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Improving Atm Security Check Using DNA Biometrics

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ABSTRACT: *This paper exposes how DNA can be used to identify account owner of a particular bank.DNA samples were obtained from body fluid. Buccal swab was used for sample collection .Buccal cell collection involves wiping a small piece of filter paper or a cotton swab against the inside of armpit in order to collect shed epithelial cells. The swab was then air dried or could be pressed against a treated collection card in order to transfer epithelial cells for storage purposes. The stored samples were later amplified and separated .The data generated from the samples were stored and saved in the database so that if a customer comes to claim money, the system checks whether it matches with what is stored in the database ,if it matches with the one in the database, access is granted to the customer,.if it does not match with what is stored in the database ,access is denied from the customer.*

Keywords: *Buccal cell, Single nucleotide polymorphism (SNP) ,polymerase chain reaction(PCR),Database,ATM*

I. INTRODUCTION

The biometric authentication technologies, typified by fingerprint, face recognition and iris scanning, have been making rapid progress. Retinal scanning, voice dynamics and handwriting recognition are also being developed. These methods have been commercialized and are being incorporated into systems that require accurate on-site personal authentication. However, these methods are based on the measurement of similarity of feature-points. This introduces an element of inaccuracy that renders existing technologies unsuitable for a universal ID system. Among the various possible types of biometric personal identification system, deoxyribonucleic acid (DNA) provides the most reliable personal identification. It is intrinsically digital, and does not change during a person's life or after his/her death. This paper addresses three questions: First, how can personally identifying information be obtained from DNA sequences in the human genome? Second, how can a personal ID be generated from DNA-based information? And finally, what are the advantages, deficiencies, and future potential for personal IDs generated from DNA data (DNA-ID)?

II. HUMAN IDENTIFICATION BASED ON DNA POLYMORPHISM

A human body is composed of approximately of 60 trillion cells. DNA, which can be thought of as the blueprint for the design of the human body, is folded inside the nucleus of each cell. DNA is a polymer, and is composed of nucleotide units that each has three parts: a base, a sugar, and a phosphate. The bases are adenine, guanine, cytosine and thymine, abbreviated A, G, C and T, respectively. These four letters represent the informational content in each nucleotide unit; variations in the nucleotide sequence bring about biological diversity, not only among human beings but among all living creatures. Meanwhile, the phosphate and sugar portions form the backbone structure of the DNA molecule. Within a cell, DNA exists in the double-stranded form, in which two ant parallel strands spiral around each other in a double helix. The bases of each strand project into the core of the helix, where they pair with the bases of the complementary strand. A pairs strictly with T, and C with G .[1]

Within human cells, DNA found in the nucleus of the cell (nuclear DNA) is divided into chromosomes. The human genome consists of 22 matched pairs of autosomal chromosomes and two sex-determining chromosomes, X and Y. In other words, human cells contain 46 different chromosomes. Males are described as XY since they possess a single copy of the X chromosome and a single copy of the Y chromosome, while females possess two copies of the X chromosome and are described as XX.

The regions of DNA that encode and regulate the synthesis of proteins are called genes; these regions consist of exons (protein-coding portions) and introns (the intervening sequences) and constitute approximately 25% of the genome .[2] The human genome contains only 20,000−25,000 genes.[3] Therefore, most of the genome, approximately 75%, is extragenic. These regions are sometimes referred to as 'junk' DNA; however, recent research suggests that they may have other essential functions. Markers commonly used to identify individual human beings are usually found in the noncoding regions, either between genes or within genes (i.e., introns).

