, mitochondrial DNA analysis or STR loci on sex chromosome or other loci can be used to overcome problems of low CPI values. From the analysis of 51 inclusion paternity trio cases, the minimum, maximum and average PI were 3.4×10^5 , 4.4×10^{11} and 9.2×10^9 , respectively (Jacewicz et al., 2004). In 139 trios analyzed, 85 non-exclusion cases presented the average probability of paternity (PP) of 99.9999%, with the average paternity index of 30,301,168.36 whereas, in the simulated duo analyses (artificial mother-deficient cases), the average PP was 98.768569% (PI:165,575.33) (Iwamura et al., 2008). A total of 112 motherless cases of parentage testing were investigated. Two criterions for paternity inclusion in motherless cases of parentage testing are the probability of exclusion and the paternity index. The threshold value of the combined probability of exclusion was 0.9999, while the threshold value of the paternity index was 10,000 for paternity inclusion (Hou et al., 2008). The Institute of Legal Medicine at Korea University has conducted some simulation studies based on data to find the most appropriate rule in each case, and currently used cut-off value which is different from 99.9% in the unrelated case (cut-off value is 99.9981% for trio case and 99.8579% for motherless case with 17 loci system) (Lee et al., 2001). In all remaining 93-deficiency cases, the putative father could be determined as being the biological father with an average probability of 99.9699%, PI:3321.26 (min. 99.5651%, PI:228.94; max. 99.9999%, PI:1,000,000) (von Wurmb-Schwark et al., 2006). The PI obtained from 67 non-exclusion cases and 22 exclusion cases typed on 10 STR loci, was calculated for the trios and also for child and alleged father in motherless cases using local frequency tables. The highest PIs for trios and duos were 53,655,218 and 341,876 for STRs, respectively (Hou et al., 2008).

Validation calculation CPI values between two methods were from testing the CPI is calculated by using a computer program FEDDS-Profile Management software compared to the normal calculation using the Microsoft Excel in two forms. The trio parentage test with 16 families (Table 11) the results are the same. During the motherless parentage test of 17 families (Table 12) the results are not changed. The

results were compared with the results of using MS Excel and FEDDS Profile Management is considered validated sufficiently.

In 1,011 parent-child allelic transfers at fifteen short tandem-repeat (STR) loci, 35 isolated STR mismatches were observed. Table 13 presents a lot of detailed characterization of the observed mutations. The event was continually repeat connected, because of either a 1-step mutation ($n = 29$), a 1.2-step mutation ($n = 1$), a 2-step mutation ($n = 1$), a 3-step mutation ($n = 2$), a 3.2-step mutation ($n = 1$) and a single point mutation ($n = 1$). Most of the STR mutation associated with gain or loss of repeat unit, but sometimes one will have more than one repeat unit or one base pair change. As can be seen in Table 46, The mutation rates at the individual STR loci were present at D21S11: 5.17×10^{-3} (7 in 1352 meioses), vWA: 4.44×10^{-3} (6 in 1350 meioses), D16S539: 3.1×10^{-3} (3 in 969 meioses), FGA: 2.97×10^{-3} (4 in 1346 meioses), D18S51: 2.97×10^{-3} (4 in 1348 meioses), D3S1358: 2.23×10^{-3} (3 in 1346 meioses), D13S317: 1.49×10^{-3} (2 in 1345 meioses), D2S1338: 1.03×10^{-3} (2 in 968 meioses), TH01: 1.03×10^{-3} (1 in 967 meioses), D7S820: 7.45×10^{-4} (1 in 1343 meioses), D5S818: 7.44×10^{-4} (1 in 1344 meioses), and D8S1179: 7.44×10^{-4} (1 in 1344 meioses), while all other loci (TPOX, D19S433, CSF1PO: $< 7.44 \times 10^{-4}$ (no mutations observed). Conclude that the mutation rate is between 7.44×10^{-4} and 5.17×10^{-3} per locus per gamete per generation. No mutations were observed in three of the fifteen loci. As with any other region of DNA, mutations can occur in STR loci. For some mechanism is not completely characterized, STR alleles can change over time. Mutational event may take the form of a change of a single base or repeat length. The molecular mechanisms by which STRs mutated are believed to involve replication slippage or the repair of DNA replication defective (Ellegen, 2004). Estimation of mutational events at a DNA marker may be achieved by comparison of genotypes from offspring to those of their parents. Genotype data from paternity trios involving a father, a mother, and at least one child (a child or more than) is examined. A discovery of an allele difference between the parents and the child is seen as evidence for a possible mutation. The search for mutation in STR loci involves examining several parent-child alleles transfer because the mutation rate is rather low in

most STRs. The majority of STR mutations involve the gain or loss of a single repeat unit. Most of these mutation rates are on the order of 1-5 mutations per 1,000 allele transfers or generational events. The STR loci with the lowest observed mutation rates are TH01 (0.01%) and TPOX (0.01%). Not surprisingly, the STR loci with the highest mutation rates – FGA (0.30%), D18S51 (0.25%), and D21S11 (0.21%) – are among the most polymorphic and possess the highest number of observed alleles. However, depending on the genotype combinations it can be difficult to ascertain from which parent the mutant allele was inherited. Since the average mutation rate is below 0.1%, approximately 1,000 parent-offspring allele transfers would have to be observed before one mutation would be seen in some STR markers (Weber and Wong, 1993). From a report that examined 10,844 parent and child allele transfers at nine STR loci and observed 23 mutations. No mutations were observed at three of the loci (TH01, F13B, CD4) (Brinkmann et al., 1998). Also reported another studied 29,640 parent-child allele transfers at five STRs and four minisatellites and observed only 18 mutational events (11 in three STR loci D3S1359, vWA, and TH01) (Sajantila, Lukka, and Syvanen 1999). There is reported mutation rates on the basis of observations can be estimated as follows; D16S539: 1.3×10^{-2} (2 in 156 meioses); D18S51: 6×10^{-3} (1 in 162 meioses); FGA: 6×10^{-3} (1 in 162 meioses); all other loci: $<6 \times 10^{-3}$ (Thomson et al., 1999). In all, 1,400 child bands were detected which corresponded to a mutation frequency of 16/1400 on 0.01143 bands per child (Cifuentes et al., 2000). The autosomal mutations observed in 389 father and child sample pairs with the 15 autosomal Identifiler STR loci are two in the Asians (Decker et al., 2008). The mutations observed were the following the most of them were either gains or losses of complete repeats and the number of additions was significantly major than the number of deletions (Di Lonardo et al., 2004). Low mutation rates are especially critical for paternity testing. This is because links are being made between the child and the alleged father based on the assumption that alleles remain the same when they are passed from one generation to the next. Parent and child allele transfer information tests for germ-line mutations. Additionally, genotypes from different kinds of tissues from the same individual are examined to demonstrate that no somatic

mutations occur. In parentage test, a high mutation rate for a STR marker could result in a false exclusion at that locus. High mutation rates help keep STR markers polymorphic and therefore useful in human identify testing. It is important to keep in mind that while mutations can potentially impact kinship reference samples they will not affect direct matches between personal effects and victims or perpetrators and crime scene evidence since any mutation that occurs will be consistent over an individual's lifetime. Point mutations have been reported a TH01 primer binding site mutation using a rare approach (Takayama et al., 2007). These mutations are found by comparison of the results of the genetic inconsistencies between parents and children.



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APPENDIX

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Table 14 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0396-51.

