

遺傳工學 技法                      韓牛   遺傳的 純粹性  
能力改良 體系確立

Genetic Identification and Improvement of Korean Cattle  
using DNA Technologies

1999

‘ \_\_\_\_\_

\_\_\_\_\_ ,

.

: 1. 10

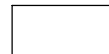
2. 1

2000 . . .

:

: ( )

:



良 體系確立 “遺傳工學 技法” 韓牛 遺傳的 純粹性 能力改

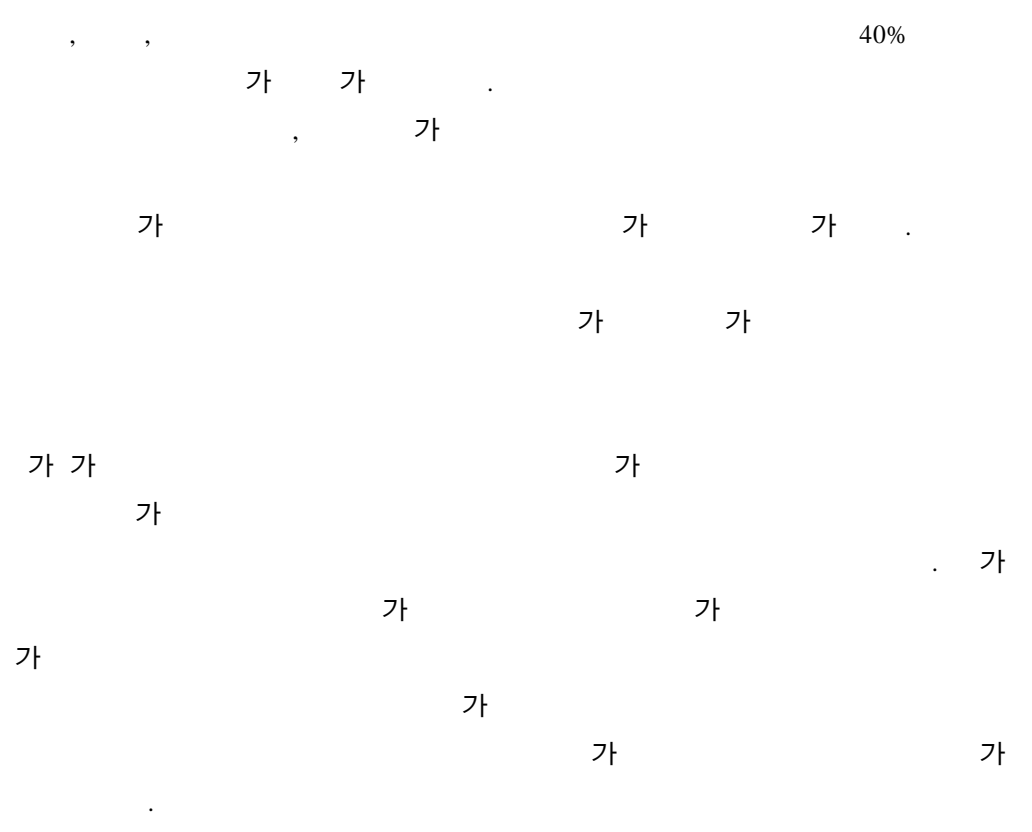
2000 . 11 . .

:  
:  
:  
:  
:

遺傳工學 技法  
體系確立

韓牛 遺傳的 純粹性

能力改良



, 가

DNA probe  
DNA marker

### 1. DNA

2001

가 , 가  
가 가 (從屬化)  
가

가 가  
가

가 , 가  
가 가  
가 1990  
(DNA)  
가 가

가 . DNA 가  
가 DNA  
(DNA Fingerprinting) ,  
(Genetic marker) program

가

가

2. DNA marker probe

가

가

가 , ,  
(AFLP, RAPD AP-PCR) 가 DNA marker DNA  
가 . DNA marker  
mechanism

DNA

가

가 가 가

DNA

가 .

, DNA

fingerprinting , DNA typing

DNA marker mapping , ,

. RFLP fingerprinting PCR

DNA typing DNA marker

cloning 가 mapping 가 .

Vos (1996) AFLP(Amplified Fragment Length

Polymorphism) RFLP PCR power 가

. DNA marker , cloning

AFLP DNA

adaptor ligation adaptor sequence bind

primer PCR .

primer 3 prime 1-3

primer

polymorphism .

DNA DNA marker

가 가 ,

가

specific DNA probe primer

### 3. DNA marker

, (神戸)

가 3 , 8

가 .

WTO

가

가

18	1974	10	1974	289.2kg	245.9kg	1998	504.9kg
315.3kg	가	가	가	가	가	가	가
	가		가		2001		

가

DNA

DNA

가 가 가 가

probe

model

DNA

DNA marker

DNA

가



가 DNA  
 marker DNA marker DNA  
 DNA probe  
 가 DNA  
 DNA ;

**DNA**

---

DNA probe DNA DNA  
 marker DNA  
 DNA (polymorphism) 가  
 가 가 .  
 enzyme) DNA (probe restriction  
 DNA marker ,  
 가 DNA marker  
 DNA  
 DNA

**DNA marker**

**probe**

---

DNA RAPD

AP-PCR DNA marker  
 DNA marker cloning sequencing marker DNA  
 AFLP  
 DNA marker marker DNA cloning  
 sequencing DNA 가 가 DNA  
 marker selection specific DNA  
 (probe primer) DNA

**DNA marker**

---

DNA  
 DNA marker

DNA marker

DNA marker (MAS, marker assisted selection)

1.

가.

421 Holstein, Aberdeen Angus, Charolais, Simmental, Brahman Kobe, 98  
 DNA probe M13 *Pst*  
 DNA marker(2.2kb), DNA probe [(AAC)n] DNA (BS=0.83)  
 가 가 가 Charolais,

가

가

DNA polymorphism

heterozygote

가

homozygote

가

(genetic homogeneity)

가

가

가

가

가

DNA

가

DNA marker

DNA marker 가 ,

DNA marker group 8.06

10.17mm 748 701g group

DNA marker group

94.4 40% 가

86.38 79.75cm . DNA marker

( , , , ,

) M13/Hae marker 11.3kb 9.4kb

가

, , 가 DNA marker

가 가

marker , , DNA

DNA primer

AFLP marker

DNA

281bp DNA marker primer(5'- ATGAGGAAC

CACAGTAGGAACC- 3', 5'- GACATGATGAGAAGAG- 3')가 high group

low group polymorphism agarose gel

marker 가

E9T2 primer AFLP  
 DNA marker sequencing 139bp DNA marker  
 primer(5'- AAGTGTGGCGGTGGA- 3', 5'- CGGACACT GT  
 GCTTC- 3') high group low group poly-  
 morphism agarose gel 가 marker  
 가 .

DNA marker MAS(Marker  
 assisted selection)

marker . 1999 DNA marker index  
 213 DNA 가  
 specific marker marker 11.3kb  
 DNA marker 9.4 3.6kb ,  
 11.3kb 9.4kb marker 가  
 ,  
 가  
 11.3kb 9.4kb  
 가 가 .

2.

가.

1. ( ) (1999. 4. ( ) )
2. (1999. 7. 20. )
3. , (2000, 7. 21. )
4. (2000. 8. 16. )
5. 가 (2000. 8. 21. 가 )
6. symposium (2000. 8. 31. )
7. (2000. 9. 1. )
8. (2000. 9. 15. )
9. symposium (2000. 9. 19. )

- 10. (2000. 11. 10. )
- 11. (2000. 11. 24. )
- 12. (2000. 12. 4. )
- 13. 1 (2000. 12. 7. )
- 14. (2000. 12. 14. )

1) 2

①. ; 10-2000-0017324  
; DNA

②. ; 10-2000-0065925  
;

2) Gene Bank

AF296448 ; 521bp marker  
AF296449 ; 402bp marker  
AF297628 ; 139bp marker

3)

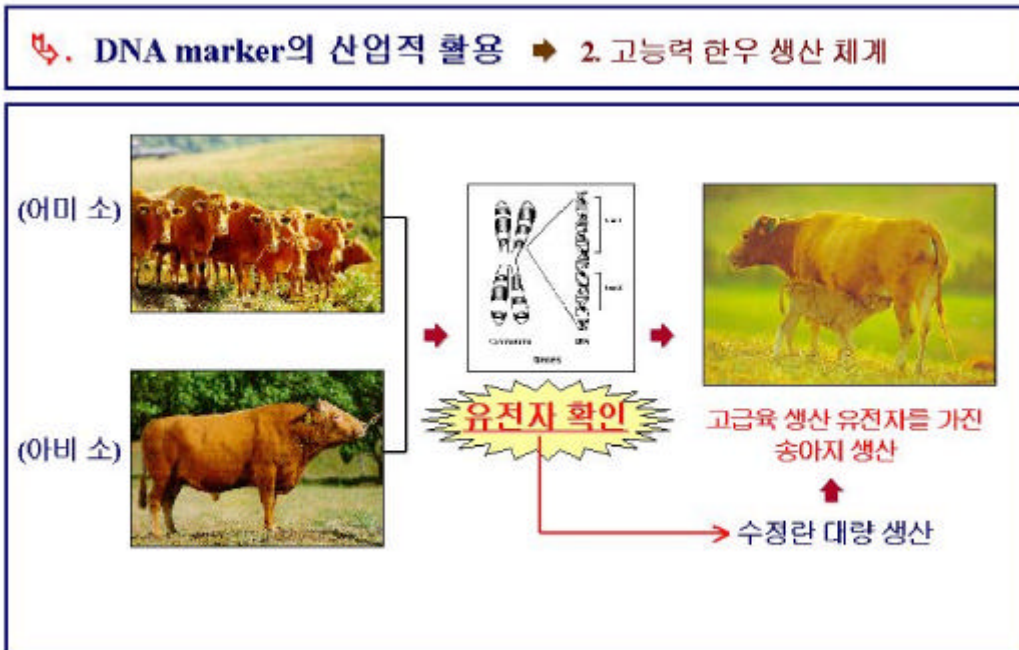
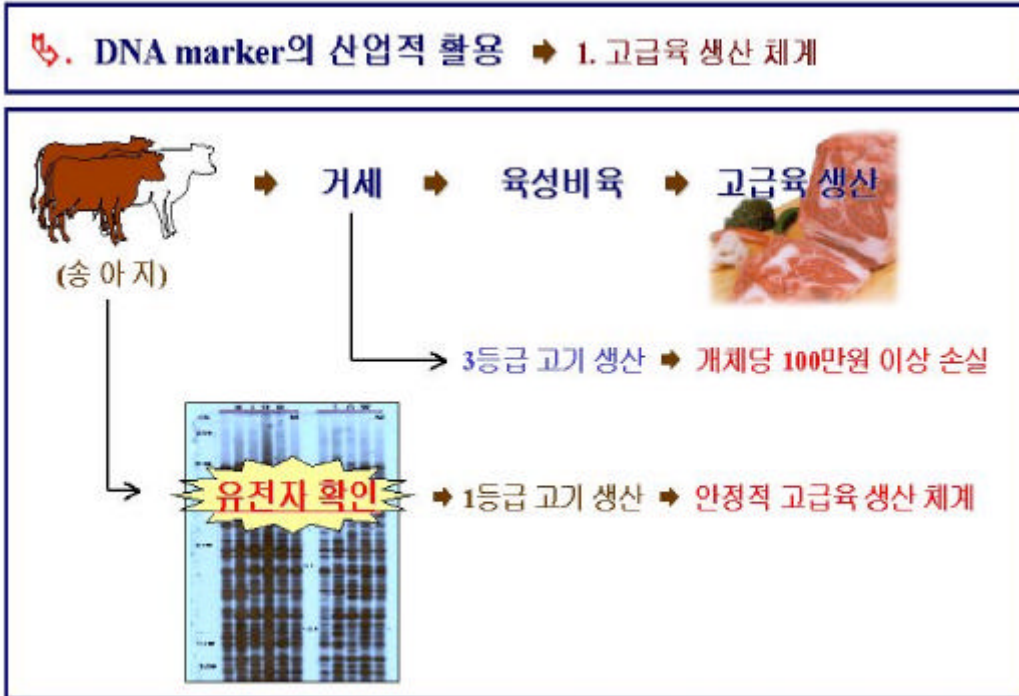
. ( ) ; 가

. ( ) ; 가

. ( , 가 ) ; 2001  
“DNA marker ” ( )

. ; 2001  
“

3)



## SUMMARY

In order to identify the genetic purity and provide new tools to genetic system of improvement in Hanwoo as a unique genetic source in Korea, this study tried several DNA techniques of DNA fingerprinting(DFP), amplified fragment length polymorphism(AFLP), random amplified polymorphic DNA(RAPD), and arbitrarily primed-polymerase chain reaction(AP-PCR). Identified DNA markers differentiated Hanwoo from other cattle breeds and related with economic traits of Hanwoo were used to apply the designed new DNA probe and primers as essential selection tools for Hanwoo improvement.