2.1. Sort tandem repeat (STR)
In the extragenic region of eukaryotic genome, there are many repeated DNA sequences (approximately 50% of the whole genome). These repeated DNA sequences come in all sizes, and are typically designated by the length of the core repeat unit and either the number of contiguous repeat units or the overall length of the repeat region. These regions are referred to as satellite DNA .[4] The core repeat unit for a medium-length repeat, referred to as a minisatellite or VNTR (variable number of tandem repeats), is in the range of approximately 8−100 bases in length .[6] DNA regions with repeat units that are 2−7 base pairs (bp) in length are called microsatellites, simple sequence repeats (SSRs), or most commonly short tandem repeats (STRs) [7]. STRs have become popular DNA markers because they are easily amplified by the polymerase chain reaction (PCR) and they are spread throughout the genome, including both the 22 autosomal chromosomes and the X and Y sex chromosomes. The number of repeats in STR markers can vary widely among individuals, making the STRs an effective means of human identification in forensic science [8]. The location of an STR marker is called its "locus." The type of STR is represented by the number of repeat called 'allele' which is taken from biological father and mother. When an individual has two copies of the same allele for a given marker, they are homozygous; when they have two different alleles, they are heterozygous.

2.2. DNA sample collection
DNA can be easily obtained from a variety of biological sources, not only body fluid but also nail, hair and used razors[9] . For biometric applications, a buccal swab is the most simple, convenient and painless sample collection method . Buccal cell collection involves wiping a small piece of filter paper or a cotton swab against the inside of the subject's cheek, in order to collect shed epithelial cells. The swab is then air dried, or can be pressed against a treated collection card in order to transfer epithelial cells for storage purposes.

2.3. DNA extraction and quantification
There are many methods available for extracting DNA. [10] The choice of which method to use depends on several factors, especially the number of samples, cost, and speed. Extraction time is the critical factor for biometric applications. The author has already reported the "5-minute DNA extraction" using an automated procedure [11]. The use of large quantities of fresh buccal cells made it possible to extract DNA in a short time.

In forensic cases, DNA quantization is an important step [12]. However, this step can be omitted in biometrics because a relatively large quantity of DNA can be recovered from fresh buccal swab samples.

2.4. DNA amplification (polymerase chain reaction: PCR
The field of molecular biology has greatly benefited from the discovery of a technique known as the polymerase chain reaction, or PCR[13]. First described in 1985 by Kary Mullis, who received the Novel Prize in Chemistry in 1993, PCR has made it possible to make hundreds of millions of copies of a specific sequence of DNA in a few hours. PCR is an enzymatic process in which a specific region of DNA is replicated over and over again to yield many copies of a particular sequence. This molecular process involves heating and cooling samples in a precise thermal cycling pattern for approximately 30 cycles. During each cycle, a copy of the target DNA sequence is generated for every molecule containing the target sequence. In recent years, it has become possible to PCR amplify 16 STRs, including the gender assignment locus called 'amelogenin,' in one tube [14].

2.5. DNA separation and detection

After STR polymorphisms have been amplified using PCR, the length of products must be measured precisely; some STR alleles differ by only 1 base-pair. Electrophoresis of the PCR products through denaturing polyacrylamide gels can be used to separate DNA molecules from 20−500 nucleotides in length with single base pair resolution [15]. Recently, the fluorescence labelling of PCR products followed by multicolour detection has been adopted by the forensic science field. Up to five different dyes can be used in a single analysis. Electrophoresis platforms have evolved from slab-gels to capillary electrophoresis (CE), which use a narrow glass filled with an cross-linked polymer solution to separate the DNA molecules [16]. After data collection by the CE, the alleles (i.e., the type or the number of STR repeat units), are analyzed by the software that accompanies the CE machine.

It takes around four hours, starting with DNA extraction, to obtain data from 16 STRs including the sex determination locus.

2.6. Single nucleotide polymorphism (SNP)

The simplest type of polymorphism is the single nucleotide polymorphism (SNP), a single base difference at a particular point in the sequence of DNA [17]. SNPs normally have just two alleles, e.g., one allele is a cytosine (C) and the other is a thymine (T) . SNPs therefore are not highly polymorphic and do not possess ideal properties for DNA polymorphism to be used in forensic analysis. However, SNPs are so abundant throughout the genome that it is theoretically possible to type hundreds of them. Furthermore, sample processing data analysis may be more fully automated because size-based separation is not required. Thus, SNPs are prospective new bio-markers in clinical medicine [18].

