
A Genetic Investigation of Two Korean Mummies from the Joseon Dynasty

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Korean mummies

- Mummification process
 - Structure of air-tight tombs
- Scientific investigation
 - Causes of death
 - Paleopathological statuses
 - Parasite loads
 - ⋮
- Genetic investigation
 - mtDNA hypervariable (HV) region sequences (in 2003)



Development of genetic investigation

- DNA extraction
 - Total Demineralization (*Forensic Sci Int Genet* 2007; 1:191-5)
 - Large scale silica column (*Croat Med J* 2007; 48:478-85)
- Small size amplicon strategy
 - Mini-primer set (*BioTechnique* 2008; 44:555-8)
- mtDNA haplogroup
 - East Asian mtDNA phylogeny (*Hum Mol Genet* 2006; 15:2076-86)
 - mtDNAmanager program (*BMC Bioinformatics* 2008; 9:483)



Danwoong-mirra



- Discovery of Yangju, Gyeonggi-do, in 2001
- A male child mummy : Ages of 4.5 to 6.6 years old
- Dating back to 550 years ago
- First mummy of scientific investigation, in Korea
- Muscles tissue



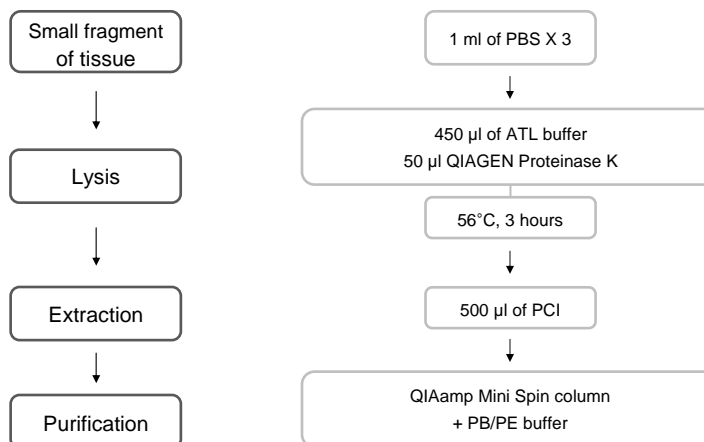
Yoon-mirra



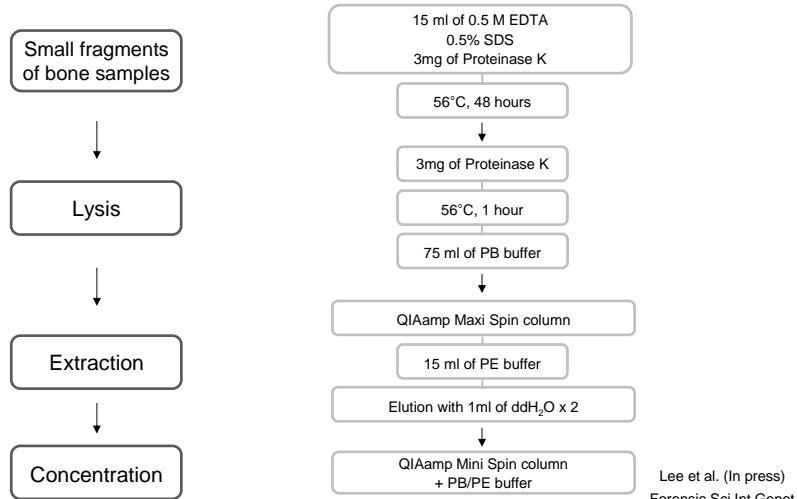
- Discovery of Paju, Gyeonggi-do, in 2002
- A pregnant female mummy : Ages of 20 to 30 years old
- Document of death date : December of 1566
- Rib bones and liver tissues



DNA extraction from mummified soft tissue



DNA extraction from bone sample

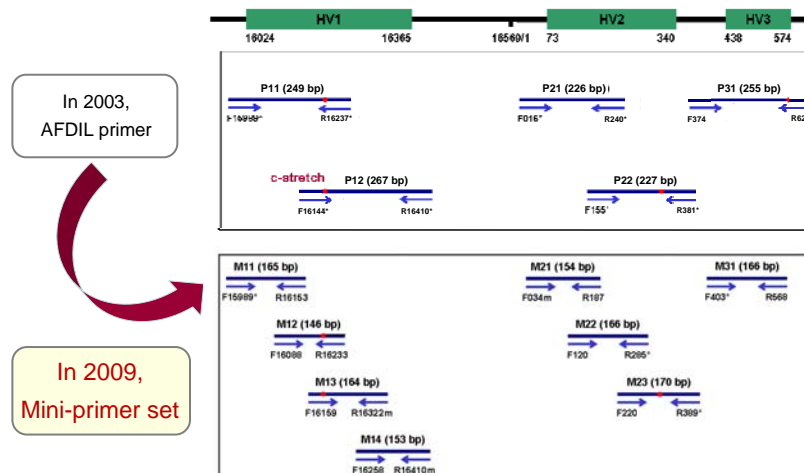


Lee et al. (In press)
Forensic Sci Int Genet



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Primer for amplification of mtDNA