### 1. Genetic differentiation Hanwoo from other cattle breeds

Specific DNA marker at 2.2kb with DNA probe M13 and restriction enzyme *Pst* was identified as most desirable preservation and selection criteria of pure individuals through DNA fingerprinting from 413 heads of Hanwoo(KPN bull and registered cow) and 98 heads of foreign cattle(Holstein, Aberdeen Angus, Charolais, Simmental, Brahman, Japanese Black Wagyu, and Chinese Yanbian Yellow). DNA probe [(AAC)<sub>n</sub>] designed from DNA marker of RAPD was satisfied with selection of pure Hanwoo genetically, comparing among several foreign cattle breeds. And also accuracy of pedigree system as the most important criteria for improvement system could be increased by DNA results. Genetic similarity estimated with band sharing between cattle breeds was found the highest(BS=0.83) between Hanwoo and Japanese Wagyu. Wagyu was suggested as synthetic model with foreign beef cattle on the basis of Hanwoo.

### 2. Genetic analysis and pedigree system

Several parameters of band frequency, allelic frequency, band sharing, population mean of the resolvable alleles, and heterozygosity were estimated from genetic analysis of cattle breeds with DNA polymorphism. Heterozygosity of DNA constitutions shown the lowest genetic homogeneity within Hanwoo population were the highest, on the other hand allelic frequency, homozygosity and band

sharing was the lowest among used cattle breeds. These results were agreed wide genetic variation of DNA constitution in Hanwoo remained still much and so Hanwoo improvement system used until now was not the best model to select superior individual genetically. In other words, this means that Hanwoo will be able to be improved gradually by strong selection intensity with exact selection model. Pedigree system to identify inheritance of desirable genetic markers to progeny using DNA technique could be also useful to genetic research of Hanwoo.

### 3. DNA markers related with economic traits

A few DNA markers related with each economic trait of Hanwoo, daily gain, backfat thickness, marbling, and *M. longissimus dorsi* area were identified with several DNA techniques. When these DNA markers were considered all together and analyzed with statistical model, it was found that critical markers located at 11.3 and 9.4kbs with M13 and *Hae* were powerful relativeness to important economic traits in Hanwoo. Significantly low backfat thickness 8.06mm to 10.17mm and significant high daily gain 748g to 701g in different DNA marker groups were found. Especially the best carcass quality of marbling were identified 15.6 to 9.35 and *M. longissimus dorsi* area were differentiated 86.38cm to 79.75cm under different DNA marker groups. And also distribution of these DNA markers of KPN bulls, registrated cows, and individuals at local farms were offered.

Identified several DNA markers related important economic traits of daily gain, back fat thickness, and carcass traits were considered as a powerful tools to utilize to improvement system in National Testing System of Hanwoo. Especially it will be more profitable to adopt to Hanwoo improvement system neglecting dam's records. These results were epochal to improve marbling in Hanwoo because selection of marbling has limitation that could not check at live and should check at carcass. And prediction to genetic possibility adopted this DNA marker is absolute process whether each individual should be castrate or not, because if castrated bull got No.2 or 3 grade, economic loss of longer management, more feed, and delayed growth are serious to farmers.



#### 4. Designed DNA primer

Identified DNA markers related with daily gain and marbling from AFLP were cloned and sequenced. Designed primer (5'-ATGAGGAACCACAGTAGGAACC-3' and 5'-GACATGATGAGAAGAG-3') for screening daily gain, and primer(5'-AAGTGTGGCGGTGGA-3' and 5'-CGGACACTGTGCTTC-3') for higher grade marbling were shown significant possibility to identify high and low performances of Hanwoo. Designed specific DNA fragments within DNA constitution related to characteristics of Hanwoo are valuable tools to adopt uniquely to identify genetic purity and selection criteria for Hanwoo improvement.

#### 5. Hanwoo breeding system with DNA markers

Application DNA results to select individuals of genetic purity in Hanwoo population and overcome restricted breeding schemes through population genetics should be recommended to low money and high efficiency comparing to present breeding schemes in Hanwoo improvement system. In considering to generation interval, economy for progeny test of Hanwoo, and selection accuracy and simpleness, DNA markers assisted selection(MAS) using 11.3 and 9.4kb for important traits of daily gain, backfat thickness, marbling, and *M. longissimus dorsi* area is the most powerful tools to make selection index for Hanwoo improvement.

## CONTENTS

Chapter 1. Introduction .....	18
Chapter 2. Identification of genetic characteristics of Hanwoo by DNA fingerprinting .....	21
1. Introduction .....	21
2. Material and Methods .....	23
3. Results and Discussion .....	27
Chapter 3. Development of probe and primer using DNA markers .....	56
1. Introduction .....	56
2. Material and Methods .....	57
3. Results and Discussion .....	63
Chapter 4. Genetic improvement of Hanwoo by DNA markers .....	89
1. Introduction .....	89
2. Material and Methods .....	90
3. Results and Discussion .....	92
Chapter 5. References .....	117

1	.....	18	
1	.....	18	
2	.....	19	
2	DNA	..... 21	
1	.....	21	
2	.....	23	
3	.....	27	
3	DNA marker	probe primer	..... 56
1	.....	56	
2	.....	57	
3	.....	63	
4	DNA marker	..... 89	
1	.....	89	
2	.....	90	
3	.....	92	
5	.....	117	

1

1

2001

가

, , , 가

가

“ ” ,

가 가  
가

가

가

가

가

가

가

가

가

가

, 가

가  
가

가  
 가 DNA (polymorphism)  
 가 DNA  
 DNA marker  
 DNA  
 DNA probe primer DNA model

## 2

DNA DNA  
 가 가  
 가 ;

- 1.
2. DNA
3. DNA probe primer
- 4.
- 5.

### DNA

· DNA probe DNA  
 · DNA DNA marker  
 · DNA DNA  
 · DNA (polymorphism) 가  
 · DNA marker  
 · DNA marker 가  
 · DNA

**DNA marker**

- DNA RAPD AP-PCR DNA marker
- DNA marker cloning sequencing marker
- AFLP DNA marker
- DNA cloning sequencing DNA marker selection
- specific DNA (probe primer)
- DNA

**DNA marker**

- DNA marker
- DNA marker , ,
- DNA marker (MAS, marker assisted selection)

## 2 DNA

### 1

가 가 genomic DNA 가 ,  
DNA DNA , 歐美  
가 가  
가  
가 DNA  
가 ,  
가  
Genomic DNA 가 , DNA  
(Molecular biological method) 가  
program 가 Plotsky (1990), Hillel (1993), Haberfeld (1993)  
, Mannen Tsuji(1993), Mannen (1993) 和牛  
DNA probe 和牛 champion  
가 DNA  
가 program  
( Hillel ,1993; Haberfeld ,1993), (Buitcamp  
,1991; Mannen Tsuji, 1993; Kikkawa ,1995; ,1997; Inoue- Murayama  
,1997), 가 (Mannen Tsuji, 1993; Inoue- Murayama ,1997; Glowatzki  
,1995), (Haberfeld ,1993; Mannen ,1993)  
DNA marker (Beever ,1990),  
DNA (MAS)(Meuwissen Van Arendonik,1992; ,1999),  
(Moody ,1995), calpastatin  
(Cockett , 1995), (Ruane Colleau,1996)

가 . gene  
mapping , (Hirano ,1998) Aberdeen Angus (Taylor  
,1998) .

가  
20  
2001  
가 가

DNA

가

repeat가 DNA core  
tandem repeat(VNTR) core repeat variable number of  
(DNA fingerprinting)

DNA



## 2

### 1.

가.

1)

가 ( )  
109 , ( ) ( )  
126 68 , 가 20  
Holstein 10 , Aberdeen Angus 10 , Charolais 10 , Simmental 10 ,  
Brahman 10 , Kobe 23 25  
.

2)

, ,  
DNA marker  
173 , 114 , ,  
DNA marker 147  
, 142 ,  
가 33가 99 marker  
.

Table 2- 1. The number of individuals and cattle breeds used for DNA fingerprinting

Application	Cattle	NLCF - HIC <sup>1)</sup> (KPN <sup>3)</sup> )	KAIA <sup>2)</sup> (Registered Hanwoo)		Foreign cattle	Local farm	Total
			Steer	Cow			
Genetic purity test		109	126	68	98	20	421
Daily gain and backfat thickness		173	114	-	-	-	287
Marbling score and <i>M. longissimus dorsi</i> area		147	142	-	-	-	289
Parentage test		33 family (Full- sib, 99 individuals)			-	-	99

1) NLCF-HIC ; National Livestock Co-operatives Federation, Hanwoo Improvement Center

2) KAIA ; Korean Animal Improvement Association

3) KPN ; Korean Proven Bull

(daily gain), (backfat thickness), (marbling score), (*M. Longissimus dorsi* area)

DNA probe

DNA probe Kobe PCR M13, YNZ22, Mo- , (GT)n, - globin, (AAC)n 7 (EcoRI, BamHI, HindIII, Hae , Hinf , Msp Pst ) Table 2- 2 .

Table 2- 2. Sequences of mini- and microsatellite probes employed in the experiments

	Sequence	Source
Probe	M 13 5' - GAGGGTGGCGGX <sup>1)</sup> TCT - 3'	(Vassart et al., 1987)
	YNZ22 5' - CTCTGGGTGTCGTGC - 3'	(Nakamura et al., 1987)
	Mo- 1 5' - TGCCCAAGTCCTCCC - 3'	(Mitani et al., 1990)
	- globin 5' - GAGCGACACGGGGG - 3'	(Higgs et al., 1986)
	(aac)n 5' - (AAC)n-3'	(Yeo et al, 2000)
	(GT)n 5' ...GTGTGTGT...3'	

1) X=C or T

2.

가.

DNA marker , 가

DNA marker

1) DNA

0.5M EDTA 가 0.2%  
 NaCl 0.16M NaCl/1mM EDTA 0.5% N-lauroyl sarcosine  
 proteinase K(10 mg/M $\emptyset$ ) DNA  
 DNA phenol phenol : chloroform : isoamylalcohol (25:24:1)  
 UV- 1201 spectrophotometer(SHIMADZU, JAPAN)  
 A $_{260}$ /A $_{280}$  1.5 1.8 가 DNA  
 TE (10mM Tris-HCl pH 8.0, 1mM EDTA) 4 .

2) DNA , Southern blotting

50  $\mu$ g DNA *EcoRI*, *BamHI*, *Hind* , *Hae* , *Hinf* , *Msp*  
*Pst* 1.0% agarose gel 2.4 volts/cm , 40  
 nitrocellulose membrane transfer . Transfer가 membrane 8  
 0 dry oven 30 baking .

3) Probe labeling hybridization

Probe M13, YNZ22, Mo- -globin BcaBest labeling kit (Takara Co.,  
 Japan) ,  $\alpha$ P- -dCTP 1  $\times$  10<sup>9</sup> cpm/ $\mu$ g DNA probe  
 hybridization solution (0.25% skim milk, 40% formamide, 6  $\times$   
 SSC, 5mM EDTA) 37 30 pre-hybridization , 24  
 hybridization , hybridization membrane 2  $\times$ SSC (0.3M NaCl,  
 30mM trisodium citrate, pH 7.0)/0.1% SDS 10 2 - 80  
 4 5 auto- radiography .

DNA marker

± 1.5 SD

10 DNA 4 DNA probe(M13, YNZ22, MO-I  
 - globin) 4 (Hae, Hinf, Msp Pst) high  
 low group DNA marker 1 screen DNA sample  
 band

10

specific

marker probe DNA 289  
 DNA marker , 7† ,  
 DNA marker

1)

- $BS(\text{band sharing}) = 2(Nab)/(Na+Nb)$   
 ; Nab : a b band , Na, Nb : a b band
- Genetic distance(D) = 1- BS

2)

- Band frequency (Falconer, 1960)

$$V_i = \frac{(P_i)^2 + f P_i(1-P_i)}{\text{homozygotes}} + \frac{2P_i(1-P_i) - 2f P_i(1-P_i)}{\text{heterozygotes}}$$

;  $V_i$  = band frequency,  $f$  = ,  $P_i$  = allelic frequency,

- Allelic frequency( )  
 $P = 1 - (1 - V)(5)$
- Mean probability( DNA random )  
 $X = [(Nab/Na) + (Nab/Nb)] / 2$
- Mean population frequency of the resolvable alleles  
 $q = 1 - (1 - X)(5)$

- Mean heterozygosity for the resolvable bands

$$h_e = 2q(1-q)/(2q-q^2)$$

- Mean homozygosity for the resolvable bands

$$h_o = 1-h_e$$

- 가 DNA 가

$$p_f = (1-2X+2X^2)$$

- 가 DNA 가

$$p_s = (2q-q^2)^{1/x}$$

### 3

#### 1.

#### DNA

probe M13 DNA probe *Pst* I

specific DNA marker 6 (8.6, 7.4, 7.1, 5.3, 2.4 2.2kb)

Figure 2-1 DNA marker 가 가

homozygote marker(7.1, 2.4, 2.2kb)가 3 ,

heterozygote marker(8.6, 7.4, 5.3kb) 3 .