2.2.1. SNP detection methods

Several SNP typing methods are available, each with its own strengths and weaknesses, unlike the STR analysis [19]. In order to achieve the same power of discrimination as that provided by STRs, it is necessary to analyse many more SNPs. 40 to 50 SNPs must be analyzed in order to obtain reasonable powerful discrimination and define the unique profile of an individual [20]. Importantly, however, we can count on the development of new SNP detection technologies, capable of high-throughput analysis, in the near future.

III. DNA POLYMORPHISM FOR BIOMETRIC SOURCE

The most commonly studied or implemented biometrics are fingerprinting, face, iris, voice, signature, retina and the patterns of vein and hand geometry [21]. No one model is best for all situations. In addition, these technologies are based on the measurement of similarity of features. This introduces an element of inaccuracy that renders the existing technologies unsuitable for a universal ID system. However, DNA polymorphism information, such as STRs and SNPs, could provide the most reliable personal identification. This data can be precisely defined the most minute level, is intrinsically digital, and does not change during a person's life or after his/her death. Therefore, DNA identification data is utilized in the forensic sciences. On the negative side, the biggest problem in using DNA is the time required for the extraction of nucleic acid and the evaluation of STR or SNP data. In addition, there are several other problems, such as the high cost of analysis, issues raised by monozygotic twins, and ethical concerns.

This section describes a method for generation of DNA personal ID (DNA-ID) based on STR and SNP data, specifically. In addition, by way of example, the author proposes DNA INK for authentic security.

3.1. DNA personal ID using STR system

We will refer to repeat counts of alleles obtained by STR analysis as (j, k). Each locus is associated with two alleles with distinct repeat counts (j, k), one allele is inherited from the father, and the other from the mother. Before (j, k) can be applied to a DNA personal ID, it is necessary to statistically analyze how the distribution of (j, k) varies at a given locus based on actual data.

We can generate a DNA-ID, αX , that includes allelic information about STR loci. The loci are incorporated in the following sequence. The repeat counts for the pair of alleles at each locus are arranged in ascending order.

Step 1. Measure the STR alleles at each locus.

Step 2. Obtain STR count values for each locus; express these in ascending order.

$$L: j \| k, j \leq k \qquad (1)$$

Depending on the measurement, the same person's STR count may appear as (j, k) or (k, j). Therefore, j and k are expressed in an ascending order, i.e., using $(j, k | j \leq k)$, in order to establish a one-to-one correspondence for each individual. This step is referred to as a ordering operation.

Step 3. Generate a DNA-ID αX according to the following series, $L_i (j, k)$:

$$\alpha X = L1 \| L2 \| L3 \| \ldots \| Ln \qquad (2)$$

where L_i indicates the ith STR count (j, k).

For example, suppose that Mr. M has the following alleles at the respective loci;

$$\alpha X = D3S1358 \| D13S317 \| D18S51 \| D21S11 \| \ldots \| D16S539 = (12,14) \| (8,11) \| (13,15) \| (29,32.2) \| \ldots \| (10,10) \quad (3)$$

The αX was thus defined as follows.

$$\alpha X = 1214811131529322 \ldots\ldots 1010 \qquad (4)$$

When the STR number of an allele had a fractional component, such as allele32.2 in D21S11, the decimal point was removed, and all of the numbers, including those after the decimal point, were retained.

Finally, αX is generated number with several tends of digits, and becomes a personal identification information that is unique with a certain probability predicted by statistical and theoretical analysis.

3.2. Establishment of the identification format

Because

αX contains personal STR information, it must be encrypted to protect privacy. This can be achieved using a one-way function that also reduces the data length of the DNA-ID. This one-way function, the secure hash algorithm-1 (SHA-1), produces an ID with a length δX of 160 bits, according to the following transformation:

$$\delta X = h (\alpha X) \qquad (5)$$

3.3. Statistical and theoretical analysis of DNA-ID

Probability p that the STR count at the same locus is identical for any two persons can be expressed as follows:

When $j=k$, $\sum_{j=1}^{m}(p_j \cdot p_k)^2$ When $j \neq k$, $\sum_{1 \leq jk \leq m}(2p_j \cdot p_k)^2 \therefore p = \sum_{j=1}^{m}(p_j)^4 + \sum_{1 \leq jk \leq m}4(p_j \cdot p_k)^2 \qquad (7)$

Here, m is the upper limit of j and k, and the information reported so far indicates m= 60. Next, a determination is made of the DNA-ID matching probability p_n, where n loci were used to generate the ID. The probability that the STR counts at the ith locus will match for any two persons is denoted as p_i. When n loci are used, the probability p_n that the DNA-IDs of any two persons will match (the DNA-ID matching probability) is as follows:

$$p_n = \prod_{i=1}^{n} p_i \qquad (8)$$

Here, it is assumed that there is no correlation among the STR loci.