Lee et al. (In press) J Forensic Sci



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PCR amplification of mtDNA HV regions

■ PCR Mixture

PCR component	volume
dH ₂ O	17.0 µl
Gold ST*R Buffer	2.5 µl
Forward Primer (10 pmol/µl)	1.5 µl
Reverse Primer (10 pmol/µl)	1.5 µl
AmpliTaq Gold (5 U/µl)	0.5 µl
DNA Template	2.0 µl
Total	25.0 µl

■ Thermal Cycling

95°C for 11 minutes , then:

95°C for 20 seconds
50°C for 20 seconds
72°C for 30 seconds
for 42 cycles, then:

72°C for 7 minutes
4°C soak



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Quality analysis using mtDNAManager

<http://mtmanager.yonsei.ac.kr/>

mtDNAManager: a Web-based tool for the management and quality analysis of mitochondrial DNA control region sequences

mtDNAManager provides a convenient web interface to analyze, query and store human mtDNA control region sequences ([BMC Bioinformatics](#) 2008,9(1):473). mtDNAManager is made free and open to all users and there is no login requirement. At the same time, mtDNAManager offers the option to store and match data with batch mode for registered users.

- [Access demo](#)

The aims of mtDNAManager are (1) to allow researchers to automatically estimate the most-probable mtDNA haplogroups of their mtDNA control region sequences, (2) to facilitate database screening with improved query tools and (3) to provide researchers with a convenient interface for managing and analysing their own data in batch mode.

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Primer for amplification of mtDNA coding region SNPs

Primer set	Haplogroup and SNP	Primer sequence (5' to 3')	Amplicon size	Concentration (μM)
PCR primer	D4-3010A	GGG ATA ACA GCG CAA TCC TA	99 bp	0.6
		ACC TTT AAT AGC GGC TGC AC		0.6
	M7-9824C	GGC ATC TAC GGC TCA ACA TT	101 bp	0.6
		ATT AGT TGG CGG ATG AAG CA		0.6
SBE primer	D4-3010A	TTT AAT AGC GGC TGC ACC AT	21 bp	0.1
	M7-9824C	GAA AGT TGA GCC AAT AAT GAC GTG	25 bp	0.1



PCR amplification of mtDNA coding region SNPs

Monoplex PCR of mtDNA Coding Region

PCR Mixture

PCR component	volume
dH ₂ O	17.0 μl
Gold ST [®] R 10X Buffer	2.5 μl
Forward Primer (10 pmol/ μl)	1.5 μl
Reverse Primer (10 pmol/ μl)	1.5 μl
AmpliTaq Gold (5 U/ μl)	0.5 μl
DNA Template	2.0 μl
Total	25.0 μl

Thermal Cycling

95°C for 11 minutes, then:
 95°C for 20 seconds
 50°C for 20 seconds
 72°C for 30 seconds
 for 42 cycles, then:
 72°C for 7 minutes
 4°C soak

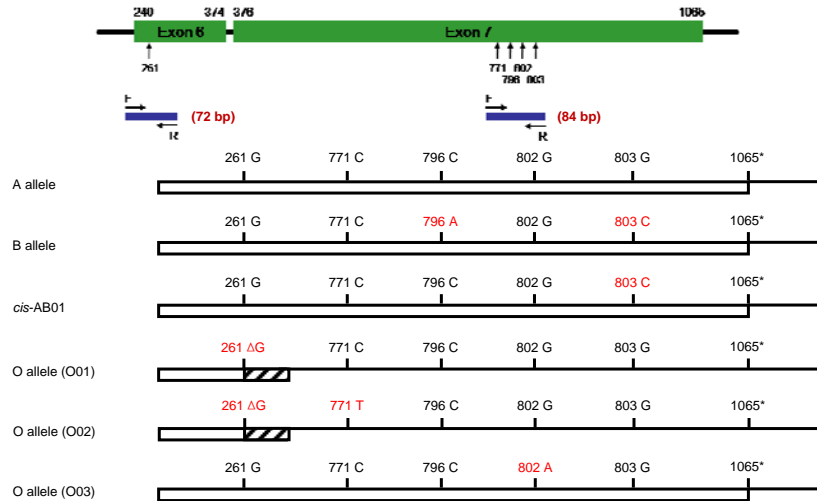
Purification of PCR Product using ExoSAP-IT

