

The genetic analysis on ancient human bone in jar coffin
excavated from Naju Bokam-ni 3rd tumulus

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ABSTRACT

We have analyzed the allele and genotype frequencies from 10 fractions of ancient human skeleton in 3 pieces of Jar coffin excavated from Naju Bokam-ni 3rd tumulus by PCR amplification, high resolution polyacrylamide gel electrophoresis and silver staining. We could isolate human genomic DNA from 3 bone fractions but the rest of them could not be used as materials due to being decayed.

We could detect sex determination as male and 3 genotypes of STR system, HUMTHO1, HUMTPOX and HUMC5F1PO from the bone fraction of left side in Jar coffin 3 and see the slightly reaction suggesting the sex as male from the bone fraction of the left side in Jar coffin 2 and female from the right side in Jar coffin 3.

We have also analyzed the genotype frequencies of mitochondria from the bone fractions of the left side and the right side in jar coffin 3, respectively. From the result of indentifying at nucleotide position between 16018 and 16378 of the base of hypervariable region(HV1) in the control region, We can presume that the both bones have the same maternal inheritance.

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404

7 가 4

1995 3

3 1996 7 8 (96)

1996 11 1998 9 3

7가 41 3

96 3

1, 2, 3 3

1998 2 19 3

10

(DNA)

(DNA)

DNA

1985 A.J.Jeffrey

가 (human genome) myoglobine gene

(hypervariable region) (restriction enzyme) southern

hybridization

1985 K.B.Mullis DNA (Polymerase Chain

Reaction : PCR) DNA thermal cycle가

PCR

3

가

1.

(nuclear)

DNA

(chromosome)가

30

46

1980 R.A.White A.Whyman

DNA 가

DNA Fig. 1

(hypervariable region)

DNA

(DNA 1ng)

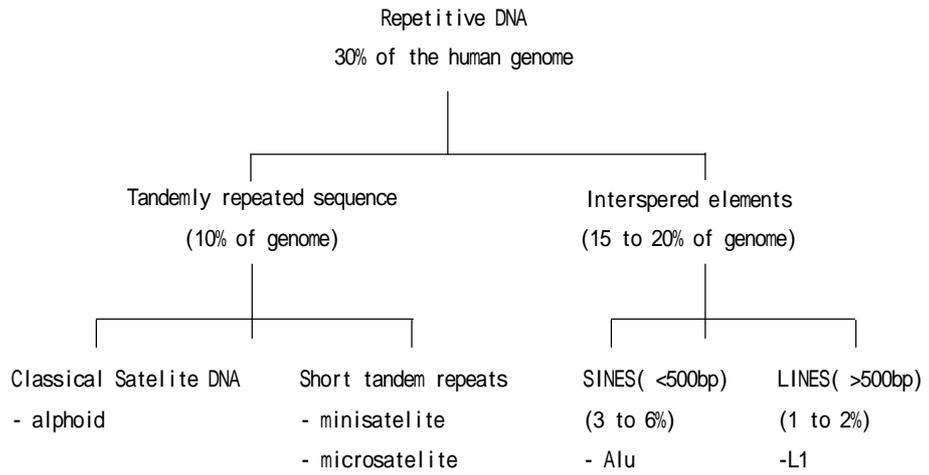
PCR

PCR

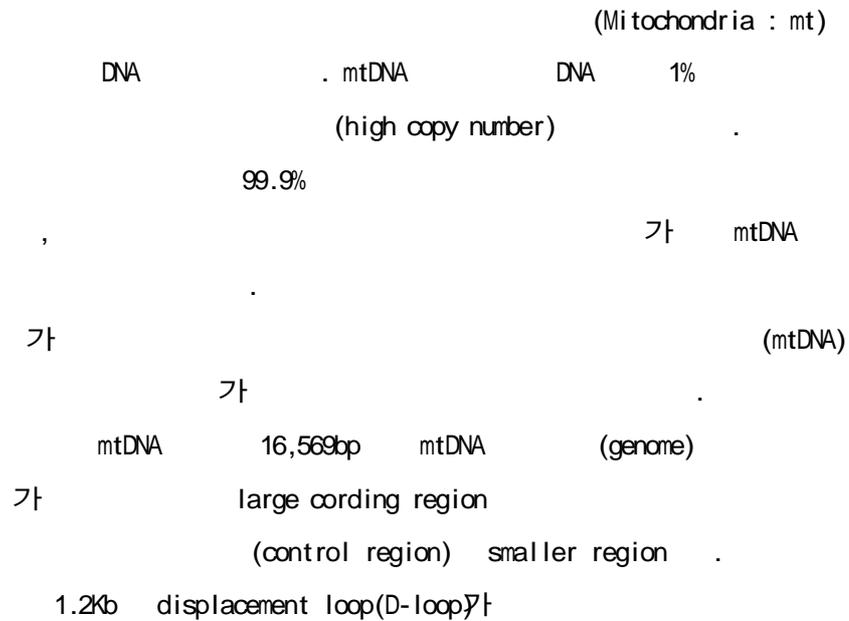
DNA

(Molecular weight)

Fig. 1.
Repetitive DNA in the human
genome



2.