3.4. Verification using validation experiment (STR)

As a validation experiment, we studied the genotype and distribution of allele frequencies at 18 STRs in 526 unrelated Japanese individuals. Data was obtained using three commercial STR typing kits: PowerPlex™ 16 system (Promega), PowerPlex SE33 (Promega), and AmpFlSTR Identifiler™ . Information about the 18 target STRs is described in Table 1.

Step 1. Perform DNA extraction, PCR amplification and STR typing

Step 2. Perform the exact test (the data were shuffled 10,000 times), the homozygosity, and likelihood ratio tests using STR data for each STR locus in order to evaluate Hardy–Weinberg equilibrium (HWE). HWE provides a simple mathematical representation of the relationship among genotype and allele frequencies within an ideal population, and is central to forensic genetics. Importantly, when a population is in HWE, the genotype frequencies can be predicted from the allele frequencies.

Step 3. Calculate parameters, the matching probability, the expected and observed heterozygosity, the power of discrimination, the polymorphic information content, the mean exclusion chance, in order to estimate the polymorphism at each STR locus.

There are some loci on the same chromosomes (chr) such as D21S11 and Penta D on chr 21, D5S818 and CSF1PO on chr 5, and TPOX and D2S1338 on chr 2. No correlation was found between any sets of loci on the same chromosome, which means they are statistically independent. In addition, the statistical data for the 18 analyzed STRs, excluding the Amelogenin locus, were analyzed and showed a relatively high rate of matching probability; no significant deviation from HWE was detected. The combined mean exclusion chance was 0.9999998995 and the combined matching probability was 1 in 9.98×10^{21}, i.e., 1.0024×10^{-22}. These values were calculated using polymorphism data from Japanese subjects; it is likely that different values would be obtained using data compiled from different ethnic groups.

Table 3.0 : Information about autosomal STR loci

Locus	Chromosome Location	Repeat Motif*	Locus	Chromosome Location	Repeat Motif*
TPOX	2 q 25.3	GAAT	TH01	11 p 15.5	TCAT
D2S1338	2 q 35	TGCC/TTCC	VWA	12 p 13.31	TCTG/TCTA
D3S1358	3 p 21.31	TCTG/TCTA	D13S317	13 q 31.1	TATC
FGA	4 q 31.3	CTTT/TTCC	Penta E	15 q 26.2	AAAGA
D5S818	5 q 23.2	AGAT	D16S539	16 q 24.1	GATA
CSF1PO	5 q 33.1	TAGA	D18S51	18 q 21.33	AGAA
SE33	6 q 14	AAAG	D19S433	19 q 12	AAGG/TAGG
D7S820	7 q 21.11	GATA	D21S11	21 q 21.1	TCTA/TCTG
D8S1179	8 q 24.13	TCTA/TCTG	Penta D	21 q 22.3	AAAGA