6 DNA band

band 7.4, 7.1 5.3kb band

2.4 2.2kb

가 . 8.6,

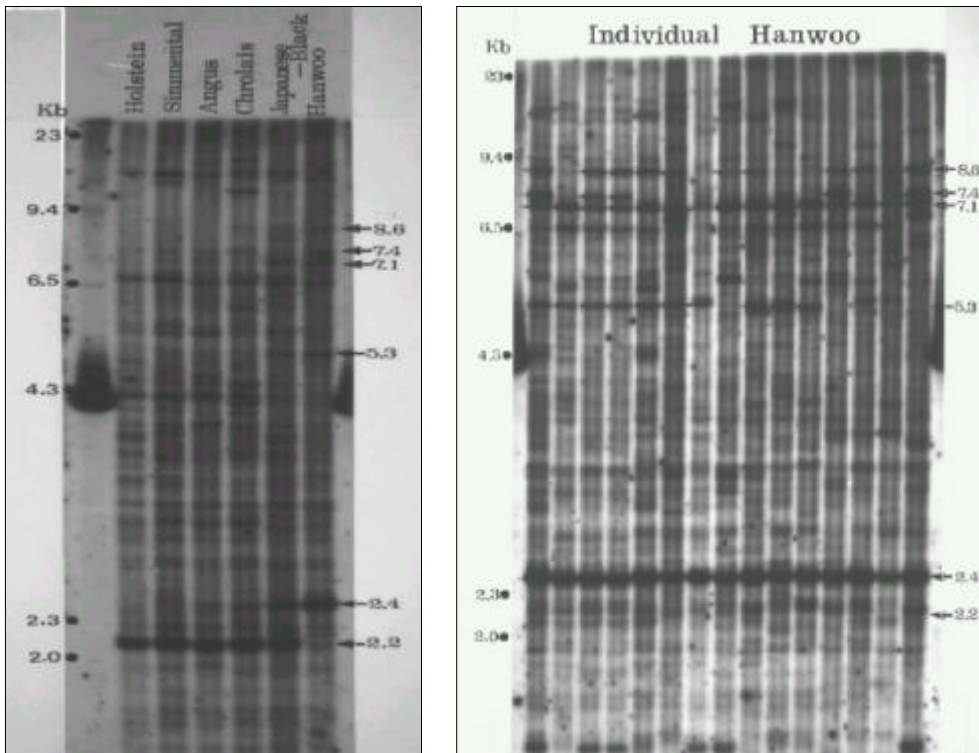


Figure 2-1. Specific DNA markers of Korean cattle compared with foreign cattle breeds from mixed samples (left) and individuals of Hanwoo (Korean Cattle) (right) using DNA fingerprinting with M13/*Pst*I.

	DNA	DNA	band
sharing	Table 2-3		
0.83		가	가
Charolais 0.73		,	
		가	.
Holstein	가	.	

Figure 2-2

Table 2-3

가 가

Table 2-3. Band sharings of between cattle breeds using mixed samples with M13/*PsfI*.

	Hanwoo	Japanese black	Charolais	Angus	Simmental	Holstein
Hanwoo	1.00					
Japanese black	0.83	1.00				
Charolais	0.73	0.79	1.00			
Angus	0.69	0.78	0.68	1.00		
Simmental	0.67	0.72	0.69	0.75	1.00	
Holstein	0.43	0.47	0.45	0.52	0.59	1.00

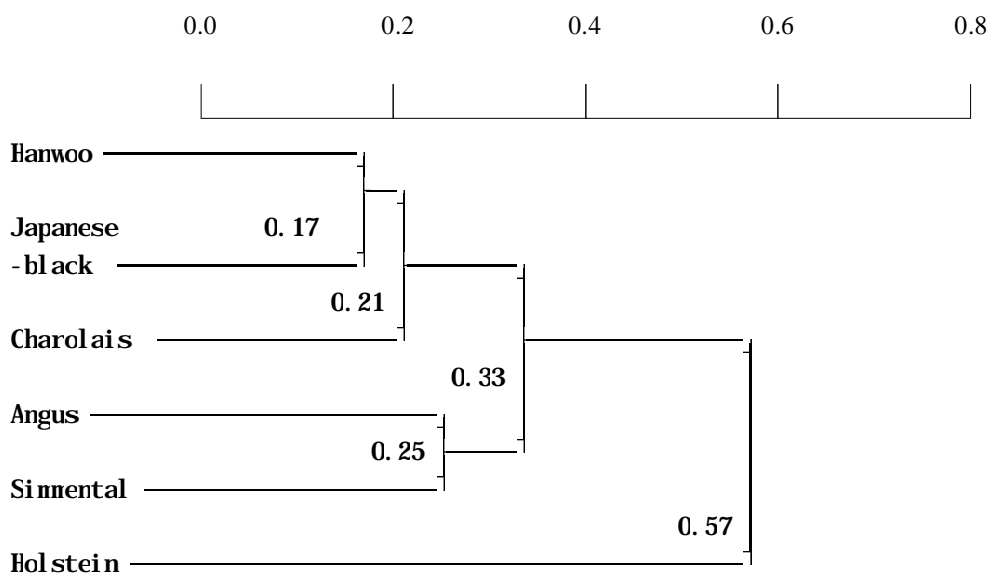


Figure 2-2. Dendrogram of genetic distance between six cattle breeds

Figure 2-3

DNA marker  
 DNA marker 2.2kb가

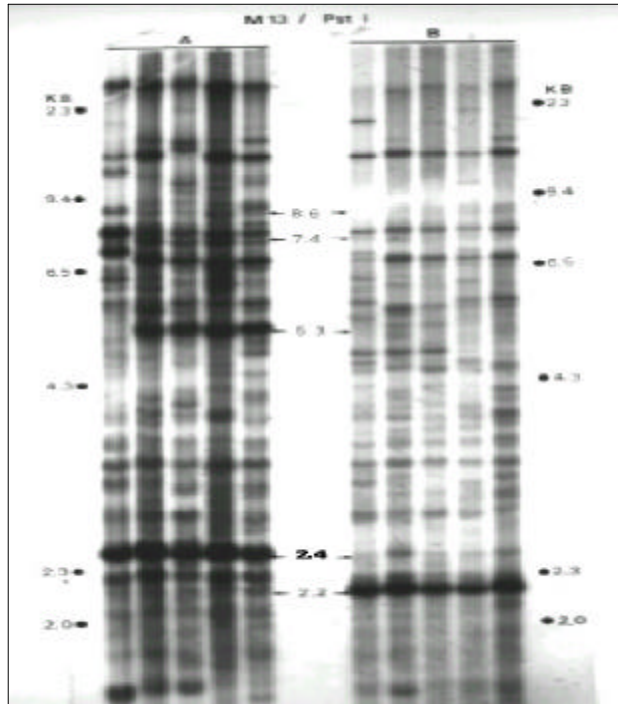


Figure 2-3. DNA fingerprinting of normal(A) and suspected(B) Hanwoo(Korean Cattle) by DNA fingerprinting with M13/*Pst* I.(Arrows : specific markers)

가 (Gawakisa , 1994 ; Jayarao , 1992 ; Buitkamp , 1991 ; Barre-Dirie , 1996 ; Haberfeld , 1993 ; Hillel , 1993 ; Mannen Tsuji, 1993 ; Glowatzki-Mullis , 1995) 가

DNA marker , , 가 Table 2-4 , 2.4kb DNA marker



가 2.2kb marker 가  
 가 105 29 가(38.2%)  
 2.2kb DNA marker 가 , 74  
 27(36.5%) 2.2kb DNA marker 가  
 가 DNA marker 가 가  
 가

Table 2-4. Distribution of specific DNA markers in Hanwoo(Korean Cattle) populations

Specific marker Hanwoo group	M13/ <i>Pst</i> I		Total No. of head
	2.4 Kb	2.2 Kb	
Korean proven bull (%)	84 (100%)	0 (0%)	84
Registered cow (%)	47 (63.5%)	27 (36.5%)	74
Progeny test bull (%)	126 (100%)	0 (0%)	126
Local Hanwoo farm bull (%)	76 (100%)	29 (38.2%)	105

2.

DNA 가 polymorphism  
 probe combination *Hae* M13 YNZ22 probe  
 4  
 probe DNA  
 , M13

Figure 2-4

Figure 2-4. DNA fingerprintings of 5 breeds cattle using two minisatellite probes M13(A) and YNZ22(B) with *Hae*

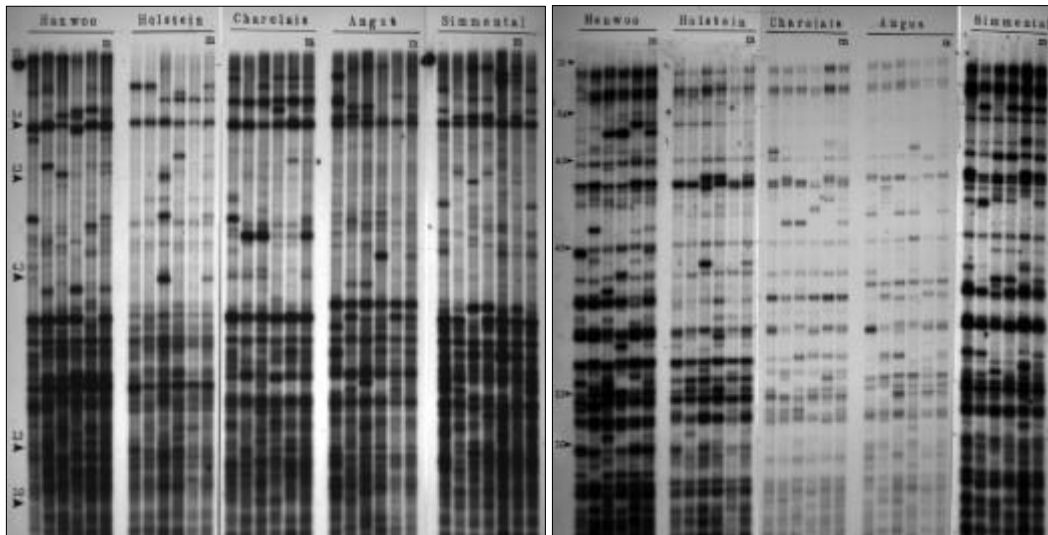


	Table 2-5		Table 2-6	
DNA band			DNA band	homozygote
intensive(dark) band			24- 25	.
가			Falconer(1960)	band
frequency	allelic frequency	.	dark band	
	DNA pattern		light band	
	band pattern,	heterozygote	(Mannen,1993; Kuhnlein,	
	1990).			
Table 2- 5	M13/ <i>Hae</i>	YNZ22/ <i>Hae</i>		intensive band
M13	0.528,	YNZ22	0.581	가
homozygote	가			Holstein
(0.617)	Charolais(0.708)가 가	.		0
	allelic frequency	intensive band		
가 M13	0.364	YNZ22	0.456	가
	0.586	0.668	가	,
	probe	가		band sharing
				.
				, DNA band
homozygote		genetic value		

가

Table 2-5. Average band frequencies, allelic frequencies and band sharing in 5 breeds of cattles without inbreeding coefficient using M13 and YNZ22 with *Hae*