Locus	Mother	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D3S1358	(15, 16)	(15, 16)	(16, 19)	0.76	$1/(2*(P[16]+P[15]))$	0.76
vWA	(17, 19)	(14, 19)	(14, 14)	3.89	$1/P[14]$	3.89
FGA	(19, 24.2)	(22.2, 24.2)	(22.2, 24)	41.67	$1/(2*P[22.2])$	41.67
D8S1179	(13, 15)	(14, 15)	(10, 14)	2.96	$1/(2*P[14])$	2.96
D21S11	(30, 31)	(30, 30)	(30, 30)	3.97	$1/P[30]$	3.97
D18S51	(12, 14)	(14, 22)	(16, 22)	71.43	$1/(2*P[22])$	71.43
D5S818	(10, 12)	(11, 12)	(11, 11)	3.69	$1/P[11]$	3.69
D13S317	(8, 8)	(8, 10)	(9, 10)	3.88	$1/(2*P[10])$	3.88
D7S820	(10, 13)	(7, 10)	(7, 11)	50.00	$1/(2*P[7])$	50.00
CPI				73,435,050.00		73,435,047.00

Table 15 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0397-51.

Locus	Mother	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D3S1358	(17, 17)	(17, 17)	(17, 17)	4.61	$1/P[17]$	4.61
vWA	(16, 17)	(14, 17)	(14, 16)	1.95	$1/(2*P[14])$	1.95
FGA	(22, 24)	(22, 22)	(21, 22)	2.42	$1/(2*P[22])$	2.42
D8S1179	(11, 13)	(11, 17)	(13, 17)	29.41	$1/(2*P[17])$	29.41
D21S11	(32.2, 32.2)	(32.2, 32.2)	(32.2, 32.2)	8.06	$1/P[32.2]$	8.06
D18S51	(14, 17)	(14, 17)	(14, 16)	1.92	$1/(2*(P[14]+P[17]))$	1.92
D5S818	(10, 12)	(12, 13)	(10, 13)	2.99	$1/(2*P[13])$	2.99
D13S317	(10, 13)	(11, 13)	(10, 11)	2.18	$1/(2*P[11])$	2.18
D7S820	(11, 12)	(11, 12)	(8, 11)	0.92	$1/(2*(P[11]+P[12]))$	0.92
CPI				59,460.85		59,460.85

Table 16 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0386-51.

Locus	Mother	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D3S1358	(17, 17)	(16, 17)	(15, 16)	1.33	$1/(2*P[16])$	1.33
vWA	(14, 14)	(14, 17)	(14, 17)	2.08	$1/(2*P[17])$	2.08
FGA	(22, 25)	(22, 25)	(22, 24)	1.67	$1/(2*(P[22]+P[25]))$	1.67
D8S1179	(13, 14)	(10, 14)	(10, 10)	6.76	$1/P[10]$	6.76
D21S11	(30, 30)	(30, 30)	(28, 30)	1.98	$1/(2*P[30])$	1.98
D18S51	(14, 17)	(15, 17)	(13, 15)	2.23	$1/(2*P[15])$	2.23
D5S818	(10, 12)	(10, 11)	(11, 12)	1.85	$1/(2*P[11])$	1.85
D13S317	(9, 13)	(9, 12)	(11, 12)	3.76	$1/(2*P[12])$	3.76
D7S820	(10, 10)	(8, 10)	(8, 12)	3.09	$1/(2*P[8])$	3.09
CPI				2,957.97		2,957.97

Table 17 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0376-51.

Locus	Mother	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D3S1358	(15, 16)	(15, 15)	(15, 18)	1.75	$1/(2*P[15])$	1.75
vWA	(17, 18)	(14, 18)	(14, 18)	1.95	$1/(2*P[14])$	1.95
FGA	(22, 24)	(22, 25)	(24, 25)	5.38	$1/(2*P[25])$	5.38
D8S1179	(11, 11)	(11, 12)	(12, 17)	3.97	$1/(2*P[12])$	3.97
D21S11	(29, 29)	(29, 29)	(29, 30)	2.00	$1/(2*P[29])$	2.00
D18S51	(14, 15)	(14, 17)	(16, 17)	6.17	$1/(2*P[17])$	6.17
D5S818	(11, 13)	(11, 13)	(12, 13)	1.14	$1/(2*(P[13]+P[11]))$	1.14
D13S317	(8, 10)	(10, 10)	(10, 11)	3.88	$1/(2*P[10])$	3.88
D7S820	(10, 11)	(11, 12)	(12, 12)	4.88	$1/P[12]$	4.88
CPI				19,335.91		19,335.91

Table 18 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0010-50.

Locus	Mother	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D3S1358	(16, 18)	(16, 17)	(16, 17)	2.30	$1/(2*P[17])$	2.30
vWA	(14, 16)	(16, 18)	(14, 18)	2.42	$1/(2*P[18])$	2.42
FGA	(18, 23)	(18, 19)	(19, 20)	10.00	$1/(2*P[19])$	10.00
D8S1179	(8, 13)	(8, 12)	(12, 15)	3.97	$1/(2*P[12])$	3.97
D21S11	(30, 30.2)	(30, 30)	(30, 30)	3.97	$1/P[30]$	3.97
D18S51	(13, 21)	(14, 21)	(14, 15)	2.79	$1/(2*P[14])$	2.79
D5S818	(10, 12)	(12, 12)	(11, 12)	2.12	$1/(2*P[12])$	2.12
D13S317	(11, 12)	(11, 12)	(10, 12)	1.38	$1/(2*(P[12]+P[11]))$	1.38
D7S820	(8, 11)	(8, 11)	(8, 12)	1.00	$1/(2*(P[8]+P[11]))$	1.00
CPI				7,163.83		7,163.83

Table 19 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0013-50.

Locus	Mother	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D3S1358	(16, 18)	(16, 16)	(16, 18)	1.33	$1/(2*P[16])$	1.33
vWA	(18, 19)	(14, 18)	(14, 14)	3.89	$1/P[14]$	3.89
FGA	(21, 24.2)	(24, 24.2)	(24, 24)	9.09	$1/P[24]$	9.09
D8S1179	(10, 15)	(15, 15)	(10, 15)	2.99	$1/(2*P[15])$	2.99
D21S11	(30, 30)	(30, 33.2)	(31, 33.2)	7.81	$1/(2*P[33.2])$	7.81
D18S51	(12, 16)	(12, 15)	(13, 15)	2.23	$1/(2*P[15])$	2.23
D5S818	(12, 13)	(12, 13)	(11, 13)	1.24	$1/(2*(P[13]+P[12]))$	1.24
D13S317	(8, 11)	(11, 11)	(10, 11)	2.18	$1/(2*P[11])$	2.18
D7S820	(10, 11)	(10, 11)	(11, 12)	0.94	$1/(2*(P[11]+P[10]))$	0.94
CPI				6,264.65		6,264.65

Table 20 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0030-50.

Locus	Mother	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D3S1358	(15, 15)	(15, 18)	(16, 18)	6.33	$1/(2*P[18])$	6.33
vWA	(14, 18)	(14, 14)	(14, 17)	1.95	$1/(2*P[14])$	1.95
FGA	(21, 24)	(22.2, 24)	(22.2, 26)	41.67	$1/(2*P[22.2])$	41.67
D8S1179	(10, 12)	(10, 12)	(12, 13)	1.82	$1/(2*(P[12]+P[10]))$	1.82
D21S11	(29, 33.2)	(29, 30)	(30, 30)	3.97	$1/P[30]$	3.97
D18S51	(14, 17)	(14, 14)	(14, 16)	2.79	$1/(2*P[14])$	2.79
D5S818	(9, 10)	(10, 10)	(10, 12)	2.34	$1/(2*P[10])$	2.34
D13S317	(10, 11)	(9, 11)	(9, 10)	2.99	$1/(2*P[9])$	2.99
D7S820	(12, 12)	(12, 12)	(8, 12)	2.44	$1/(2*P[12])$	2.44
CPI				177,064.00		177,064.00

Table 21 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0032-50.