* Two types of motif means a compound or complex repeat sequence

Table 3.1: Data Generated from sweat

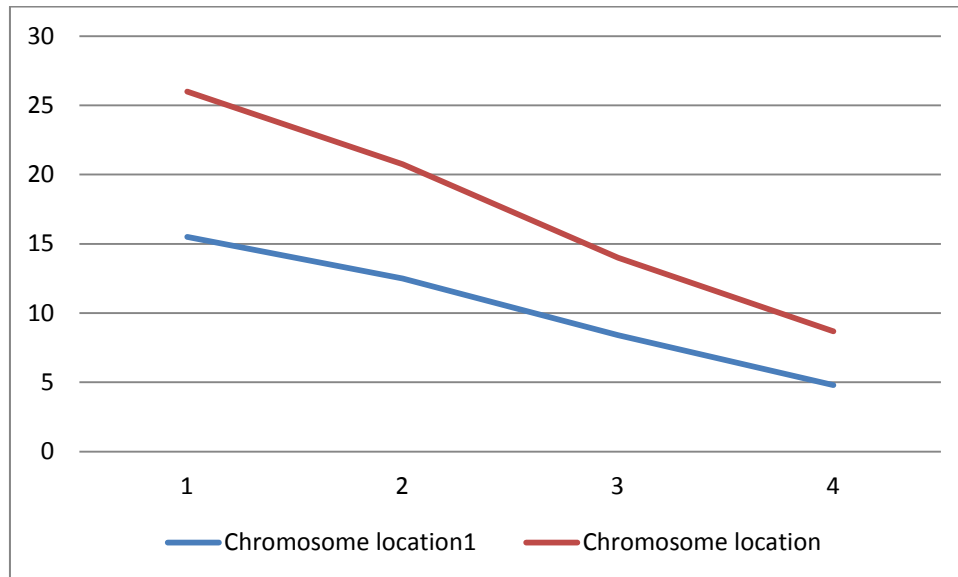| Locus1	Chromosome location1	Locus2	Chromosome location
TPOX	15.5	GAAT	10.5
FGA	12.5	PENTA E	8.25
SE33	8.4	AAAG	5.6
D7S820	4.8	GSTA	3.87

Fig.3.2: Graph of chromosome location

3.3 Analysis of Data: The graph above shows how the chromosome representation of rightful should be. If a customer comes to withdraw money, fluid will be extracted from the customer's armpit in order to ascertain whether he or she is the rightful owner of the money or not. The data gotten from the customer will be processed and matched with the graph in fig.3.2, if it matches with it, access is granted to the customer, in case it does not match with it, access is denied from the customer.

3.4. DNA personal ID using SNP system

The vast majority of SNPs are biallelic, meaning that they have two possible alleles and therefore three possible genotypes. For example, if the alleles for a SNP locus are R and S (where 'R' and 'S' could represent a A(adenine), G(guanine), C(cytosine) and T(thymine) nucleotide), three possible genotypes would be RR, RS (SR) or SS. Because a single biallelic SNP by itself yields less information than a multiallelic STR marker, it is necessary to analyze a larger number of SNPs in order to obtain a reasonable power of discrimination to define a unique profile. Computational analysis have shown that on average, 25 to 45 SNP loci are needed in order to yield equivalent random match probabilities comparable to those obtained with the 13 core STR loci that have been adopted by the FBI's DNA database (COmbined DNA Index System, CODIS).

The steps of creating a DNA-ID using SNPs are as follows;

Step 1. Define alleles 1 and 2 for each SNP locus. Since DNA has a double helix structure, the single nucleotide polymorphism of A or G is the same polymorphism of T or C, respectively (Fig. 4). In other words, it is important to specify which strand of the double helix is to be analyzed, and to define allele 1 and allele 2 at the outset.

Step 2. Analyze the SNP loci and place them in the following order.

$$L : \text{allele 1} \| \text{allele 2} \tag{9}$$

Step 3. Generate the DNA-ID αX according to the following series of L_i (allele1, allele2):

$$\alpha X = L1 \| L2 \| L3 \| \ldots \| Ln \tag{10}$$

where L_i indicates the ith SNP nucleotide (allele1, allele2).