Probe / Restriction enzyme	Genetic group	No. of different band scored	Average No. bands scored per cattles	Band frequency	Allelic frequency	Band sharing
M13 / <i>Hae</i>	Hanwoo	25	13.2 ± 0.66	0.528 ± 0.056	0.364 ± 0.053	0.586 ± 0.038
	Holstein	24	14.8 ± 0.97	0.617 ± 0.067	0.495 ± 0.075	0.727 ± 0.033
	Charolais	25	14.0 ± 0.95	0.560 ± 0.059	0.419 ± 0.065	0.652 ± 0.031
	Angus	24	13.8 ± 0.73	0.575 ± 0.062	0.445 ± 0.071	0.634 ± 0.033
	Simmental	25	13.4 ± 0.68	0.536 ± 0.055	0.387 ± 0.060	0.575 ± 0.030
YNZ22 / <i>Hae</i>	Hanwoo	32	18.6 ± 0.81	0.581 ± 0.057	0.456 ± 0.063	0.668 ± 0.016
	Holstein	23	19.2 ± 0.97	0.662 ± 0.064	0.576 ± 0.075	0.797 ± 0.013
	Charolais	26	18.4 ± 0.68	0.708 ± 0.059	0.608 ± 0.075	0.760 ± 0.013
	Angus	27	16.0 ± 0.63	0.593 ± 0.059	0.462 ± 0.067	0.679 ± 0.022
	Simmental	33	23.2 ± 0.86	0.703 ± 0.056	0.608 ± 0.067	0.760 ± 0.021

Table 2-6      Figure 2-4      가      band  
 가      band  
 (Jeffreys , 1985; Georges , 1988; Mannen Tsuji, 1993) .  
     band가      mean probability(X)      M13  
     0.536      YNZ22      0.656      가 가      , band가  
          mean population frequency(q)      가 0.319(M13)  
 0.413(YNZ22)      가 .  
     heterozygote      M13      0.810,  
 YNZ22      0.740      가      homozygote  
          DNA  
 가

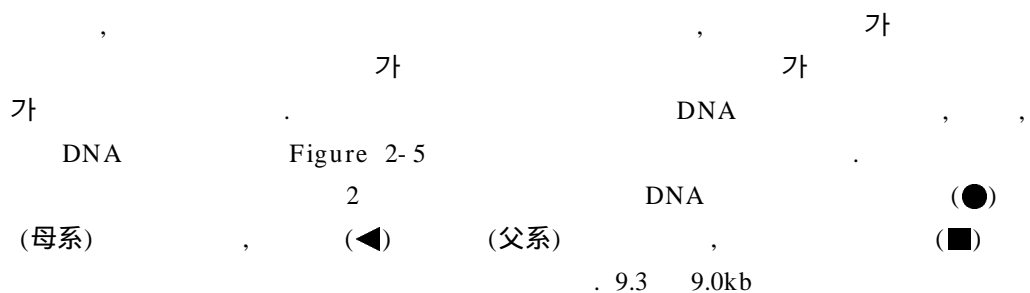
가 , DNA M13 1.1 × 10-6  
 YNZ22 1.5 × 10-8 , 2 가 DNA  
 (pf) 1.2 × 10-11 1.1 × 10-11  
 homozygote , 가

Table 2-6. Genetic characterization of 5 breeds of cattle using DNA fingerprints with M13 and YNZ22 probes with *Hae*

probe/restriction enzyme		Hanwoo	Holstein	Charolais	Angus	Simmental
M13 / <i>Hae</i>	f	23.2 ± 1.11	29.0 ± 1.90	27.0 ± 1.58	29.0 ± 1.48	27.4 ± 1.29
	x	0.536	0.670	0.601	0.725	0.556
	q	0.319	0.426	0.368	0.476	0.334
	he	0.810	0.729	0.775	0.688	0.800
	ho	0.190	0.270	0.225	0.312	0.200
	ps	1.1 × 10-6	3.7 × 10-6	8.7 × 10-7	2.8 × 10-5	1.7 × 10-7
	pf	1.2 × 10-13	1.1 × 10-11	1.8 × 10-13	1.0 × 10-9	2.7 × 10-15
YNZ22 / <i>Hae</i>	f	40.2 ± 1.01	41.8 ± 1.24	38.4 ± 1.33	37.2 ± 1.28	44.8 ± 1.69
	x	0.656	0.740	0.778	0.689	0.782
	q	0.413	0.490	0.529	0.442	0.533
	he	0.740	0.675	0.640	0.716	0.637
	ho	0.260	0.325	0.360	0.284	0.363
	ps	1.5 × 10-8	6.0 × 10-7	1.3 × 10-5	2.6 × 10-7	2.5 × 10-6
	pf	1.1 × 10-16	1.2 × 10-12	9.2 × 10-10	7.5 × 10-14	4.2 × 10-11

### 3. DNA marker 가

가.



band가 O1 , 3.5kb  
 가 band가 O1 O2 band  
 . 7.1 5.3kb band가  
 2 band , 7.1  
 2.4kb band band

DNA band

(Bruford Burke, 1990;  
 Ikeda ,1992; Mannen Tsuji,1993; Glowatzki- Mullis ,1995).  
 21가 2

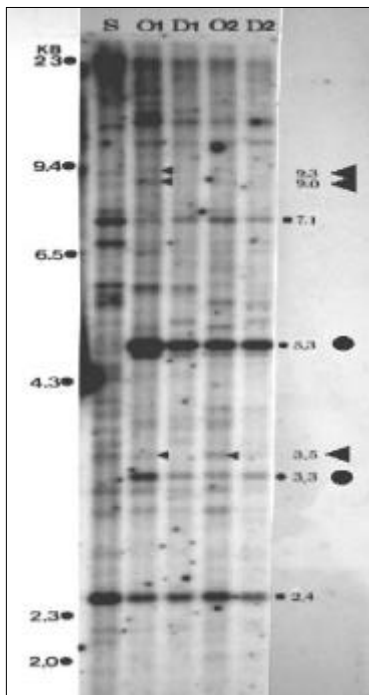


Figure 2- 5. DNA fingerprintings of sire(S), dam(D), and offsprings(O) in Hanwoo(Korean cattle)

. 가

Figure 2- 5 (full- sib) 10가 dark  
 band , band 가  
 , 480 band ,  
 Table 2- 7 2- 8 .

Table 2-7 DNA band

62 480 band 12.9% , band 182  
 (37.9%), band 236 (49.2%)  
 가

Table 2-8 specific marker(8.6,  
 가  
 7.4, 7.1, 5.3, 2.4 2.2kb)  
 band 3 35 band 8.6% ,  
 band 11 (31.4%), band 21  
 (60.0%) specific marker  
 band

Table 2-7. Pedigree analysis of DNA bands in full-sibs of Hanwoo(Korean Cattle)

	S	D	S+D	TOTAL
No. of bands	62	182	236	480 bands
Frequency	12.9%	37.9%	49.2%	100%

\* S: sire, D: dam

Table 2-8. Pedigree analysis of specific DNA bands in full-sibs of Hanwoo (Korean cattle)

	S	D	S+D	TOTAL
No. of bands	3	11	21	35 bands (6 offspring)
Frequency	8.6%	31.4%	60.0%	100%

\* S: sire, D: dam

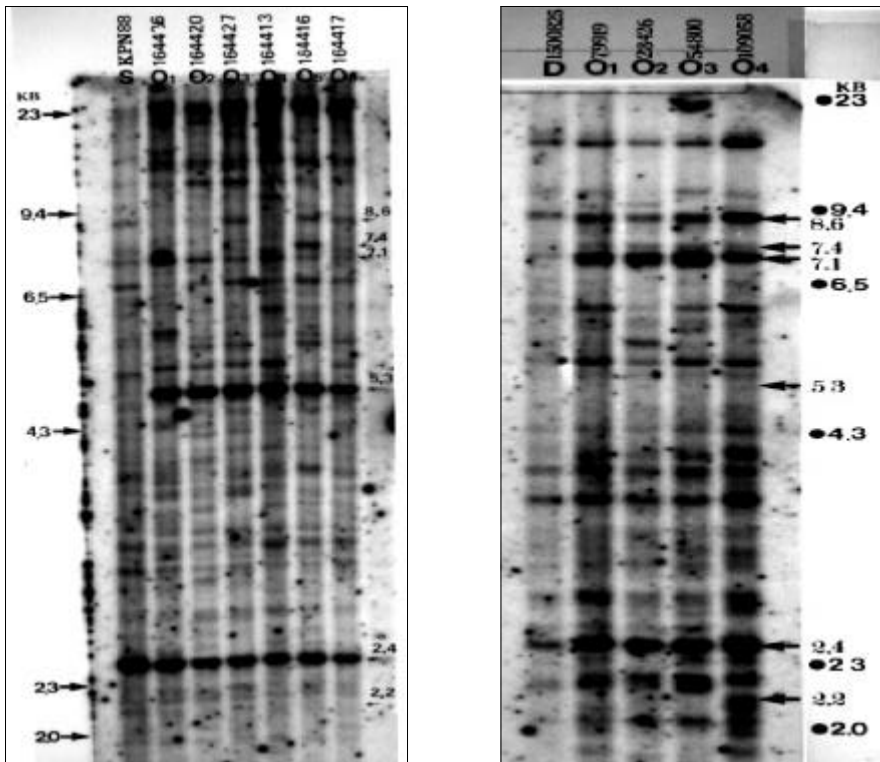


Figure 2-6. DNA fingerprintings of paternal(left) and maternal(right) half-sibs in Hanwoo(Korean Cattle)

Figure 2-6 6 paternal half-sib 4  
 maternal half-sib DNA specific band  
 子孫 . 7.1 2.4kb  
 paternal half-sib band가 , maternal  
 half-sib (母) band가 homozygote  
 band band  
 . 2.2kb band  
 band . 5.3kb 가 (paternal half-sib)  
 band가 , 가 (maternal half-sib)  
 가 band 가 band가 ,  
 5.3kb band .

4. ( ) DNA marker

가

가

DNA

가

가

가

DNA marker

가	가	가	287
Table 2-9	704.5		588.3kg
781g	0.90cm		(high)
10	(X+1.5SD)	0.949kg	(low) 10 (X- 1.5SD)
0.732kg			10 (X+1.5SD) 1.61cm
10	(X- 1.5SD)	0.18cm	

Table 2-9. Individual performance of daily gain and backfat thickness at high and low groups of normal distribution in Hanwoo(Korean Cattle)

Group	Traits	Growth			Backfat thickness		
		Market day	Market weight(kg)	Daily gain(g)	Market day	Thickness (cm)	
High (Steer)	No. of head	10	10	10	10	10	
	Mean	718 ± 21	676 ± 22	949 ± 43	723 ± 22	1.61 ± 0.35	
Low (Steer)	No. of head	10	10	10	10	10	
	Mean	716 ± 11	524 ± 19	732 ± 19	694 ± 14	0.18 ± 0.04	
Total	No. of head			173			
		Bull					
		Steer			114		
	Mean ± SD	Bull	704 ± 23	593 ± 42	809 ± 71	704 ± 23	0.68 ± 0.38
		Steer	720 ± 32	563 ± 52	748 ± 77	720 ± 32	1.10 ± 0.47



10 mixed DNA 4 probe 4  
 enzyme probe enzyme  
 DNA marker가 1 screen Figure 2-7  
 Figure 2-8 DNA .  
 lane mixed sample(MH ML)  
 group marker .