Locus	Mother	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D3S1358	(15, 17)	(15, 15)	(15, 17)	1.75	$1/(2*P[15])$	1.75
vWA	(14, 14)	(14, 18)	(18, 18)	4.83	$1/P[18]$	4.83
FGA	(21, 25)	(21, 25)	(21, 21)	4.50	$1/(P[21]+P[25])$	4.50
D8S1179	(14, 14)	(11, 14)	(11, 14)	4.27	$1/(2*P[11])$	4.27
D21S11	(29, 30)	(29, 30)	(30, 30)	1.99	$1/(P[30]+P[29])$	1.99
D18S51	(12, 16)	(13, 16)	(13, 14)	3.76	$1/(2*P[13])$	3.76
D5S818	(13, 13)	(10, 13)	(10, 12)	2.34	$1/(2*P[10])$	2.34
D13S317	(8, 12)	(8, 8)	(8, 10)	1.71	$1/(2*P[8])$	1.71
D7S820	(10, 11)	(10, 12)	(12, 12)	4.88	$1/P[12]$	4.88
CPI				23,680.14		23,680.14

Table 22 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0033-50.

Locus	Mother	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D3S1358	(16, 18)	(16, 16)	(16, 16)	2.66	$1/P[16]$	2.66
vWA	(17, 17)	(16, 17)	(16, 17)	3.45	$1/(2*P[16])$	3.45
FGA	(24, 25)	(23, 25)	(23, 25)	2.69	$1/(2*P[23])$	2.69
D8S1179	(13, 15)	(13, 16)	(14, 16)	6.02	$1/(2*P[16])$	6.02
D21S11	(29, 30)	(30, 30)	(30, 32.2)	1.98	$1/(2*P[30])$	1.98
D18S51	(14, 21)	(14, 18)	(14, 18)	15.15	$1/(2*P[18])$	15.15
D5S818	(10, 12)	(10, 12)	(11, 12)	1.11	$1/(2*(P[12]+P[10]))$	1.11
D13S317	(9, 12)	(9, 10)	(10, 10)	7.75	$1/P[10]$	7.75
D7S820	(11, 13)	(11, 11)	(10, 11)	1.48	$1/(2*P[11])$	1.48
CPI				56,886.57		56,886.57

Table 23 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0039-50.

Locus	Mother	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D3S1358	(15, 16)	(16, 16)	(16, 16)	2.66	$1/P[16]$	2.66
vWA	(17, 18)	(17, 17)	(16, 17)	2.08	$1/(2*P[17])$	2.08
FGA	(22, 23)	(22, 23)	(22, 25)	1.27	$1/(2*(P[22]+P[23]))$	1.27
D8S1179	(16, 18)	(10, 18)	(10, 16)	3.38	$1/(2*P[10])$	3.38
D21S11	(29, 31)	(31, 31.2)	(29, 31.2)	7.04	$1/(2*P[31.2])$	7.04
D18S51	(14, 15)	(14, 16)	(14, 16)	2.56	$1/(2*P[16])$	2.56
D5S818	(11, 12)	(9, 11)	(9, 10)	7.25	$1/(2*P[9])$	7.25
D13S317	(8, 9)	(9, 11)	(11, 11)	4.37	$1/P[11]$	4.37
D7S820	(9, 12)	(9, 10)	(10, 13)	2.59	$1/(2*P[10])$	2.59
CPI				55,253.47		55,253.47

Table 24 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0041-50.

Locus	Mother	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D3S1358	(16, 17)	(15, 17)	(15, 15)	3.50	$1/P[15]$	3.50
vWA	(14, 14)	(14, 19)	(17, 19)	4.39	$1/(2*P[19])$	4.39
FGA	(18, 19)	(18, 23)	(19, 23)	2.69	$1/(2*P[23])$	2.69
D8S1179	(10, 15)	(10, 15)	(15, 16)	1.59	$1/(2*(P[15]+P[10]))$	1.59
D21S11	(29, 31.2)	(30.2,31.2)	(29, 30.2)	10.42	$1/(2*P[30.2])$	10.42
D18S51	(14, 15)	(15, 16)	(15, 16)	2.56	$1/(2*P[16])$	2.56
D5S818	(7, 12)	(7, 12)	(11, 12)	1.91	$1/(2*(P[12]+P[7]))$	1.91
D13S317	(8, 10)	(8, 11)	(8, 11)	2.18	$1/(2*P[11])$	2.18
D7S820	(9, 10)	(10, 13)	(8, 13)	13.89	$1/(2*P[13])$	13.89
CPI				101,146.40		101,146.40

Table 25 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0071-50.

Locus	Mother	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D3S1358	(16, 17)	(16, 16)	(16, 17)	1.33	$1/(2*P[16])$	1.33
vWA	(14, 16)	(14, 14)	(14, 18)	1.95	$1/(2*P[14])$	1.95
FGA	(23, 24)	(21, 24)	(21, 22)	3.88	$1/(2*P[21])$	3.88
D8S1179	(11, 12)	(11, 14)	(13, 14)	2.96	$1/(2*P[14])$	2.96
D21S11	(29, 29)	(29, 31.2)	(30, 31.2)	7.04	$1/(2*P[31.2])$	7.04
D18S51	(13, 17)	(12, 13)	(12, 18)	7.25	$1/(2*P[12])$	7.25
D5S818	(10, 11)	(10, 10)	(7, 10)	2.34	$1/(2*P[10])$	2.34
D13S317	(10, 11)	(10, 11)	(11, 12)	1.40	$1/(2*(P[11]+P[10]))$	1.40
D7S820	(11, 12)	(11, 12)	(11, 12)	1.84	$1/(P[11]+P[12])$	1.84
CPI				9,098.27		9,098.27

Table 26 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0089-50.

Locus	Mother	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D3S1358	(15, 16)	(15, 17)	(16, 17)	2.30	$1/(2*P[17])$	2.30
vWA	(18, 18)	(17, 18)	(17, 18)	2.08	$1/(2*P[17])$	2.08
FGA	(20, 21)	(20, 26)	(25, 26)	12.50	$1/(2*P[26])$	12.50
D8S1179	(12, 13)	(12, 14)	(14, 15)	2.96	$1/(2*P[14])$	2.96
D21S11	(29, 32)	(29, 33.2)	(28, 33.2)	7.81	$1/(2*P[33.2])$	7.81
D18S51	(15, 15)	(15, 15)	(13, 15)	2.23	$1/(2*P[15])$	2.23
D5S818	(12, 13)	(11, 13)	(11, 11)	3.69	$1/P[11]$	3.69
D13S317	(8, 11)	(8, 11)	(8, 11)	1.92	$1/(P[8]+P[11])$	1.92
D7S820	(10, 11)	(10, 12)	(9, 12)	2.44	$1/(2*P[12])$	2.44
CPI				53,376.58		53,376.58

Table 27 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0107-50.