For example, suppose that a person has the following alleles at the respective loci;

$$\alpha X = \text{SNP 1} \| \text{SNP 2} \| \text{SNP 3} \| \text{SNP 4} \| . . . \| \text{SNP 50}   = (A,A) \| (C,T) \| (T,C) \| (C,C \| \ldots \| (G,A) \qquad (11)$$

Then α_X would be defined as follows.

$$\alpha X = \text{AACTTCCC} \ldots \text{GA} \qquad (12)$$

Next, the four types of nucleotide, A, G, C and T, are translated into binary notation.

$$A=00, G=01, C=10, T=11 \qquad (13)$$

Finally, the α_X is described as a string of 100 bits (digits of value 0 or 1).

$$\alpha X = 0000101111101010 \ldots 0100 \qquad (14)$$

This α_X must be encrypted for privacy protection using the secure hash algorithm-1 (SHA-1) for the same reasons as described above for STRs. The resulting DNA-ID (SNP) has a length δ_X of 160 bits, according to the following transformation:

$$\delta X = h (\alpha X) \qquad (15)$$

3.5. Verification using validation experiment (SNP)
As a validation experiment, the author analyzed 120 autosomal SNPs in 100 unrelated Japanese subjects using the TaqMan® method (Applied Biosystems), and built a Japanese SNP database for identification. Although several SNPs were located on the same autosomal chromosome, no correlation was found between alleles at any SNP loci. Furthermore, no significant deviation from Hardy−Weinberg Equilibrium (HWE) was detected. The macthing probability (MP) of each SNP ranged from 0.375−0.465 . The MP for 41 SNPs (3.63×10^{-18}), which have high MP in each loci, was very similar to the MPs obtained with the current STR multiplex kits, PowerPlex™ 16 System(Promega) and AmpFlSTR Identifiler (Applied Biosystems), which were 5.369×10^{-18} and 1.440×10^{-17}, respectively in Japanese population.

3.6. Rapid analysis system of SNP
A reduction of the time required for DNA analysis is necessary in order to make practical use of DNA biometrics. In the STR system, it is difficult to decrease the analysis time because it is necessary to perform electrophoresis after PCR amplification. From DNA extraction to STR typing, the entire process takes 4−5 hours. However, there are many methods for analyzing SNPs that do not demand such a lengthy process. The author developed the SNP typing methodology using the modified TaqMan® method, which is capable of amplifying the DNA and typing the SNPs at the same time. The author modified the number of PCR cycles and the annealing/extension time, and selected SNP loci that yield successful results under the modified PCR conditions. This new method is capable of detecting and typing 96 SNPs within 30 minutes .

III.   IV PROBLEMS OF DNA BIOMETRICS
There can be no doubt that DNA-ID is potentially useful as a biometric. It has many advantages, including accuracy, strictness, discriminatory power (and ease of increasing this power), and the ability to use the same analysis platform all over the world. However, DNA polymorphism information is not widely used in biometrics at this point. The most serious flaw is that DNA analysis is time-consuming compared to other authentication methods. It takes at least 4 hours to get STR identification data by common methods used in forensic science. Most of the time required for DNA analysis is taken up by PCR amplification and electrophoresis. It is impossible to dramatically shorten the duration of these steps using existing technologies. SNP analysis may be faster, however: it is possible to analyze 96 SNPs within 30 minutes (Hashiyada, Itakura et al., 2009). Thus, a SNP system could use a specific usage, for example in passports or in very large-scale mercantile transactions

IV.   CONCLUSION
Development of biometric authentication technologies has progressed rapidly in the last few years. Personal identification devices based on unique patterns of fingerprints, iris, or subcutaneous veins in the finger have all been commercialized. All of these methods of verification are based on matching analog patterns or feature-point comparisons. Because they lack absolute accuracy, they have not yet achieved a universal standard. Among the various types of biometric information source, the DNA-ID is thought to be the most reliable method for personal identification. DNA information is

intrinsically digital, and does not change either during a person' life or after his/her death. The discriminatory power of the data can be enhanced by increasing the number of STR or SNP loci. The DNA-ID could be encrypted via the one-way function (SHA-1) to protect privacy and to reduce data length. Using the STR system, it is currently difficult to complete analysis within 3 hours; however, using the SNP system, it is possible to analyse 96 SNPs within 30 minutes. Both systems yielded verifiable results in validation experiments. The author also introduced the idea of DNA-INK as a practical application of DNA-ID.

DNA-ID has some disadvantages, as well, including long analysis time, ethical concerns, high cost, and the impossibility of discrimination of monozygotic twins. However, the author believes that the DNA-ID must be employed as a biometric methodology, using breakthrough methods developed in the near future.

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