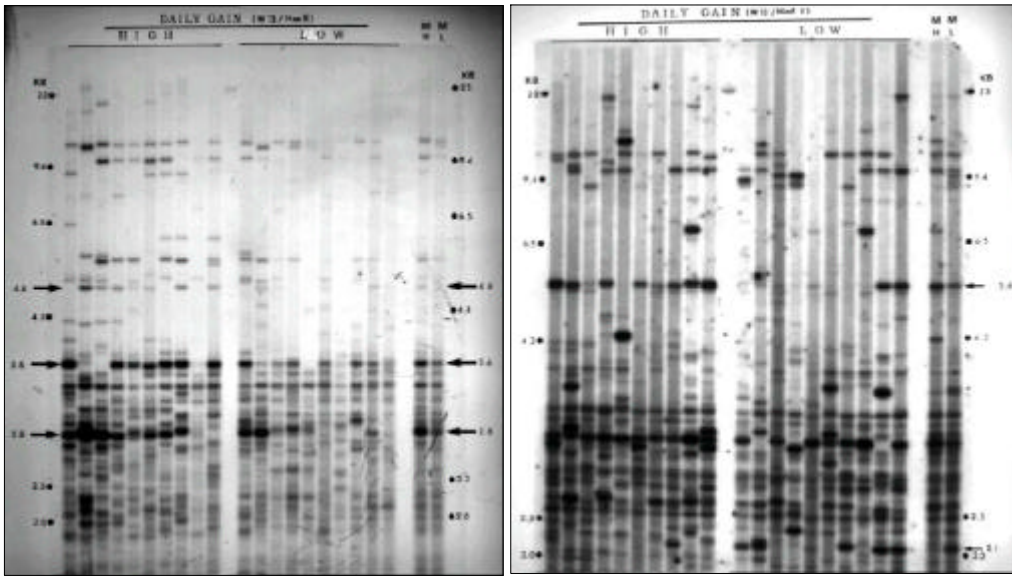


Figure 2-7. DNA fingerprintings for daily gains of high and low groups in Hanwoo (Korean Cattle) with M13/*Hae* (left) and M13/*Hinf* (right).  
 (← : specific marker)

mixed DNA band  
 probe enzyme high low group  
 band가 1-2 band marker  
 가 . DNA  
 high group low group 70%  
 가 DNA band 가 ,  
 M13/*Hae* 3 (4.6, 3.6, 2.8kb) M13/*Hinf* 2 (5.6  
 2.1kb) high group low group specific DNA marker Figure 2-7

M13/*Hae* 3 (12.4, 11.3, 9.8kb)  
 Mo-1/*Hinf* 1 (2.3kb) high group low group specific DNA marker  
 Figure 2-8

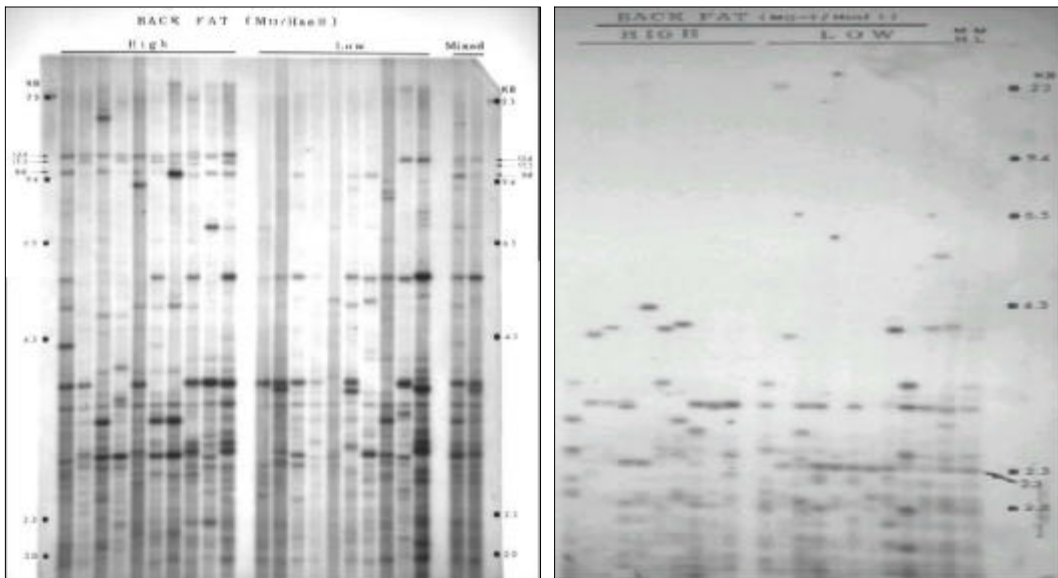


Figure 2-8. DNA fingerprintings for backfat thickness of high and low groups in Hanwoo (Korean Cattle) with M13/*Hae* (left) and MO-1/*Hinf* (right).  
 (◄ : specific marker)

Figure 2-9  
 specific marker DNA  
 Table 2-10  
 4.6/3.6/2.8kb ) 가 M13/*Hinf*

M13/*Hae* 287  
 specific bands  
 M13/*Hae* 3.6, 3.6/2.8, 4.6kb none(specific band marker)

M13/*Hinf* screen

specific marker 가

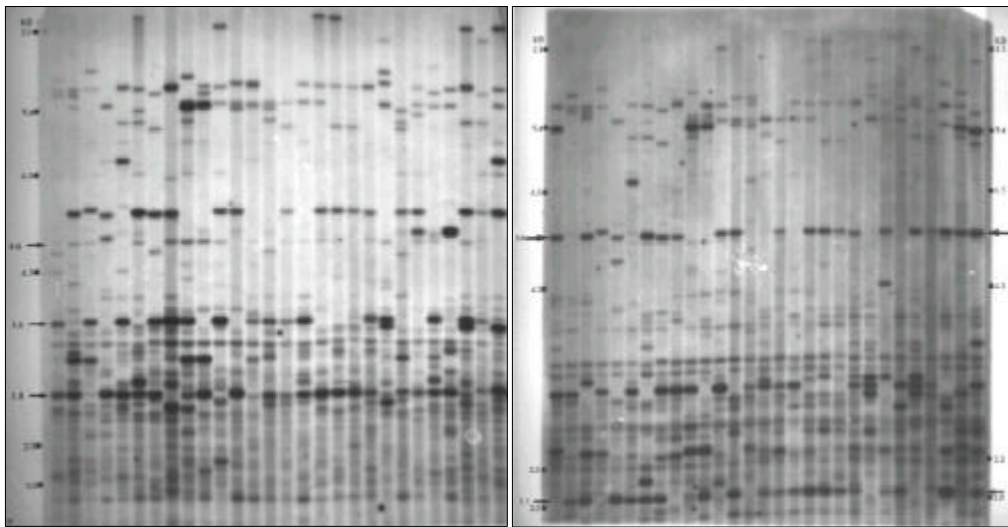


Figure 2-9. Individual check for specific DNA markers of daily gains in Hanwoo (Korean Cattles) with M13/*Hae* (left) and M13/*Hinj* (right). (◄ : specific marker)

Table 2-10. Distribution of specific DNA markers for daily gain of Hanwoo(Steer, Bull, KPN bull and Registered cow) by DNA fingerprinting with M13/*Hae* .

Marker	M13 / <i>Hae</i>								Total
	4.6	3.6	2.8	4.6/3.6	4.6/2.8	3.6/2.8	4.6/3.6/2.8	none	
Hanwoo Steer (%)	13 (6.3)	27 (13.1)	18 (8.7)	20 (9.7)	22 (10.7)	55 (26.7)	29 (14.1)	22 (10.7)	206 (100)
Progeny test bull(%)	9 (6.5)	12 (8.6)	10 (7.2)	16 (11.5)	18 (12.9)	30 (21.6)	38 (27.3)	6 (4.3)	139 (100)
KPN bull (%)	7 (4.9)	12 (8.4)	18 (12.6)	15 (10.5)	10 (7.0)	29 (20.3)	42 (29.4)	10 (7.0)	143 (100)
Registered cow (%)	3 (4.0)	9 (11.8)	6 (7.9)	13 (17.1)	8 (10.5)	13 (17.1)	15 (19.8)	9 (11.8)	76 (100)

Table 2-11. Distribution of specific DNA markers for daily gain of Hanwoo(Steer, Bull, KPN bull and Registered cow) by DNA fingerprinting with M13/*Hae* and MO-1/*Hinj* .

Table 2- 11. Distribution of specific DNA markers for backfat thickness of Hanwoo (Steer, Bull, KPN bull, and Registered cow) by DNA fingerprinting with M13/Hae .

Marker	M13 / Hae								Total
	12.4	11.3	9.4	12.4/11.3	12.4/9.4	11.3/9.4	12.4/11.3/9.4	none	
Hanwoo									
Steer (%)	28 (13.6)	12 (5.8)	37 (18.0)	15 (7.3)	47 (22.8)	23 (11.2)	26 (12.6)	18 (8.7)	206 (100)
Progeny test bull (%)	25 (18.0)	14 (10.1)	26 (18.7)	11 (7.9)	44 (31.7)	11 (7.9)	6 (4.3)	2 (1.4)	139 (100)
KPN bull (%)	17 (11.9)	9 (6.3)	17 (11.9)	11 (7.7)	30 (21.0)	20 (13.9)	23 (16.1)	16 (11.2)	143 (100)
Registered cow (%)	8 (10.5)	6 (7.9)	9 (11.8)	6 (7.9)	8 (10.5)	9 (11.9)	20 (26.3)	10 (13.2)	76 (100)

Figure 2- 10 DNA marker mechanism , full-sib 가 DNA marker 가 . M13/Hae specific marker 4.6kb , 2.8 3.6kb marker . M13/Hinf marker 5.6kb . , Figure 2- 11 marker 12.4kb 가 가 가 가 , 9.8kb 가 가 .

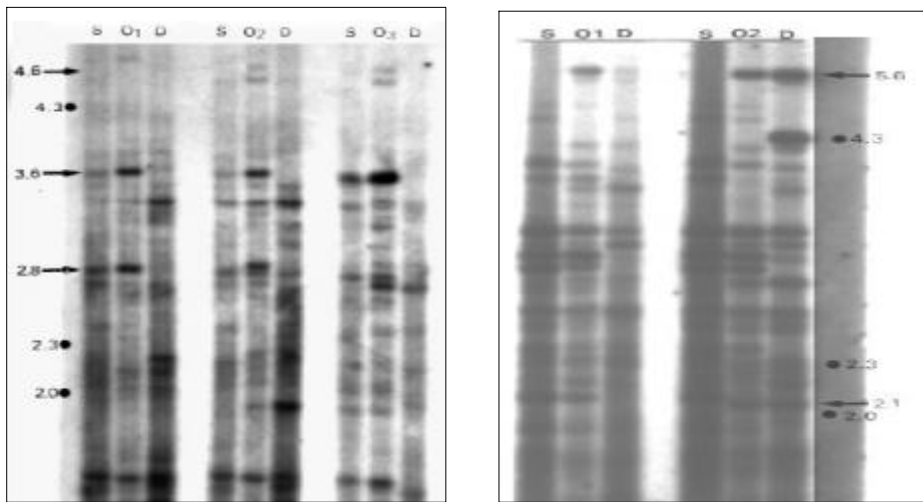


Figure 2- 10. Inheritance of specific marker related with daily gain of Hanwoo (Korean Cattle) using DNA fingerprinting with M13/Hae (left) and M13/Hinf (right). (S : sire, D : dam, O : offspring)

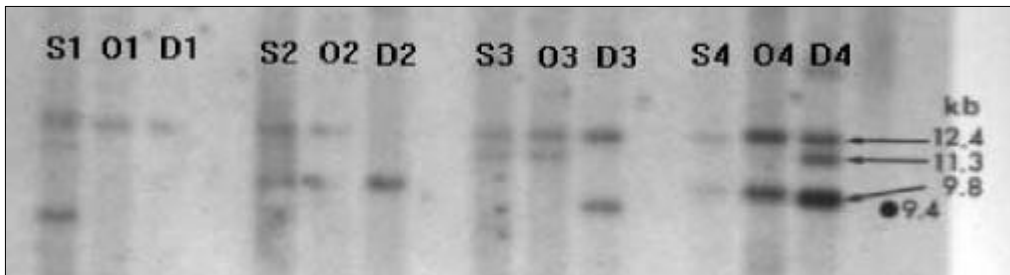


Figure 2-11. Inheritance of specific marker related with backfat thickness of Hanwoo (Korean Cattle) using DNA fingerprinting with M13/*Hae* . (S : sire, D : dam, O : offspring)

## 5. DNA marker

가  
DNA

DNA marker

289

low high group,

Table 2-12 . 1-19

2.54

10.74

가

가 85.37cm<sup>2</sup>

80.30cm<sup>2</sup>

Table 2- 12. Individual performance of marbling score and *M. longissimus dorsi* area between high and low groups in Hanwoo(Korean Cattle)

Items	Traits		Market day	Marbling score (1-19)	Market day	<i>M. longissimus dorsi</i> (cm <sup>2</sup> )
	High	No. of head		10	10	10
Mean ± SD			715 ± 44	19 ± 0.00	723 ± 30	93.6 ± 3.84
Low	No. of head		10	10	10	10
	Mean ± SD		709 ± 21	1.7 ± 0.66	705 ± 36	67.9 ± 3.55
Total	No. of head	Bull			147	
		Steer			142	
	Mean	Bull	702 ± 25	2.54 ± 2.26	702 ± 25	85.37 ± 9.01
	± SD	Steer	720 ± 35	10.74 ± 4.71	720 ± 35	80.30 ± 8.17

(high) 10 (X+1.5SD) 19  
 (low) 10 (X- 1.5SD) 1.7  
 가 , 1- 19  
 low high group . 10  
 (X+1.5SD) 93cm<sup>2</sup> 10 (X- 1.5SD) 67.9cm<sup>2</sup> .  
 10 mixed DNA 4 probe 4 enzyme  
 VNTR(variable number of tandem repeat) probe  
 enzyme DNA marker가 1 screen  
 , marker M13/*Hae* M13/*Hinf* DNA Figure  
 2- 12 Figure 2- 13  
 . high low group 가 band  
 70% DNA band low high group  
 .  
 high group  
 low group 70% 가 DNA band 가  
 , M13/*Hae* 2 (9.4 3.6kb)  
 M13/*Hinf* 2 (9.4 2.9kb) high group low group specific DNA  
 marker M13/*Hae* 5.6kb  
 M13/*Hinf* 2 (5.6 4.3kb) marker가 marker