(HV) HV1, HV2 . mtDNA (HV) 가
 HV1 HV2 가 400bp .
 (TWGDAM: Technical Working Group on DNA Analysis Method) HV1
 16024 16365 , HV2 00073 00340 mt
 DNA database .

3. 3
 3 1,2,3 1,500

. (Photo 1~3)

가
 1 2 4 , 3 2
 10 . (Table 1, Fig. 2)

Table 1.

1	3	1	(1)
2	3	1	(2)
3	3	1	(1)
4	3	1	(2)
5	3	2	(1)
6	3	2	(2)
7	3	2	(1)
8	3	2	(2)
9	3	3	(1)
10	3	3	(1)

1
Photo 1.
3



2
Photo 2.
3



3
Photo 3.
3



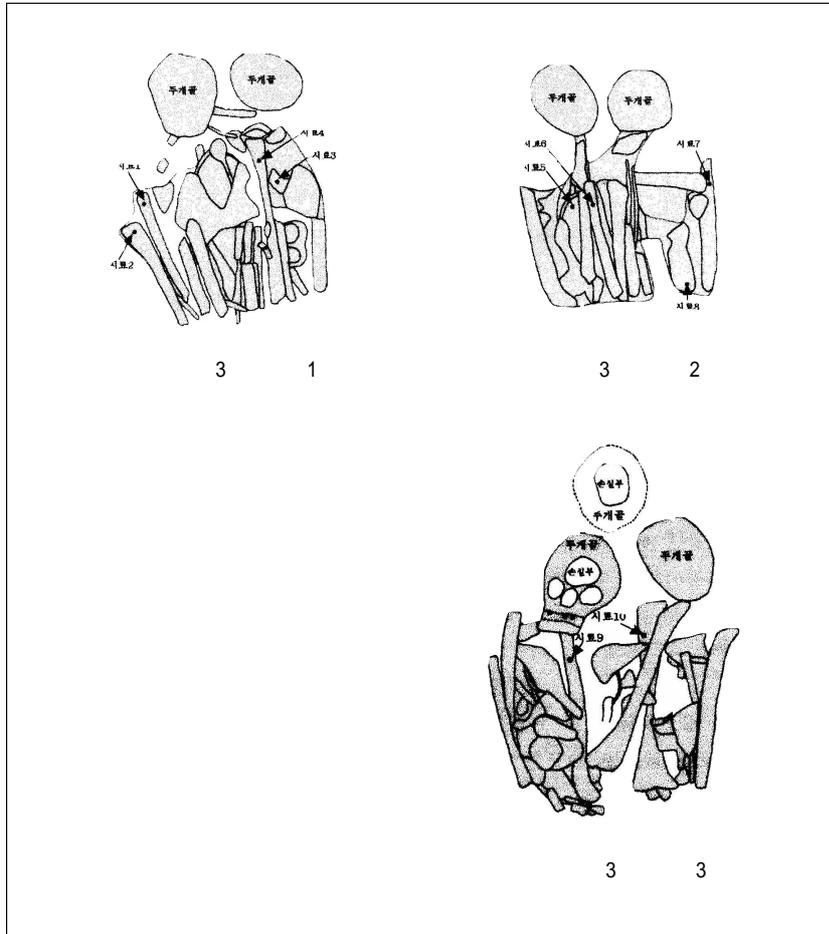


Fig. 2.

4.
1)

(6,9,10)
5,7,8)

가

10
3 (6,9,10)

3
7 (1

90 % , 0.5M EDTA 50Mℓ
 7
 EDTA .

2) DNA

가 1
 Mℓ TEN (10mM Tris-HCl, pH 8.0, 10mM EDTA, 150mM NaCl) 50μℓ
 proteinase K(10ng/Mℓ Promega) 100μℓ 10% SDS 가 56

phenol/chloroform/ isoamylalcohol(25:24:1)

chloroform
 Centricon100(Amicon, USA)

DNA . DNA 1% Agarose Gel

DNA .

3) TH01-Amelogenin-TPOX-CSF1PO

TH01-Amelogenin-TPOX-CSF1PO 4 Geneprint Human
 Identification Kit(Promega, USA)

. PCR , 가 DNA
 (PCR)

DNA thermal cycler(Perkin-Elmer 480) Table 2

4)

loading dye(10mM NaOH, 95%
 formamide, 0.05% bromophenol blue, 0.05% xylene cyanol FF) 2

Table 2. (PCR)

Initial denaturation	96 for 2 min
First cycling (10 cycles)	94 for 1 min
Denaturation	64 for 1 min
Primer annealing	70 for 1.5 min
Extension	
Second cycling (20 cycles)	90 for 1 min
Denaturation	64 for 1 min
Primer annealing	70 for 1.5 min
Extension	

95 denaturation 10 μ l 7M urea denaturing polyacrylamide gel (6% T, 5% C, 42cm long, 0.4mm thickness and 0.5X TBE)

30W 3.5

(silver staining), allelic ladder

5)

10 3

EDTA

microcon 100(Amicon, U.S.A.)