Locus	Mother	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D3S1358	(16, 16)	(14, 16)	(14, 17)	16.13	$1/(2*P[14])$	16.13
vWA	(14, 17)	(14, 17)	(14, 14)	2.01	$1/(P[14]+P[17])$	2.01
FGA	(22, 23)	(20, 22)	(20, 22)	6.33	$1/(2*P[20])$	6.33
D8S1179	(11, 13)	(11, 16)	(16, 17)	6.02	$1/(2*P[16])$	6.02
D21S11	(32.2, 32.2)	(29, 32.2)	(29, 32.2)	2.00	$1/(2*P[29])$	2.00
D18S51	(16, 19)	(17, 19)	(13, 17)	6.17	$1/(2*P[17])$	6.17
D5S818	(11, 13)	(10, 13)	(10, 10)	4.67	$1/P[10]$	4.67
D13S317	(9, 12)	(9, 11)	(9, 11)	2.18	$1/(2*P[11])$	2.18
D7S820	(11, 11)	(11, 11)	(9, 11)	1.48	$1/(2*P[11])$	1.48
CPI				230,555.70		230,555.70

Table 28 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0114-50.

Locus	Mother	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D3S1358	(16, 16)	(15, 16)	(15, 16)	1.75	$1/(2*P[15])$	1.75
vWA	(14, 16)	(16, 16)	(14, 16)	3.45	$1/(2*P[16])$	3.45
FGA	(22, 24)	(22, 24)	(22, 23)	1.58	$1/(2*(P[22]+P[24]))$	1.58
D8S1179	(10, 12)	(11, 12)	(11, 14)	4.27	$1/(2*P[11])$	4.27
D21S11	(30, 32.2)	(30, 31)	(31, 32.2)	6.33	$1/(2*P[31])$	6.33
D18S51	(15, 21)	(13, 21)	(13, 16)	3.76	$1/(2*P[13])$	3.76
D5S818	(7, 11)	(7, 9)	(9, 12)	7.25	$1/(2*P[9])$	7.25
D13S317	(8, 9)	(8, 9)	(8, 11)	1.09	$1/(2*(P[8]+P[9]))$	1.09
D7S820	(11, 11)	(11, 11)	(11, 11)	2.96	$1/P[11]$	2.96
CPI				22,530.90		22,530.90

Table 29 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0115-50.

Locus	Mother	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D3S1358	(15, 15)	(15, 16)	(16, 17)	1.33	$1/(2*P[16])$	1.33
vWA	(14, 19)	(14, 17)	(15, 17)	2.08	$1/(2*P[17])$	2.08
FGA	(23, 23.2)	(23.2, 24)	(23, 24)	4.55	$1/(2*P[24])$	4.55
D8S1179	(11, 14)	(11, 13)	(13, 14)	2.99	$1/(2*P[13])$	2.99
D21S11	(28, 33.2)	(30, 33.2)	(30, 30)	3.97	$1/P[30]$	3.97
D18S51	(12, 15)	(15, 15)	(15, 15)	4.46	$1/P[15]$	4.46
D5S818	(9, 10)	(9, 11)	(10, 11)	1.85	$1/(2*P[11])$	1.85
D13S317	(9, 11)	(8, 11)	(8, 10)	1.71	$1/(2*P[8])$	1.71
D7S820	(11, 12)	(9, 11)	(8, 9)	9.09	$1/(2*P[9])$	9.09
CPI				19,117.61		19,117.61

Table 30 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0181-51.

Locus	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D8S1179	(13, 13)	(12, 13)	2.99	$1/(2*P[13])$	2.99
D21S11	(29, 30)	(29, 30)	1.99	$(P[29]+P[30])/(4*P[29]*P[30])$	1.99
D7S820	(9, 11)	(8, 9)	4.55	$1/(4*P[9])$	4.55
CSF1PO	(7, 12)	(11, 12)	0.66	$1/(4*P[12])$	0.66
D3S1358	(15, 17)	(16, 17)	1.15	$1/(4*P[17])$	1.15
TH01	(8, 9)	(7, 9)	0.70	$1/(4*P[9])$	0.70
D13S317	(8, 11)	(8, 8)	1.71	$1/(2*P[8])$	1.71
D16S539	(11, 12)	(10, 11)	0.84	$1/(4*P[11])$	0.84
D2S1338	(17, 23)	(19, 23)	1.52	$1/(4*P[23])$	1.52
D19S433	(13, 15.2)	(13, 14.2)	0.89	$1/(4*P[13])$	0.89
vWA	(17, 20)	(14, 17)	1.04	$1/(4*P[17])$	1.04
TPOX	(8, 9)	(9, 10)	1.91	$1/(4*P[9])$	1.91
D18S51	(14, 21)	(12, 14)	1.40	$1/(4*P[14])$	1.40
D5S818	(12, 13)	(9, 13)	1.50	$1/(4*P[13])$	1.50
FGA	(21, 23)	(21, 24)	1.94	$1/(4*P[21])$	1.94
CPI			228.71		228.71

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Table 31 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0380-51.

Locus	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D8S1179	(11, 14)	(11, 13)	2.14	$1/(4*P[11])$	2.14
D21S11	(29, 30)	(29, 29)	2.00	$1/(2*P[29])$	2.00
D7S820	(11, 12)	(11, 12)	1.96	$(P[11]+P[12])/(4*P[11]*P[12])$	1.96
CSF1PO	(13, 13)	(10, 13)	6.33	$1/(2*P[13])$	6.33
D3S1358	(16, 18)	(16, 17)	0.66	$1/(4*P[16])$	0.66
TH01	(7, 7)	(7, 10)	1.61	$1/(2*P[7])$	1.61
D13S317	(12, 12)	(9, 12)	3.76	$1/(2*P[12])$	3.76
D16S539	(11, 12)	(9, 11)	0.84	$1/(4*P[11])$	0.84
D2S1338	(19, 23)	(18, 23)	1.52	$1/(4*P[23])$	1.52
D19S433	(13, 14)	(13, 13)	1.78	$1/(2*P[13])$	1.78
vWA	(14, 17)	(17, 17)	2.08	$1/(2*P[17])$	2.08
TPOX	(8, 11)	(8, 11)	1.45	$(P[8]+P[11])/(4*P[8]*P[11])$	1.45
D18S51	(14, 14)	(14, 24)	2.79	$1/(2*P[14])$	2.79
D5S818	(11, 13)	(11, 13)	2.42	$(P[11]+P[13])/(4*P[11]*P[13])$	2.42
FGA	(21, 23)	(22, 23)	1.34	$1/(4*P[23])$	1.34
CPI			13,352.27		13,352.27

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Table 32 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0042-50.

Locus	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D8S1179	(13, 13)	(13, 14)	2.99	$1/(2*P[13])$	2.99
D21S11	(30, 31)	(30, 32.2)	0.99	$1/(4*P[30])$	0.99
D7S820	(10, 12)	(11, 12)	1.22	$1/(4*P[12])$	1.22
CSF1PO	(11, 12)	(11, 12)	1.50	$(P[11]+P[12])/(4*P[11]*P[12])$	1.50
D3S1358	(15, 16)	(15, 16)	1.54	$(P[15]+P[16])/(4*P[15]*P[16])$	1.54
TH01	(9, 9)	(7, 9)	1.41	$1/(2*P[9])$	1.41
D13S317	(8, 8)	(8, 8)	3.41	$1/P[8]$	3.41
D16S539	(12, 12)	(11, 12)	2.63	$1/(2*P[12])$	2.63
D2S1338	(22, 22)	(17, 22)	13.16	$1/(2*P[22])$	13.16
D19S433	(13, 16.2)	(13, 15.2)	0.89	$1/(4*P[13])$	0.89
vWA	(17, 20)	(17, 20)	26.04	$(P[17]+P[20])/(4*P[17]*P[20])$	26.04
TPOX	(8, 10)	(8, 8)	0.89	$1/(2*P[8])$	0.89
D18S51	(13, 16)	(10, 16)	1.28	$1/(4*P[16])$	1.28
D5S818	(11, 12)	(11, 12)	1.98	$(P[11]+P[12])/(4*P[11]*P[12])$	1.98
FGA	(19, 21)	(19, 22)	5.00	$1/(4*P[19])$	5.00
CPI			364,108.90		364,108.90

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Table 33 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0051-50.