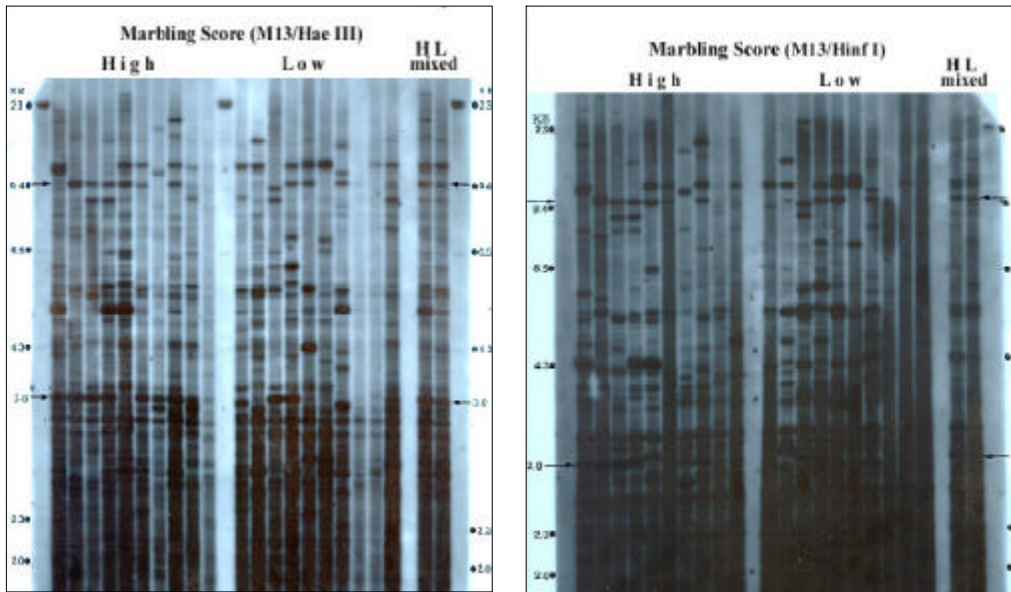


Figure 2- 12. DNA fingerprintings for marbling scores of high and low groups in Hanwoo(Korean Cattle) using DNA fingerprinting with M13/*Hae* (left) and M13/*Hinf* (right). (◀ : specific marker)

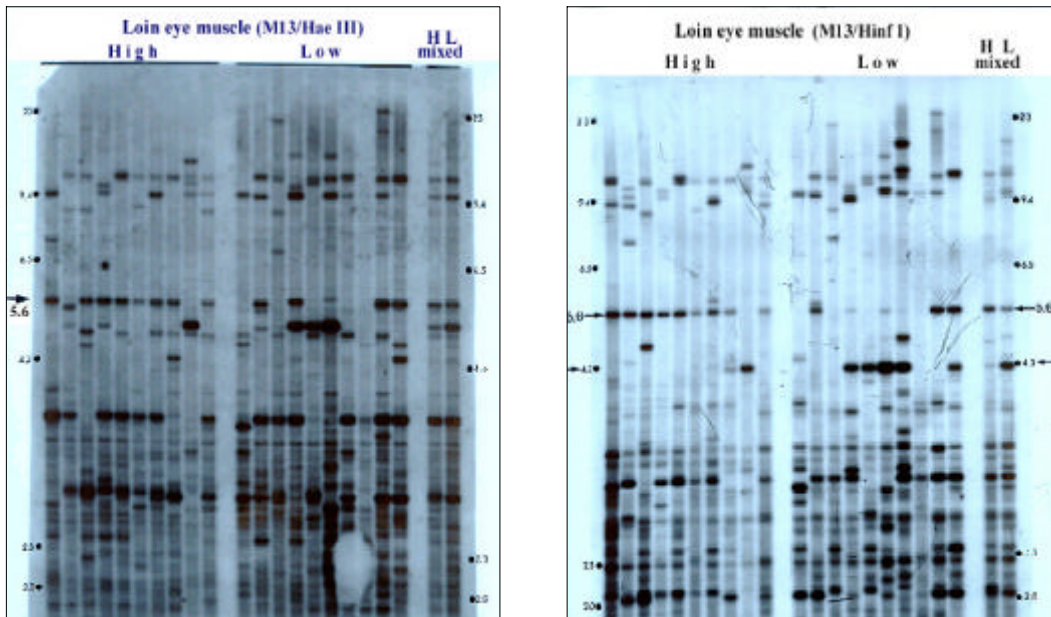


Figure 2- 13. DNA fingerprintings for *M. longissimus dorsi* area of high and low groups in Hanwoo(Korean Cattle) using DNA fingerprinting with M13/*Hae* (left) and M13/*Hinf* (right). (◀ : specific marker)

screen marker specific markers M13/Hae M13/Hinf  
 Table 2- 13 142 147 289  
 , Table 2- 14  
 1- 19  
 (1- 3) (1- 5) DNA marker

Table 2- 13 M13/Hae steer 9.4kb marker 가  
 3 2 가  
 1 4- 5 94.4% specific  
 marker가 1 54.4%  
 . M13/Hinf marker(9.4kb) 가 steer 3  
 가 1 77.3% marker가 1 53.3%  
 24% . M13/Hinf 9.4 2.9kb 가  
 5 56.3% marker  
 DNA marker

가  
 1 10 . 가  
 가 DNA marker  
 Table 2- 14 .



Table 2- 13. Distribution of specific DNA markers for marbling score in the steer of Hanwoo(Korean Cattle) using DNA fingerprinting with M13/*Hae* and M13/*Hinf*

Grade		Marker	M13/ <i>Hae</i>					M13/ <i>Hinf</i>				
			9.4	3.6	9.4/3.6	None	Total	9.4	2.9	9.4/2.9	None	Total
3 Grade	1	㉠	0	0	0	0	0	0	0	0	0	0
		㉡	0	0	2	0	2	0	0	1	0	1
		㉢	0	0	2	2	4	0	1	2	1	4
		3Grade	0	0	4	2	6	0	1	3	1	5
		Total	(0%)	(0%)	(4.8%)	(6.7%)	(3.2%)	(0%)	(2.4%)	(4.6%)	(2.6%)	(2.6%)
2 Grade	2	㉣	1	1	4	3	9	2	0	2	5	9
		㉤	0	0	2	0	2	0	0	1	0	1
		㉥	0	1	7	1	9	0	4	4	1	9
		㉣-㉥	1 (2.8%)	2 (5%)	13 (15.7%)	4 (13.3%)	20 (10.6%)	2 (4.6%)	4 (9.5%)	7 (10.8%)	6 (15.8%)	19 (10.1%)
	3	㉦	0	2	4	4	10	1	1	5	2	9
		㉧	1	1	3	4	9	2	2	2	2	8
		㉨	0	2	3	4	9	1	1	2	4	8
		㉦-㉨	1 (2.8%)	5 (12.5%)	10 (12%)	12 (40%)	28 (14.8%)	4 (9.1%)	4 (9.5%)	9 (13.9%)	8 (21.1%)	25 (13.2%)
		2Grade	2	7	23	16	48	6	8	16	14	44
		Total	(5.6%)	(17.5%)	(27.7%)	(53.3%)	(23.4%)	(13.6%)	(19.1%)	(24.6%)	(36.8%)	(23.3%)
1 Grade	4		2	2	7	4	15	1	4	4	7	16
			3	2	10	3	18	3	4	7	2	16
			0	5	2	1	8	1	3	3	2	9
		-	5 (13.9%)	9 (22.5%)	19 (22.9%)	8 (26.7%)	41 (21.7%)	5 (13.9%)	11 (26.2%)	14 (21.5%)	11 (28.9%)	41 (21.7%)
	5		0	5	6	1	12	3	5	2	2	12
			6	3	6	1	16	6	2	8	3	19
			4	4	9	0	17	2	3	7	6	18
		?	6	6	5	0	17	4	5	7	1	17
		?	3	2	2	1	8	6	4	1	0	11
		?	4	3	3	0	10	4	0	5	0	9
		?	6	1	6	1	14	8	3	2	0	13
		- ?	29 (80.6%)	24 (60%)	37 (44.6%)	4 (13.3%)	94 (49.7%)	33 (75.0%)	22 (52.4%)	32 (49.2%)	12 (31.6%)	99 (52.4%)
		1Grade	34	33	56	12	135	38	33	46	23	140
		Total	(94.4%)	(82.5%)	(67.5%)	(40%)	(71.4%)	(86.4%)	(78.6%)	(70.8%)	(60.5%)	(74.1%)
Total		36 (100%)	40 (100%)	83 (100%)	30 (100%)	189 (100%)	44 (100%)	42 (100%)	65 (100%)	38 (100%)	189 (100%)	

81%  
M13/Hae 9.4 3.6kb marker 가 3  
2, 3 27% . marker가 100% 3  
DNA marker  
가 . M13/Hinf marker  
가 .

Table 2- 14. Distribution of specific DNA markers for marbling scores in the bull of Hanwoo(Korean Cattle) using DNA fingerprinting with M13/Hae and M13/Hinf

marker Grade	M13/Hae					M13/Hinf					
	9.4	3.6	9.4/3.6	None	Total	9.4	2.9	9.4/2.9	None	Total	
No.3		7	20	24	10	61	9	17	23	12	61
		5	8	18	6	37	8	9	15	4	36
		3	9	7	2	21	3	11	3	5	22
	No.3 ( - )	15 (78.9%)	37 (86.0%)	49 (73.1%)	18 (100%)	119 (81.0%)	20 (76.9%)	37 (88.1%)	41 (82.0%)	21 (72.4%)	119 (81.0%)
No.2		0	2	6	0	8	2	0	4	2	8
		0	0	3	0	3	1	1	0	1	3
		1	1	3	0	5	1	1	3	0	5
		1	1	1	0	3	0	1	0	2	3
		1	2	0	0	3	0	1	0	2	3
		0	0	2	0	2	1	1	0	0	2
	No.2 ( - )	3 (15.8%)	6 (14.0%)	15 (22.4%)	0 (0%)	24 (16.3%)	5 (19.2%)	5 (11.9%)	7 (14.0%)	7 (24.1%)	24 (16.3%)
No.1		0	0	2	0	2	0	0	1	1	2
		1	0	0	0	1	0	0	1	0	1
		0	0	0	0	0	0	0	0	0	0
		0	0	1	0	1	1	0	0	0	1
	No.1 ( - )	1 (5.3%)	0 (0%)	3 (4.5%)	0 (0%)	4 (2.7%)	1 (3.8%)	0 (0%)	2 (4.0%)	1 (3.4%)	4 (2.7%)
Total	19	43	67	18	147	26	42	50	29	147	



Table 2- 16. Distribution of specific DNA markers for *M. longissimus dorsi* area of Hanwoo(steer, Bull, KPN bull and Registered cow) using DNA fingerprinting with M13/*Hae* and M13/*Hinf* .