ABI PRISM[®] SNaPshot[®] Multiplex Kit

Purification of SNaPshot[®] Product using CIAP



Selection of SNPs for ABO blood group typing



Primer for amplification of ABO blood type

Primer set	Region	Primer sequence (5' to 3')	Amplicon size	Concentration (μM)
PCR primer	Exon 6	CTC CAT GTG CAG TAG GAA GGA	72 bp	0.4
		AAT GTG CCC TCC CAG ACA A		0.4
	Exon 7	CCA GTC CCA GGC CTA CAT C	84 bp	0.4
		TGC A \underline{Y} C TCT TGC ACC GAC		0.4
SBE primer	ABO261	AGG AAG GAT GTC CTC GTG GT	21 bp	0.23
	ABO771	(T) ₁₄ GTC CCA GGC CTA CAT CCC	33 bp	0.30
	ABO796	(T) ₁₆ GGA CGA GGG CGA TTT CTA CTA C	39 bp	0.27
	ABO802	(T) ₂₄ GGC GAT TTC TAC TAC \underline{A} TG GGG	46 bp	0.30
		(T) ₂₅ GGC GAT TTC TAC TAC \underline{C} TG GGG	47 bp	0.20
ABO803	(T) ₃₆ CAC CGA CCC CCC GAA GAA C	56 bp	0.35	



PCR amplification of ABO blood type

□ Monoplex PCR of ABO exon 6 and 7

■ PCR Mixture

PCR component	volume
dH ₂ O	18.0 µl
Gold ST [®] R 10X Buffer	2.5 µl
Forward Primer (10 pmol/µl)	1.0 µl
Reverse Primer (10 pmol/µl)	1.0 µl
AmpliTaq Gold (5 U/µL)	0.5 µl
DNA Template	2.0 µl
Total	25.0 µl

■ Thermal Cycling

95°C for 11 minutes, then:

94°C for 20 seconds

63°C for 1 minute

72°C for 30 seconds

for 45 cycles, then:

72°C for 7 minutes

4°C soak

□ Purification of PCR Product using ExoSAP-IT

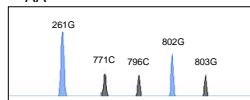
□ ABI PRISM[®] SNaPshot[®] Multiplex Kit

□ Purification of SNaPshot[®] Product using CIAP

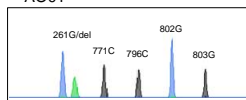


SBE electropherograms of ABO blood type

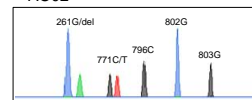
■ AA



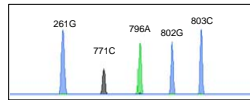
■ AO01



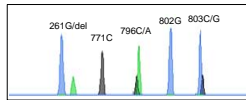
■ AO02



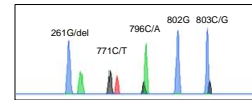
■ BB



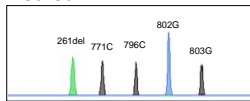
■ BO01



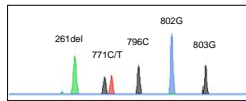
■ BO02



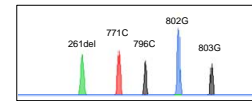
■ O01O01



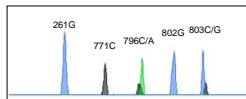
■ O01O02



■ O02O02



■ AB

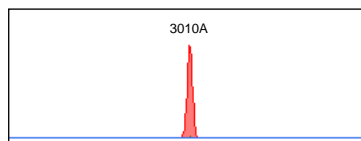


mtDNA HV region sequence and haplogroup specific SNP analysis

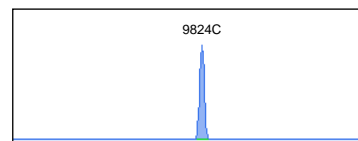
- Mummies mtDNA sequence analysis by mtDNAManager

Mummy	Haplogroup	mtDNA hypervariable region sequence
Danwoong-mirra	D4/G	16223T-16362C-73G-263G-309.1C-315.1C-489C
Yoon-mirra	M7c1	16223T-16294T-16295T-16391A-73G-146C-199C-263G-315.1C-489C-523d-524d

- Danwoong-mirra (D4)



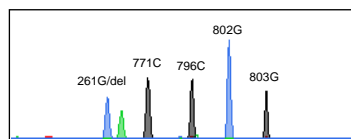
- Yoon-mirra (M7)



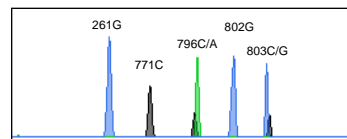
ABO blood type of Korean mummies

- Multiplex SBE reaction
- Monoplex SBE reaction
- Cloning analysis

- Danwoong-mirra (AO01)



- Yoon-mirra (AB)



Concluding remarks

- The authenticity of the results was confirmed by obtaining **reproducible results** from **repetitive analysis of multiple extracts**.
- The **mtDNA haplogroup determination** based on **HV region sequence polymorphisms** and **diagnostic coding region SNP** information can help confirm the absence of contamination and/or artificial recombination due to sample mix-up.
- mtDNA sequences and ABO blood types of ancient Korean mummies were successfully analyzed using a **small size amplicon strategy** and the **authentication process**, that would be used effectively in future genetic analyses of various forensic and ancient samples.