Locus	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D8S1179	(10, 11)	(10, 10)	3.38	$1/(2*P[10])$	3.38
D21S11	(29, 31)	(31, 31.2)	3.16	$1/(4*P[31])$	3.16
D7S820	(11, 12)	(9, 11)	0.74	$1/(4*P[11])$	0.74
CSF1PO	(11, 12)	(10, 12)	0.66	$1/(4*P[12])$	0.66
D3S1358	(15, 16)	(15, 16)	1.54	$(P[15]+P[16])/(4*P[15]*P[16])$	1.54
TH01	(7, 9)	(6, 9)	0.70	$1/(4*P[9])$	0.70
D13S317	(9, 10)	(9, 10)	3.43	$(P[9]+P[10])/(4*P[9]*P[10])$	3.43
D16S539	(11, 14)	(11, 11)	1.68	$1/(2*P[11])$	1.68
D2S1338	(22, 23)	(20, 22)	6.58	$1/(4*P[22])$	6.58
D19S433	(14.2, 15.2)	(15.2, 15.2)	2.87	$1/(2*P[15.2])$	2.87
vWA	(16, 17)	(16, 18)	1.72	$1/(4*P[16])$	1.72
TPOX	(8, 8)	(8, 8)	1.77	$1/P[8]$	1.77
D18S51	(15, 17)	(14, 17)	3.09	$1/(4*P[17])$	3.09
D5S818	(10, 10)	(10, 11)	2.34	$1/(2*P[10])$	2.34
FGA	(22, 23)	(23, 24)	1.34	$1/(4*P[23])$	1.34
CPI			18,396.71		18,396.71

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Table 34 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0054-50.

Locus	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D8S1179	(10, 13)	(13, 13)	2.99	$1/(2*P[13])$	2.99
D21S11	(30, 32.2)	(29, 30)	0.99	$1/(4*P[30])$	0.99
D7S820	(11, 11)	(9, 11)	1.48	$1/(2*P[11])$	1.48
CSF1PO	(10, 11)	(11, 12)	0.84	$1/(4*P[11])$	0.84
D3S1358	(16, 18)	(16, 16)	1.33	$1/(2*P[16])$	1.33
TH01	(7, 8)	(7, 7)	1.61	$1/(2*P[7])$	1.61
D13S317	(10, 11)	(8, 10)	1.94	$1/(4*P[10])$	1.94
D16S539	(9, 11)	(9, 12)	1.15	$1/(4*P[9])$	1.15
D2S1338	(17, 21)	(17, 21)	6.94	$(P[17]+P[21])/(4*P[17]*P[21])$	6.94
D19S433	(13, 15.2)	(13, 14)	0.89	$1/(4*P[13])$	0.89
vWA	(14, 18)	(14, 16)	0.97	$1/(4*P[14])$	0.97
TPOX	(8, 11)	(9, 11)	1.01	$1/(4*P[11])$	1.01
D18S51	(14, 17)	(15, 17)	3.09	$1/(4*P[17])$	3.09
D5S818	(10, 13)	(10, 11)	1.17	$1/(4*P[10])$	1.17
FGA	(20, 23)	(22, 23)	1.34	$1/(4*P[23])$	1.34
CPI			517.89		517.89

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Table 35 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0068-50.

Locus	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D8S1179	(15, 15)	(13, 15)	2.99	$1/(2*P[15])$	2.99
D21S11	(29, 32.2)	(29, 32.2)	3.02	$(P[29]+P[32.2])/(4*P[29]*P[32.2])$	3.02
D7S820	(9, 11)	(9, 11)	5.29	$(P[9]+P[11])/(4*P[9]*P[11])$	5.29
CSF1PO	(10, 11)	(10, 11)	2.01	$(P[10]+P[11])/(4*P[10]*P[11])$	2.01
D3S1358	(15, 16)	(15, 17)	0.87	$1/(4*P[15])$	0.87
TH01	(8, 9)	(7, 8)	4.81	$1/(4*P[8])$	4.81
D13S317	(8, 11)	(8, 11)	1.94	$(P[8]+P[11])/(4*P[8]*P[11])$	1.94
D16S539	(8, 10)	(9, 10)	1.46	$1/(4*P[10])$	1.46
D2S1338	(19, 23)	(19, 24)	1.11	$1/(4*P[19])$	1.11
D19S433	(14, 14)	(14, 14.2)	2.30	$1/(2*P[14])$	2.30
vWA	(14, 14)	(14, 14)	3.89	$1/P[14]$	3.89
TPOX	(8, 11)	(8, 11)	1.45	$(P[8]+P[11])/(4*P[8]*P[11])$	1.45
D18S51	(14, 20)	(13, 14)	1.40	$1/(4*P[14])$	1.40
D5S818	(10, 11)	(11, 12)	0.92	$1/(4*P[11])$	0.92
FGA	(19, 23.2)	(19, 19)	10.00	$1/(2*P[19])$	10.00
CPI			212,290.30		212,290.30

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Table 36 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0079-50.

Locus	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D8S1179	(13, 16)	(16, 16)	6.02	$1/(2*P[16])$	6.02
D21S11	(29, 32.2)	(29, 32.2)	3.02	$(P[29]+P[32.2])/(4*P[29]*P[32.2])$	3.02
D7S820	(8, 10)	(8, 11)	1.54	$1/(4*P[8])$	1.54
CSF1PO	(10, 12)	(10, 12)	1.83	$(P[10]+P[12])/(4*P[10]*P[12])$	1.83
D3S1358	(16, 17)	(16, 16)	1.33	$1/(2*P[16])$	1.33
TH01	(9, 10)	(9, 9)	1.41	$1/(2*P[9])$	1.41
D13S317	(11, 14)	(11, 11)	2.18	$1/(2*P[11])$	2.18
D16S539	(10, 12)	(10, 12)	2.78	$(P[10]+P[12])/(4*P[10]*P[12])$	2.78
D2S1338	(18, 23)	(18, 21)	3.62	$1/(4*P[18])$	3.62
D19S433	(15.2, 16)	(13, 16)	17.86	$1/(4*P[16])$	17.86
vWA	(14, 18)	(15, 18)	1.21	$1/(4*P[18])$	1.21
TPOX	(8, 9)	(9, 11)	1.91	$1/(4*P[9])$	1.91
D18S51	(13, 14)	(13, 16)	1.88	$1/(4*P[13])$	1.88
D5S818	(7, 13)	(12, 13)	1.50	$1/(4*P[13])$	1.50
FGA	(23, 25)	(23, 25)	4.03	$(P[23]+P[25])/(4*P[23]*P[25])$	4.03
CPI			987,903.60		987,903.60

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Table 37 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0099-50-1.