DNA

DNA 1%

가 (agarose gel)

EtBr

9(3)

6(2)

DNA가

10(

3)

DNA

(Photo 4)

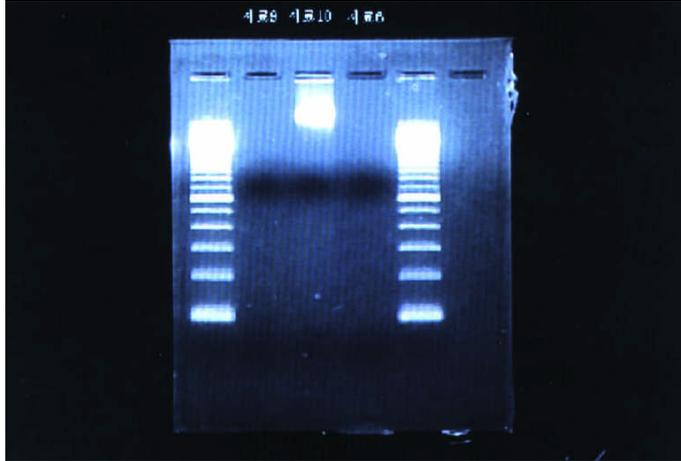


Photo 4.

1% 가

DNA

9 Amelogenin 212-218
 , TH01 7-9,
 TPOX 8-8, CSF1PO 10-12 . 6 Amelogenin
 212-218 , 10 Amelogenin 212-212
 . (Photo 5)

DNA

10(3)

DNA

STR(Short tandem repeats)

DNA

DNA

5.

1)

가

DNA

DNA

HV1(15971 16410)

F15917/R16410 primer

Dye Terminator Cycle

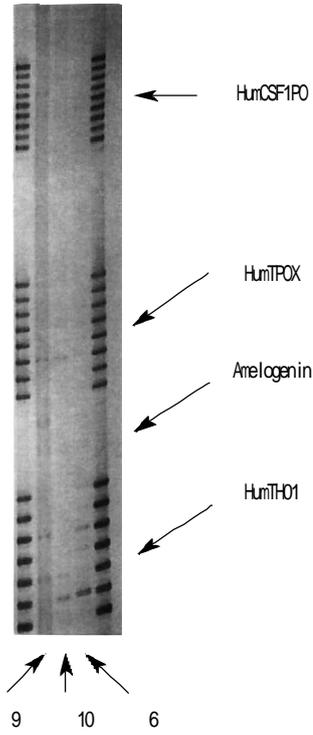


Photo 5.

Sequencing Kit	Perkin Elmer Prism 377 DNA Sequencer			
	Sequence Navigator			DNA
Forward	Reverse sequence	Anderson sequence		
2)				
mtDNA	3	3	(9)	(10)
base	,		HV1	16018 base
			mtDNA	16378
3	3			가

(Table 3)

Ref. sequence	16018	16030	16040	16050	16060
Anderson	T C T	CTGTTCTTTC	ATGGGGGAAGC	AGATTTGGGT	ACCACCCAAG
시료 9	-	-	-	-	-
시료 10	-	-	-	-	-
	16070	16080	16090	16100	16110
	T A T T G A C T C A	C C C A T C A A C A	A C C G C T A T G T	A T T T C G T A C A	T T A C T G C C A G
	-	-	-	-	-
	-	-	-	-	-
	16120	16130	16140	16150	16160
	C C A C C A T G A A	T A T T G T A C G G	T A C C A T A A A T	A C T T G A C C A C	C T G T A G T A C A
	-	-	-	-	-
	-	-	-	-	-
	16170	16180	16190	16200	16210
	T A A A A A C C C A	A T C C A C A T C A	A A A C C C C C T C	C C C A T G C T T A	C A A G C A A G T A
	-	-	-	-	-
	-	-	-	-	-
	16220	16230	16240	16250	16260
	C A G C A A T C A A	C C C T C A A C T A	T C A C A C A T C A	A C T G C A A C T C	C A A A G C C A C C
	-	-	-	-	-
	-	-	-	-	-
	16270	16280	16290	16300	16310
	C C T C A C C C A C	T A G G A T A C C A	A C A A A C C T A C	C C A C C C T T A A	C A G T A C A T A G
	-	-	-	-	-
	-	-	-	-	-
	16320	16330	16340	16350	16360
	T A C A T A A A G C	C A T T T A C C G T	A C A T A G C A C A	T T A C A G T C A A	A T C C C T T C T C
	-	-	-	-	-
	-	-	-	-	-
	16370	16380			
	G T C C C C A T G G	A T G A C C C C C C			
	-	-			
	-	-			

3
mtDNA HVI

3 3 , 3 가
TH01 , TPOX
, CSF1PO 3 3
, 2 Amelogenin 가
3 TH01 , TPOX , CSF1PO 3
3 , 3

HV1

3

가

3

1,500

3 STR

3

가

가

3

3

10

(DNA)

3

7

3

STR(Short tandem repeat)

TH01 , TPOX , CSF1PO

3

2

3

3

HV1

16018

16378 base

3

가

(男妹)

(母子)

가

(近親相姦)

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