Cattle \ Marker	M13/ <i>Hae</i>			M13/ <i>Hinf</i>				
	5.6kb	None	Total	5.6kb	4.3kb	5.6/4.3kb	None	Total
Steer (%)	54 (39.4)	83 (60.6)	137 (100)	48 (37.8)	12 (9.5)	13 (10.2)	54 (42.5)	127 (100)
Progeny test bull (%)	67 (44.7)	83 (55.3)	150 (100)	79 (51.0)	4 (2.6)	7 (4.5)	65 (41.9)	155 (100)
KPN bull (%)	30 (34.1)	58 (65.9)	88 (100)	27 (30.7)	9 (10.2)	20 (22.7)	32 (36.4)	88 (100)
Registered cow (%)	58 (63.0)	34 (37.0)	92 (100)	28 (30.4)	16 (17.4)	23 (25.0)	25 (27.2)	92 (100)

Figure 2- 14 DNA marker mechanism

Figure 2- 14 DNA marker mechanism

가 , , full-sib 가 DNA marker

가 . M13/*Hae* Specific marker 9.4kb

가

가 가 , 3.6kb

marker . M13/*Hinf* marker 9.4kb 2.9kb

, M13/*Hae* 9.4kb marker

가 가

DNA marker 가

Figure 2- 15 marker M13/*Hae*

M13/*Hinf* Specific marker 5.6kb 가

가 가

marker , M13/*Hinf* specific marker 4.3kb

DNA marker

specific marker DNA marker homozygote 가

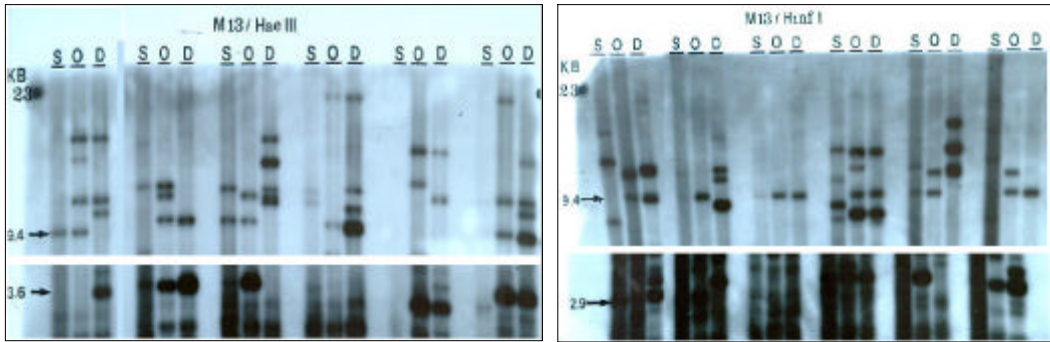


Figure 2-14. Inheritance of specific marker related with marbling scores using DNA fingerprinting with M13/*Hae* (left) and M13/*Hinf* (right).  
(S : sire, D : dam, O : offspring)

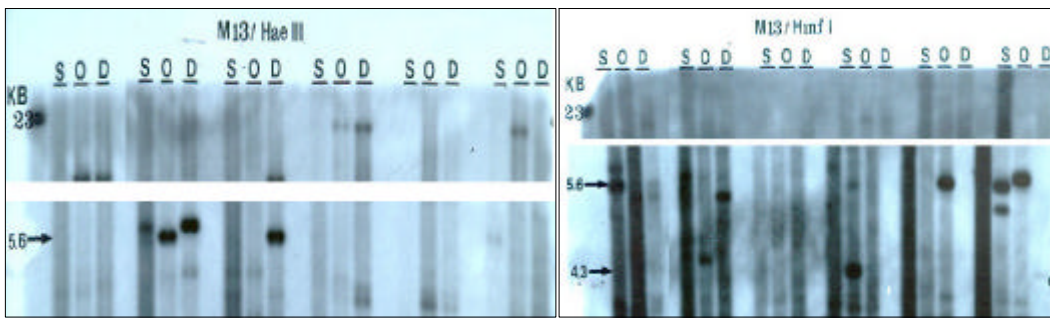


Figure 2-15. Inheritance of specific marker related with loin eye muscle using DNA fingerprinting with M13/*Hae* (left) and M13/*Hinf* (right).  
(S : sire, D : dam, O : offspring)

6. DNA marker

가

가

DNA marker

DNA maker

가

가

DNA marker

Table 2-17

DNA marker 가

marbling 17.3%, 11.3%, 36.7%,  
12.4kb none marker

26.6% 가

Table 2- 17. Specific markers and frequencies for marbling score, daily gain, backfat thickness and *M. longissimus dorsi* area in Korean Proven Bull of Hanwoo(Korean Cattle)

Marbling score(M13/Hae )									
Marker	9.4	3.6	9.4/3.6		None			Total	
No. of head	26	33	65		26			150	
Frequency(%)	17.3	22.0	43.3		17.3			100	
Daily gain(M13/Hae )									
Marker	4.6	3.6	2.8	4.6/3.6/ ×	4.6/ ×/2.8	×/3.6/2.8	4.6/3.6/2.8	None	Total
No. of head	7	12	18	15	10	29	42	17	150
Frequency(%)	4.7	8.0	12.0	10.0	6.7	19.3	28.0	11.3	100
Backfat thickness(M13/Hae )									
Marker	12.4	11.3	9.4	12.4/11.3/ ×	12.4/11.3/ ×	12.4/ ×/9.4	×/11.3/9.4	12.4/11.3/9.4	None
No. of head	17	9	17	11	30	20	23	23	150
Frequency(%)	11.3	6.0	11.3	7.3	20.0	13.3	15.3	15.3	100
<i>M. longissimus dorsi</i> area(M13/Hinf )									
Marker	5.6	4.3	5.6/4.3		None			Total	
No. of head	24	8	18		29			79	
Frequency(%)	30.4	10.1	22.8		36.7			100	

Table 2- 18

가 DNA marker  
 , DNA marker  
 가  
 , 가  
 , DNA maker 가  
 ,  
 DNA marker

Table 2-18. Specific markers and frequencies for marbling score, daily gain and backfat thickness in local farm individuals of Hanwoo(Korean Cattle)

<b>Marbling score(M13/Hae )</b>									
Marker	9.4	3.6	9.4/3.6		None	Total			
No. of head	205	346	625		111	1,287			
Frequency(%)	15.9	26.9	48.6		8.6	100			

<b>Daily gain(M13/Hae )</b>									
Marker	4.6	3.6	2.8	4.6/3.6/ ×	4.6/ ×/2.8	×/3.6/2.8	4.6/3.6/2.8	None	Total
No. of head	26	143	100	147	162	234	447	28	1,287
Frequency(%)	2.0	11.1	7.8	11.4	12.6	18.2	34.7	2.2	100

<b>Backfat thickness(M13/Hae )</b>									
Marker	12.4	11.3	9.4	12.4/11.3/ ×	12.4/ ×/9.4	×/11.3/9.4	12.4/11.3/9.4	None	Total
No. of head	233	65	256	95	374	139	61	64	1,287
Frequency(%)	18.1	5.0	19.9	7.4	29.1	10.8	4.7	5.0	100

Table 2-19. Distribution of DNA markers related with marbling score, daily gain and backfat thickness in Hanwoo(Korean Cattle) at different area

<b>Marbling score(M13/Hae )</b>						
Kyungki	Marker	9.4	3.6	9.4/3.6	none	Total
	No. of head	80	105	195	36	416
	%	19.2	25.2	46.9	8.7	100
Kyung sang	Marker	9.4	3.6	9.4/3.6	none	Total
	No. of head	86	155	275	53	569
	%	15.1	27.2	48.3	9.3	100
Junra	Marker	9.4	3.6	9.4/3.6	none	Total
	No. of head	29	69	121	13	232
	%	12.5	29.7	52.2	5.6	100
Jeju	Marker	9.4	3.6	9.4/3.6	none	Total
	No. of head	10	17	34	9	70
	%	14.3	24.3	48.6	12.9	100
<b>Total</b>	Marker	9.4	3.6	9.4/3.6	none	Total
	No. of head	205	346	625	111	1,287
	%	15.9	26.9	48.6	8.6	100

\* Next page Continue

Daily gain(M13/Hae )										
Kyungki	Marker	4.6	3.6	2.8	4.6/3.6/ x	4.6/ x/2.8	x/3.6/2.8	4.6/3.6/2.8	None	T total
	No. of head	10	37	35	42	65	65	156	6	416
	%	2.4	8.9	8.4	10.1	15.6	15.6	37.5	1.4	100
Kyung sang	Marker	4.6	3.6	2.8	4.6/3.6/ x	4.6/ x/2.8	x/3.6/2.8	4.6/3.6/2.8	None	T total
	No. of head	11	70	47	69	64	107	184	17	569
	%	1.9	12.3	8.3	12.1	11.3	18.8	32.3	3.0	100
Junra	Marker	4.6	3.6	2.8	4.6/3.6/ x	4.6/ x/2.8	x/3.6/2.8	4.6/3.6/2.8	None	T total
	No. of head	3	26	15	26	22	53	85	2	232
	%	1.3	11.2	6.5	11.2	9.5	22.8	36.6	0.9	100
Jeju	Marker	4.6	3.6	2.8	4.6/3.6/ x	4.6/ x/2.8	x/3.6/2.8	4.6/3.6/2.8	None	T total
	No. of head	2	10	3	10	11	9	22	3	70
	%	2.9	14.3	4.3	14.3	15.7	12.9	31.4	4.3	100
Total	Marker	4.6	3.6	2.8	4.6/3.6/ x	4.6/ x/2.8	x/3.6/2.8	4.6/3.6/2.8	None	T total
	No. of head	26	143	100	147	162	234	447	28	1,287
	%	2.0	11.1	7.8	11.4	12.6	18.2	34.7	2.2	100
Backfat thickness(M13/Hae )										
Kyungki	Marker	12.4	11.3	9.4	12.4/11.3/ x	12.4/ x/9.4	x/11.3/9.4	12.4/11.3/9.4	None	T total
	No. of head	65	25	86	31	109	53	27	20	416
	%	15.6	6.0	20.7	7.5	26.2	12.7	6.5	4.8	100
Kyung sang	Marker	12.4	11.3	9.4	12.4/11.3/ x	12.4/ x/9.4	x/11.3/9.4	12.4/11.3/9.4	None	T total
	No. of head	110	25	123	38	163	56	19	35	569
	%	19.3	4.4	21.6	6.7	28.7	9.8	3.3	6.2	100
Junra	Marker	12.4	11.3	9.4	12.4/11.3/ x	12.4/ x/9.4	x/11.3/9.4	12.4/11.3/9.4	None	T total
	No. of head	43	12	34	19	82	24	10	8	232
	%	18.5	5.2	14.7	8.2	35.3	10.3	4.3	3.5	100
Jeju	Marker	12.4	11.3	9.4	12.4/11.3/ x	12.4/ x/9.4	x/11.3/9.4	12.4/11.3/9.4	None	T total
	No. of head	15	3	13	7	20	6	5	1	70
	%	21.4	4.3	18.6	10.0	28.6	8.6	7.1	1.4	100
Total	Marker	12.4	11.3	9.4	12.4/11.3/ x	12.4/ x/9.4	x/11.3/9.4	12.4/11.3/9.4	None	T total
	No. of head	233	65	256	95	374	139	61	64	1,287
	%	2.0	11.1	7.8	11.4	12.6	18.2	34.7	2.2	100

Table 2-19 가 1,295  
DNA marker marker 1  
가 가 9.4kb 가 19.2%  
, DNA marker  
가 12.9% 가 ,  
marker 가  
가 가  
DNA marker 가 가  
0.9% 3.5% 가



DNA marker

Table 2-20

가

가

가

189

가

DNA marker

가

139

DNA marker

, 1

가

9.4kb

94.4% 가 1

가

50%

1

가

가

가

1

Table 2-20. Distribution of DNA markers related with marbling score in Hanwoo(Korean Cattle) between good and poor feeding systems

Items \ Marker(kb)	9.4	3.6	9.4/3.6	None	Total
<b>Total number of heads</b>	<b>60</b> (18.3%)	<b>73</b> (22.3%)	<b>146</b> (44.5%)	<b>49</b> (14.9%)	<b>328</b> (100%)
Good feeding systems	36 (19.0%)	40 (21.2%)	83 (43.9%)	30 (15.9%)	189 (100%)
Heads and ratio of No. 1 marbling grade	34 (94.4%)	33 (82.5%)	56 (67.5%)	12 (40.0%)	135 (71.4%)
Poor feeding systems	24 (17.3%)	33 (23.7%)	63 (45.3%)	19 (13.7%)	139 (100%)
Heads and ratio of No. 1 marbling grade	12 (50.0%)	16 (48.5%)	13 (20.6%)	4 (21.1%)	45 (32.3%)

### 3 DNA marker probe primer

#### 1

가 가 가

DNA

가

, DNA

DNA fingerprinting RAPD(random amplified polymorphic DNA), DAF(DNA amplified fragment), AP-PCR(arbitrary primed- polymerase chain reaction) PCR

RFLP가 fingerprinting

DNA typing DNA marker mapping

. RFLP

fingerprinting PCR DNA typing

DNA marker cloning 가 mapping

Vos (1995)

AFLP(amplified fragment length

polymorphism) PCR fingerprinting

DNA

가

AFLP RFLP PCR power 가

DNA marker

, cloning

. AFLP

DNA

adaptor ligation

adaptor sequence

bind primer PCR

primer 3'

1-3

primer

DNA

polymorphism

DNA specific DNA marker  
DNA DNA probe Steffen (1993),  
Glowatzki-Mullis (1995), Huebscher (1995), Kashi (1990), Tsuji (1995)  
. Animal  
Genetic Institute, Animal Improvement Center  
DNA DNA DNA probe  
. Kobe  
100 DNA Marker  
. DNA fingerprinting RFLP advanced  
AFLP  
DNA marker DNA cloning DNA sequencing  
specific DNA probe primer  
.

## 2

### 1.

가 150 Aberdeen  
Angus, Simmental, Charolais, Brahman Holstein 50  
Primers(Table 3-1 ), dNTPs, *Taq* polymerase RAPD  
AP-PCR DNA marker .