Locus	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D8S1179	(12, 16)	(15, 16)	3.01	$1/(4*P[16])$	3.01
D21S11	(32.2, 32.2)	(30, 32.2)	4.03	$1/(2*P[32.2])$	4.03
D7S820	(11, 12)	(10, 12)	1.22	$1/(4*P[12])$	1.22
CSF1PO	(11, 12)	(11, 12)	1.50	$(P[11]+P[12])/(4*P[11]*P[12])$	1.50
D3S1358	(15, 17)	(15, 17)	2.03	$(P[15]+P[17])/(4*P[15]*P[17])$	2.03
TH01	(6, 9)	(6, 6)	4.67	$1/(2*P[6])$	4.67
D13S317	(11, 11)	(8, 11)	2.18	$1/(2*P[11])$	2.18
D16S539	(11, 11)	(11, 12)	1.68	$1/(2*P[11])$	1.68
D2S1338	(20, 24)	(23, 24)	1.67	$1/(4*P[24])$	1.67
D19S433	(13, 15.2)	(13, 14)	0.89	$1/(4*P[13])$	0.89
vWA	(16, 18)	(16, 18)	2.93	$(P[16]+P[18])/(4*P[16]*P[18])$	2.93
TPOX	(8, 8)	(8, 9)	0.89	$1/(2*P[8])$	0.89
D18S51	(15, 16)	(15, 16)	2.40	$(P[15]+P[16])/(4*P[15]*P[16])$	2.40
D5S818	(10, 11)	(11, 13)	0.92	$1/(4*P[11])$	0.92
FGA	(21, 23)	(19, 21)	1.94	$1/(4*P[21])$	1.94
CPI			12,766.12		12,766.12

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Table 38 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0099-50-2.

Locus	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D8S1179	(15, 16)	(15, 16)	4.51	$(P[15]+P[16])/(4*P[15]*P[16])$	3.01
D21S11	(31, 32.2)	(30, 32.2)	2.02	$1/(4*P[32.2])$	4.03
D7S820	(11, 12)	(10, 12)	1.22	$1/(4*P[12])$	1.22
CSF1PO	(11, 12)	(11, 12)	1.50	$(P[11]+P[12])/(4*P[11]*P[12])$	1.50
D3S1358	(15, 15)	(15, 17)	1.75	$1/(2*P[15])$	2.03
TH01	(6, 6)	(6, 6)	9.35	$1/P[6]$	4.67
D13S317	(8, 11)	(8, 11)	1.94	$(P[8]+P[11])/(4*P[8]*P[11])$	2.18
D16S539	(9, 12)	(11, 12)	1.32	$1/(4*P[12])$	1.68
D2S1338	(20, 24)	(23, 24)	1.67	$1/(4*P[24])$	1.67
D19S433	(13, 15.2)	(13, 14)	0.89	$1/(4*P[13])$	0.89
vWA	(16, 16)	(16, 18)	3.45	$1/(2*P[16])$	2.93
TPOX	(8, 8)	(8, 9)	0.89	$1/(2*P[8])$	0.89
D18S51	(16, 16)	(15, 16)	2.56	$1/(2*P[16])$	2.40
D5S818	(10, 13)	(11, 13)	1.50	$1/(4*P[13])$	0.92
FGA	(21, 23)	(19, 21)	1.94	$1/(4*P[21])$	1.94
CPI			23,506.30		23,506.30

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Table 39 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0103-50.

Locus	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D8S1179	(14, 15)	(14, 15)	2.98	$(P[14]+P[15])/(4*P[14]*P[15])$	2.98
D21S11	(29, 30)	(29, 30)	1.99	$(P[29]+P[30])/(4*P[29]*P[30])$	1.99
D7S820	(10, 12)	(10, 11)	1.30	$1/(4*P[10])$	1.30
CSF1PO	(11, 12)	(11, 12)	1.50	$(P[11]+P[12])/(4*P[11]*P[12])$	1.50
D3S1358	(17, 18)	(17, 18)	4.32	$(P[17]+P[18])/(4*P[17]*P[18])$	4.32
TH01	(7, 9.3)	(7, 7)	1.61	$1/(2*P[7])$	1.61
D13S317	(8, 10)	(10, 11)	1.94	$1/(4*P[10])$	1.94
D16S539	(12, 13)	(10, 12)	1.32	$1/(4*P[12])$	1.32
D2S1338	(19, 24)	(19, 24)	2.77	$(P[19]+P[24])/(4*P[19]*P[24])$	2.77
D19S433	(13, 13)	(13, 13.2)	1.78	$1/(2*P[13])$	1.78
vWA	(14, 14)	(14, 14)	3.89	$1/P[14]$	3.89
TPOX	(8, 9)	(8, 8)	0.89	$1/(2*P[8])$	0.89
D18S51	(15, 17)	(14, 17)	3.09	$1/(4*P[17])$	3.09
D5S818	(12, 13)	(12, 12)	2.12	$1/(2*P[12])$	2.12
FGA	(21, 21)	(21, 21)	7.75	$1/P[21]$	7.75
CPI			176,897.10		176,897.10

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Table 40 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0106-50-1.

Locus	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D8S1179	(10, 16)	(10, 15)	1.69	$1/(4*P[10])$	1.69
D21S11	(31, 32.2)	(29, 32.2)	2.02	$1/(4*P[32.2])$	2.02
D7S820	(10, 11)	(10, 11)	2.03	$(P[10]+P[11])/(4*P[10]*P[11])$	2.03
CSF1PO	(10, 11)	(10, 11)	2.01	$(P[10]+P[11])/(4*P[10]*P[11])$	2.01
D3S1358	(15, 16)	(16, 18)	0.66	$1/(4*P[16])$	0.66
TH01	(7, 7)	(7, 7)	3.23	$1/P[7]$	3.23
D13S317	(8, 11)	(8, 11)	1.94	$(P[8]+P[11])/(4*P[8]*P[11])$	1.94
D16S539	(10, 11)	(11, 11)	1.68	$1/(2*P[11])$	1.68
D2S1338	(23, 24)	(21, 24)	1.67	$1/(4*P[24])$	1.67
D19S433	(13, 13.2)	(13, 15.2)	0.89	$1/(4*P[13])$	0.89
vWA	(14, 17)	(14, 17)	2.01	$(P[14]+P[17])/(4*P[14]*P[17])$	2.01
TPOX	(8, 8)	(8, 8)	1.77	$1/P[8]$	1.77
D18S51	(14, 14)	(14, 15)	2.79	$1/(2*P[14])$	2.79
D5S818	(10, 12)	(11, 12)	1.06	$1/(4*P[12])$	1.06
FGA	(20, 23)	(20, 21)	3.16	$1/(4*P[20])$	3.16
CPI			4,828.39		4,828.39

Table 41 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0106-50-2.

Locus	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D8S1179	(14, 15)	(14, 15)	2.51	$(P[14]+P[15])/(4*P[14]*P[15])$	2.51
D21S11	(14, 17)	(14, 17)	2.01	$(P[14]+P[17])/(4*P[14]*P[17])$	2.01
D7S820	(8, 11)	(8, 11)	1.94	$(P[8]+P[11])/(4*P[8]*P[11])$	1.94
CSF1PO	(11, 11)	(10, 11)	1.68	$1/(2*P[11])$	1.68
D3S1358	(10, 11)	(11, 11)	1.68	$1/(2*P[11])$	1.68
TH01	(11, 11)	(10, 11)	1.48	$1/(2*P[11])$	1.48
D13S317	(16, 16)	(16, 18)	1.33	$1/(2*P[16])$	1.33
D16S539	(10, 12)	(11, 12)	1.06	$1/(4*P[12])$	1.06
D2S1338	(13, 13.2)	(13, 15.2)	0.89	$1/(4*P[13])$	0.89
D19S433	(12, 15)	(10, 15)	1.50	$1/(4*P[15])$	1.50
vWA	(20, 22)	(20, 21)	3.16	$1/(4*P[20])$	3.16
TPOX	(21, 23)	(21, 24)	4.03	$1/(4*P[21])$	4.03
D18S51	(29, 31)	(29, 32.2)	1.00	$1/(4*P[29])$	1.00
D5S818	(7, 7)	(7, 7)	3.23	$1/P[7]$	3.23
FGA	(8, 8)	(8, 8)	1.77	$1/P[8]$	1.77
CPI			5,613.74		5,613.74

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Table 42 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0132-50.

Locus	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D8S1179	(13, 14)	(10, 14)	1.48	$1/(4*P[14])$	1.48
D21S11	(30, 32.2)	(32.2, 33.2)	2.02	$1/(4*P[32.2])$	2.02
D7S820	(9, 10)	(9, 12)	4.55	$1/(4*P[9])$	4.55
CSF1PO	(7, 12)	(10, 12)	0.66	$1/(4*P[12])$	0.66
D3S1358	(15, 17)	(16, 17)	1.15	$1/(4*P[17])$	1.15
TH01	(6, 6)	(6, 9)	4.67	$1/(2*P[6])$	4.67
D13S317	(8, 11)	(8, 11)	1.94	$(P[8]+P[11])/(4*P[8]*P[11])$	1.94
D16S539	(9, 12)	(9, 11)	1.15	$1/(4*P[9])$	1.15
D2S1338	(19, 25)	(19, 25)	6.92	$(P[19]+P[25])/(4*P[19]*P[25])$	6.92
D19S433	(14, 15.2)	(13, 14)	1.15	$1/(4*P[14])$	1.15
vWA	(17, 18)	(16, 17)	1.04	$1/(4*P[17])$	1.04
TPOX	(8, 8)	(8, 14)	0.89	$1/(2*P[8])$	0.89
D18S51	(14, 16)	(16, 16)	2.56	$1/(2*P[16])$	2.56
D5S818	(9, 11)	(7, 11)	0.92	$1/(4*P[11])$	0.92
FGA	(23, 23)	(23, 24.2)	2.69	$1/(2*P[23])$	2.69
CPI			5,090.19		5,090.19

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Table 43 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0147-50-1.

Locus	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D8S1179	(13, 16)	(15, 16)	3.01	$1/(4*P[16])$	3.01
D21S11	(30, 32)	(30, 32)	10.61	$(P[30]+P[32])/(4*P[30]*P[32])$	10.61
D7S820	(9, 10)	(9, 11)	4.55	$1/(4*P[9])$	4.55
CSF1PO	(9, 11)	(9, 9)	26.32	$1/(2*P[9])$	26.32
D3S1358	(15, 16)	(15, 16)	1.54	$(P[15]+P[16])/(4*P[15]*P[16])$	1.54
TH01	(9, 9)	(9, 9.3)	1.41	$1/(2*P[9])$	1.41
D13S317	(11, 11)	(10, 11)	2.18	$1/(2*P[11])$	2.18
D16S539	(9, 11)	(9, 9)	2.30	$1/(2*P[9])$	2.30
D2S1338	(18, 19)	(17, 19)	1.11	$1/(4*P[19])$	1.11
D19S433	(14, 14)	(14, 14)	4.61	$1/P[14]$	4.61
vWA	(19, 19)	(17, 19)	4.39	$1/(2*P[19])$	4.39
TPOX	(8, 8)	(8, 8)	1.77	$1/P[8]$	1.77
D18S51	(17, 20)	(16, 17)	3.09	$1/(4*P[17])$	3.09
D5S818	(10, 12)	(10, 11)	1.17	$1/(4*P[10])$	1.17
FGA	(23.2, 24)	(22, 24)	2.27	$1/(4*P[24])$	2.27
CPI			13,538,910.00		13,538,910.00

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Table 44 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0147-50-2.

Locus	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D8S1179	(11, 16)	(15, 16)	3.01	$1/(4*P[16])$	3.01
D21S11	(32, 33.2)	(30, 32)	9.62	$1/(4*P[32])$	9.62
D7S820	(9, 11)	(9, 11)	5.29	$(P[9]+P[11])/(4*P[9]*P[11])$	5.29
CSF1PO	(9, 14)	(9, 9)	26.32	$1/(2*P[9])$	26.32
D3S1358	(15, 17)	(15, 16)	0.87	$1/(4*P[15])$	0.87
TH01	(7, 9)	(9, 9.3)	0.70	$1/(4*P[9])$	0.70
D13S317	(10, 11)	(10, 11)	3.03	$(P[10]+P[11])/(4*P[10]*P[11])$	3.03
D16S539	(9, 11)	(9, 9)	2.30	$1/(2*P[9])$	2.30
D2S1338	(17, 18)	(17, 19)	2.91	$1/(4*P[17])$	2.91
D19S433	(14, 14)	(14, 14)	4.61	$1/P[14]$	4.61
vWA	(17, 19)	(17, 19)	3.23	$(P[17]+P[19])/(4*P[17]*P[19])$	3.23
TPOX	(8, 9)	(8, 8)	0.89	$1/(2*P[8])$	0.89
D18S51	(17, 20)	(16, 17)	3.09	$1/(4*P[17])$	3.09
D5S818	(11, 12)	(10, 11)	0.92	$1/(4*P[11])$	0.92
FGA	(23.2, 24)	(22, 24)	2.27	$1/(4*P[24])$	2.27
CPI			4,302,935.00		4,302,935.00

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Table 45 Comparison of combined paternity index (CPI) calculation between the FEDDS-ProfileManagement software and MS Excel manual in case 0160-50.

Locus	Child	Alleged Father	PI for FEDDS	Formula for manual calculation	PI Manual
D8S1179	(10, 11)	(10, 11)	3.83	$(P[10]+P[11])/(4*P[10]*P[11])$	3.83
D21S11	(29, 33.2)	(32.2, 33.2)	3.91	$1/(4*P[33.2])$	3.91
D7S820	(10, 11)	(10, 12)	1.30	$1/(4*P[10])$	1.30
CSF1PO	(10, 12)	(10, 12)	1.83	$(P[10]+P[12])/(4*P[10]*P[12])$	1.83
D3S1358	(15, 17)	(16, 17)	1.15	$1/(4*P[17])$	1.15
TH01	(8, 9.3)	(9.3, 9.3)	6.17	$1/(2*P[9.3])$	6.17
D13S317	(8, 8)	(8, 9)	1.71	$1/(2*P[8])$	1.71
D16S539	(9, 13)	(9, 13)	3.53	$(P[9]+P[13])/(4*P[9]*P[13])$	3.53
D2S1338	(17, 21)	(21, 24)	4.03	$1/(4*P[21])$	4.03
D19S433	(13, 15)	(13, 13)	1.78	$1/(2*P[13])$	1.78
vWA	(18, 18)	(14, 18)	2.42	$1/(2*P[18])$	2.42
TPOX	(8, 11)	(8, 8)	0.89	$1/(2*P[8])$	0.89
D18S51	(14, 15)	(13, 14)	1.40	$1/(4*P[14])$	1.40
D5S818	(10, 13)	(11, 13)	1.50	$1/(4*P[13])$	1.50
FGA	(21, 23)	(22, 23)	1.34	$1/(4*P[23])$	1.34
CPI			65,694.06		65,694.06

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Table 46 Characteristics of the observed mutation case results.

Case no.	STR System	Child	Mother	Father	Origin	Gain(+)/ loss(-)	Sequence
0408/48	D21S11	28	n.t.	29	Paternal	-1	[TCTA] ₄ [TCTG] ₆ [TCTA] ₃ TA[TCTA] ₃ TCA[TCTA] ₂ TCCATA[TCTA] ₁₁₋₁₀
0113/49	D21S11	30, 33.2	30, 30.2	30,32.2	Paternal	+1	[TCTA] ₅ [TCTG] ₆ [TCTA] ₃ TA[TCTA] ₃ TCA[TCTA] ₂ TCCATA[TCTA] ₁₂₋₁₃ TATCTA
0469/50	D21S11	29	30.2	29,30	Maternal	-1.2	[TCTA] ₅ [TCTG] ₆ [TCTA] ₃ TA[TCTA] ₃ TCA[TCTA] ₂ TCCATA[TCTA] ₁₀ TATCTA
0541/50	D21S11	30,31	32, 32.2	n.t.	Maternal	-1	[TCTA] ₆ [TCTG] ₅ [TCTA] ₃ TA[TCTA] ₃ TCA[TCTA] ₂ TCCATA[TCTA] ₁₃₋₁₂
0012/51	D21S11	29,31	30, 32.2	n.t.	Maternal	+1/-1	[TCTA] ₆ [TCTG] ₅ [TCTA] ₃ TA[TCTA] ₃ TCA[TCTA] ₂ TCCATA[TCTA] _{11-12 or 10}
0690/51	D21S11	30.2, 32.2	29, 31.2	29,32.2	Maternal	-1	[TCTA] ₅ [TCTG] ₆ [TCTA] ₃ TA[TCTA] ₃ TCA[TCTA] ₂ TCCATA[TCTA] ₁₁₋₁₀ TATCTA
0132/52	D21S11	29	32.2	n.t.	Maternal	-3.2	[TCTA] ₄ [TCTG] ₆ [TCTA] ₃ TA[TCTA] ₃ TCA[TCTA] ₂ TCCATA[TCTA] ₁₃₋₁₁ TATCTA

Table 46 Characteristics of the observed mutation case results (continued).

Case no.	STR System	Child	Mother	Father	Origin	Gain(+)/ loss(-)	Sequence
0103/48	vWA	18	n.t.	17,19	Paternal	+1/-1	TCTA[TCTG] ₄ [TCTA] ₁₂₋₁₁ or 10-11 TCCATCTA
0037/50	vWA	17,19	14,19	14,18	Paternal	-1	TCTA[TCTG] ₄ [TCTA] ₁₁₋₁₀ TCCATCTA
0302/50	vWA	16,20	n.t.	18,19	Paternal	+1	TCTA[TCTG] ₄ [TCTA] ₁₂₋₁₃ TCCATCTA
0324/50	vWA	16,17	n.t.	18,19	Paternal	-1	TCTA[TCTG] ₄ [TCTA] ₁₁₋₁₀ TCCATCTA
0325/50	vWA	17,18	14,17	16,19	Paternal	-1	TCTA[TCTG] ₄ [TCTA] ₁₂₋₁₁ TCCATCTA
0118/52	vWA	14,16	n.t.	17	Paternal	-1	TCTA[TCTG] ₄ [TCTA] ₁₀ TCCATCTA
0359/47	FGA	21,26	n.t.	22,25	Paternal	+1/-1	[TTTC] ₃ TTTTTCT[CTTT] ₁₃₋₁₄ CTCC[TTCC] ₂ or [TTTC] ₃ TTTTTCT[CTTT] ₁₈₋₁₇ CTCC[TTCC] ₂
0293/50	FGA	23,25	22,25	22	Paternal	+1	[TTTC] ₃ TTTTTCT[CTTT] ₁₄₋₁₅ CTCC[TTCC] ₂
0285/51	FGA	19,2, 22	21,23	n.t.	Maternal	+1/-1	[TTTC] ₃ TTTTTCT[CTTT] ₁₃₋₁₄ or 15- 14 CTCC[TTCC] ₂

Table 46 Characteristics of the observed mutation case results (continued).

Case no.	STR System	Child	Mother	Father	Origin	Gain(+)/ loss(-)	Sequence
0588/51	FGA	21,26	n.t.	23,25	Paternal	+1	[TTTC] ₃ TTTTTCT[CTTT] ₁₇₋₁₈ CTCC[TTCC] ₂
0125/49	D18S51	13,14	12,13	13,15	Paternal	-1	[AGAA] ₁₅₋₁₄
0376/49	D18S51	16,17	14,16	14,16	Unassigned	+1	[AGAA] ₁₆₋₁₇
0067/51	D18S51	14	n.t.	13,17	Paternal	-1	[AGAA] ₁₃₋₁₄
0493/51	D18S51	17,19	n.t.	14,20	Paternal	-1	[AGAA] ₂₀₋₁₉
0145/48	D16S539	9,13	n.t.	11	Paternal	+2/-2	[GATA] _{11-13 or 11-9}
0303/50	D16S539	12	n.t.	9,11	Paternal	+1	[GATA] ₁₁₋₁₂
0029/52	D16S539	10	9,11	n.t.	Maternal	+1/-1	[GATA] ₉₋₁₀ or [GATA] ₁₁₋₁₀
0647/50	D3S1358	14,15	14,15	16	Paternal	-1	TCTA[TCTG] ₃ [TCTA] ₁₂₋₁₁
0661/51	D3S1358	17,19	n.t.	16,18	Paternal	+1/-1	TCTA[TCTG] ₃ [TCTA] ₁₂₋₁₃ or TCTA[TCTG] ₃ [TCTA] ₁₄₋₁₃ or TCTA[TCTG] ₃ [TCTA] ₁₄₋₁₅
0183/52	D3S1358	15,18	n.t.	16,17	Paternal	+1/-1	TCTA[TCTG] ₃ [TCTA] ₁₃₋₁₄ or TCTA[TCTG] ₃ [TCTA] ₁₂₋₁₁
0368/47	D2S1338	20,23	n.t.	17,19	Paternal	+1	[TGCC] ₇ [TTCC] ₁₂₋₁₃
0611/51	D2S1338	18,23	20,24	n.t.	Maternal	-1	[TGCC] ₇ [TTCC] ₁₇₋₁₆
0211/48	D13S317	11	8	11	Maternal	+3	[TATC] ₈₋₁₁

Table 46 Characteristics of the observed mutation case results (continued).

Case no.	STR System	Child	Mother	Father	Origin	Gain(+)/ loss(-)	Sequence
0211/48	D13S317	<i>11</i>	<i>8</i>	<i>11</i>	Maternal	+3	[TATC] ₈₋₁₁
0302/50	D13S317	<i>12,13</i>	n.t.	<i>11,14</i>	Paternal	+1/-1	[TATC] ₁₁₋₁₂ or [TATC] ₁₄₋₁₃
0395/48	D5S818	<i>10</i>	<i>11</i>	<i>10,12</i>	Maternal	-1	[AGAT] ₁₁₋₁₀
0285/51	D7S820	<i>8</i>	n.t.	<i>11</i>	Paternal	-3	[GATA] ₁₁₋₈
0130/49	D8S1179	<i>15,16</i>	<i>11,15</i>	<i>15</i>	Unassigned	+1	[TCTA] _{1,2} [TCTG] ₁ [TCTA] ₁₃
0316/48	TH01	<i>9.3</i>	n.t.	<i>7</i>	Paternal	+A	primer binding site (A insertion)

Alleles affected by the mutational event are shown in italics

Sequence gain or loss affected by the mutational event are shown in bolds

n.t. not available for typing

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BIOGRAPHY

Mister Tawat Rinthachai was born in Roi Et province on the 27th of July 1979. He graduated in Bachelor Degree from Chulalongkorn University for Faculty of Science; major Genetics in 2004. Consequently, he started to study his Master Degree in Genetics from Faculty of Science, Chulalongkorn University.



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