Table 3-1. RAPD primers used in this study

Primer No.	Primer sequences (5' 3')	Primer No.	Primer sequences (5' 3')
1	CAGGCCCTTC	H8	GCCGCTACTA
2	GTGACGTAGG	H9	GGGCCCCGAGG
3	GGGTAACGCC	H10	TACGATGACG
4	GTTTCGCTCC	H11	TTCCCGGAGC
5	AATCGGGCTG	P1	CAGGCCCTTC
6	CAATCGCCGT	P2	CAATCGCCGT
7	TCGGCGATAG	P3	AGGGGTCTTG
8	TACAACGAGG	P4	TCGGCGATAG
9	GATCATAGCG	P5	GAAACGTAGG
10	GTCCACACGG	P6	AGCCAGCGAA
11	GATCATAGCG	P7	GTGACGTAGG
12	CCCGCCGTTG	P8	TCCGCTCTGG
H1	AACGCGTAGA	P9	GGGTAACGCC
H2	ACATCCTGCG	P10	CTGAGACGGA
H3	AGCGGCTAGG	P11	GTGATCGCAG
H4	ATACGGCGTC	P12	TAGAACGAGG
H5	ATCGGGTCCG	P13	GTTTCGCTCC
H6	ATCTGCGAGC	P14	TGGATTGGTC
H7	CGGTGGCGAA	P15	GGACTGGAGT

Table 3-2. Sequences of arbitrary primers used for AP-PCR analysis in this study

Primer	Sequence(5' 3')	Abbreviation
M13 reverse sequencing primer	GGAAACAGCTATGACCATG	M13 reverse
T7 sequencing primer	GTAATACGACTCACTATAG	T7
pBS reverse sequencing primer	GGAAACAGCTATGACCATGA	pBS
T3 sequencing primer	GCAATTAACCCTCACTAAAG	T3
KPN-X primer	CTTGCGCGCATAACGCACAAC	KPN-X
KPN-M primer	CTTGCGCGCATGTACATGAC	KPN-M
universal M13 sequencing primer	TTATGTAAAACGACGGCCAGT	M13 universal
KPN-R primer	CCAAGTCGACATGGCACRTGTATA CATAYGTAAC	KPN-R



. AFLP(amplified fragment length polymorphism)

DNA 500ng *TaqI* 65 1  
 Table 3-3 *EcoRI*, T4 DNA ligase, *EcoRI* adapter, *TaqI* adaptor 가  
 ligation 37 1 . DNA  
 ethanol 70% ethanol . DNA TE  
 buffer . DNA PCR *TaqI*  
 primer, *EcoRI* primer *Taq* polymerase 95 1 , 60 1 ,  
 72 2 cycle 35 cycle . cycle PAGE  
 1% agarose gel

PCR DNA sample NaOH formamide 95 , 2  
 가 denaturation 6% denaturing polyacrylamide gel 1,800  
 Volts 3 . Molecular weight marker 100bp ladder  
 . gel 10% acetic acid 20 fixing silver  
 staining kit(Promega cat. No. DQ7050) silver staining .

### 3. DNA marker DNA

RAPD, AP-PCR, AFLP DNA marker

(1) RAPD AP-PCR marker band  
 band agarose gel eluter elution kit DNA

AFLP marker band primer  
 PCR cloning .

(2) Cloning vector PCR product cloning pGEM- T  
 vector Invitrogen pCR<sup>®</sup> 2.1 vector , vector  
 marker DNA subcloning.

(3) Cloning DNA vector primer  
 Sanger's method ABI PRISM 377 automatic  
 sequencer .

Table 3-3. DNA sequence of adaptors and PCR primers for AFLP

	Name	Sequence
Adapters <i>EcoR</i>	<i>Eco</i> top strand	5 - CTCGTAGACTGCGTACC
	<i>Eco</i> bottom strand	5 - AATGGTACGCAGTCTAC
Adapters <i>Taq</i>	<i>Taq</i> top strand	5 - GACGATGAGTCCTGAC
	<i>Taq</i> bottom strand	5 - CGGTCAGGACTCAT
Primers <i>EcoR</i>	E 1	5 - GAC TGC GTA CCA ATT CA
	E 2	5 - GAC TGC GTA CCA ATT CAA C
	E 3	5 - GAC TGC GTA CCA ATT CAA G
	E 4	5 - GAC TGC GTA CCA ATT CAC A
	E 5	5 - GAC TGC GTA CCA ATT CAC T
	E 6	5 - GAC TGC GTA CCA ATT CAG A
	E 7	5 - GAC TGC GTA CCA ATT CAG T
	E 8	5 - GAC TGC GTA CCA ATT CAT C
	E 9	5 - GAC TGC GTA CCA ATT CAT G
Primers <i>Taq</i>	T 1	5 - GAT GAG TCC TGA CCG AA
	T 2	5 - GAT GAG TCC TGA CCG AAA C
	T 3	5 - GAT GAG TCC TGA CCG AAA G
	T 4	5 - GAT GAG TCC TGA CCG AAC A
	T 5	5 - GAT GAG TCC TGA CCG AAC T
	T 6	5 - GAT GAG TCC TGA CCG ACA C
	T 7	5 - GAT GAG TCC TGA CCG ACA G
	T 8	5 - GAT GAG TCC TGA CCG ACA T
	T 9	5 - GAT GAG TCC TGA CCG ACC A

4. Probe primer

repetitive sequence, RAPD, AP-PCR, AFLP, DNA marker, probe, marker, probe

PRIMER program, secondary structure가, primer, melting temperature( $T_m$ )가 50, primer, GC content 50%

, DNA marker, primer → DNA marker

primer, AFLP, restriction enzyme, primer design, DNA marker

, DNA marker sequence, selective nucleotide, sequence, primer design

, marker sequence, design, primer, random primer, PCR



### 3

#### 1. DNA

RAPD  
 Figure 3-1  
 marker

DNA marker  
 primer  
 , No.10 primer  
 P4 P6 primer

RAPD  
 521bp

Figure 3-2  
 primer  
 primer  
 296bp

Figure 3-2

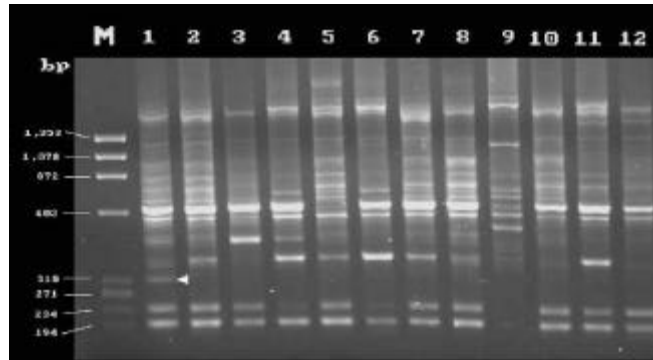


Figure 3-1. RAPD analysis with No. 10 primer in six cattle breeds  
 lane M : Molecular marker( X174 DNA/*Hae* )  
 lane 1, 2 : Korean Cattle(Hanwoo), lane 3, 4 : Holstein, lane 5, 6 : Angus  
 lane 7, 8 : Charolais, lane 9, 10 : Simmental, lane 11, 12 : Brahman

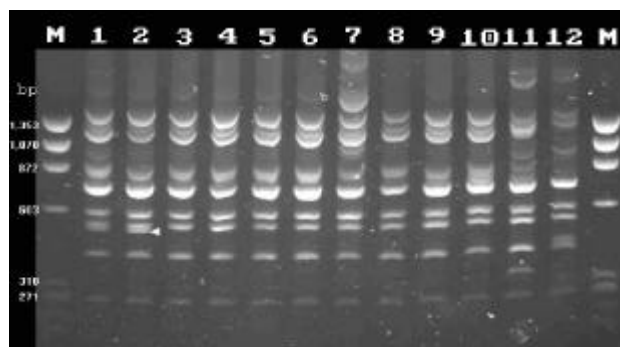


Figure 3-2. RAPD analysis with P4 & P6 primer in six cattle breeds  
 lane M : Molecular marker( X174 DNA/*Hae* )  
 lane 1, 2 : Korean Cattle(Hanwoo), lane 3, 4 : Holstein, lane 5, 6 : Angus  
 lane 7, 8 : Charolais, lane 9, 10 : Simmental, lane 11, 12 : Brahman

RAPD 296bp 521bp  
 296bp marker 85.3%  
 , 521bp marker  
 85.9%, 79.4% .(Table 3-4)

Table 3-4. Genetic frequency of genetic markers in individuals of Hanwoo(Korean Cattle) found by RAPD analysis

Primer	DNA marker (bp)	Male			Female			Total		
		Tested	Positive	(%)	Tested	Positive	(%)	Tested	Positive	(%)
No.10	296	85	0	0	68	58	85.3	153	58	37.9
P4&P6	521	85	73	85.9	68	54	79.4	153	127	83.0

Figure 3-3 AP-PCR marker KPN- X primer(20mer) , 284bp marker  
 . marker ,  
 81.2%, 79.4% 153 80.4%

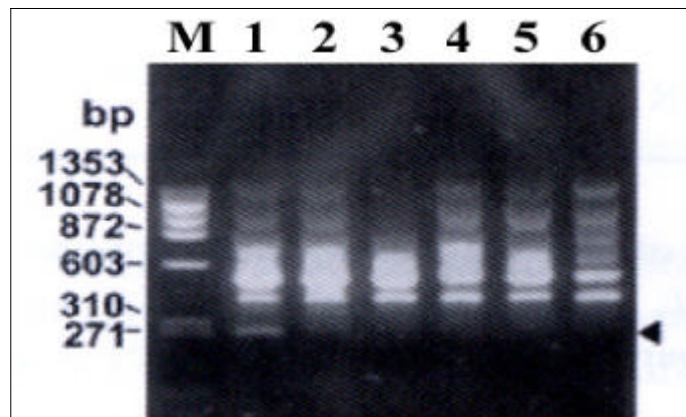


Figure 3-3. AP-PCR analysis with KPN- X primer in 6 bovine breeds  
 lane M : molecular marker( X174 DNA/Hae )  
 lane 1 : Hanwoo(Korean Cattle), lane 2 : Holstein,  
 lane 3 : Angus, lane 4 : Charolais, lane 5 : Simmental,  
 lane 6 : Brahman

Table 3-5. Genetic frequency of the 284bp AP-PCR marker in individuals of Korean native cattle(Hanwoo) when amplified with the KPN- X primer

Male			Female			Total		
Tested	Positive	Frequency (%)	Tested	Positive	Frequency (%)	Tested	Positive	Frequency (%)
85	69	81.2	68	54	79.4	153	123	80.4

## 2. DNA marker DNA

가. RAPD AP-PCR marker band gel eluter elution kit  
DNA

RAPD AP-PCR DNA marker band  
agarose gel . DNA가  
negative charge DNA gel eluter (GE 200  
SIXPAC GEL ELUTER, HOEFER) agarose bead bind  
bind DNA elution JET pure kit (GENOMED)  
agarose gel DNA (data not shown).  
DNA subcloning elution product template  
marker primer primer PCR DNA  
subcloning .

. Cloning vector marker DNA subcloning

PCR DNA blunt Taq polymerase가  
adenine 가  
sticky end cloning thymine 가  
cloning vector pGEM- T vector (Promega) DNA ligation  
, *E.coli* JM109 . Insert 가 clone  
vector가 T7 promoter site SP6 promoter site  
primer 가 PCR , insert marker DNA  
primer 가 PCR . (Figure 3-4)

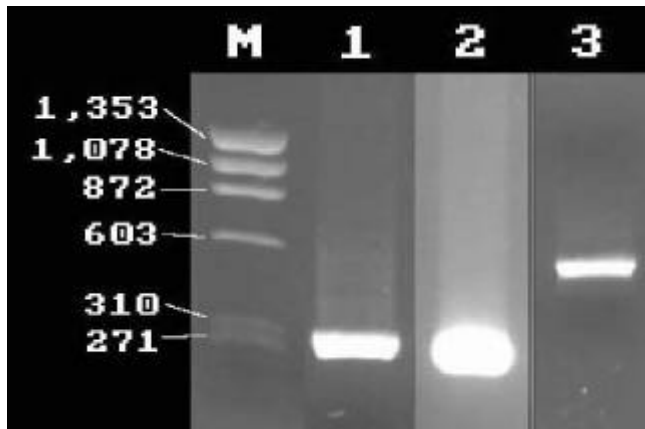


Figure 3-4. Confirm of transformant inserts.

lane M : X 174 DNA/*Hae* digest fragments,

lane 1 : RAPD No.10 primer marker

lane 2 : AP-PCR KPN- X primer marker

lane 3 : RAPD P4 & P6 primer marker

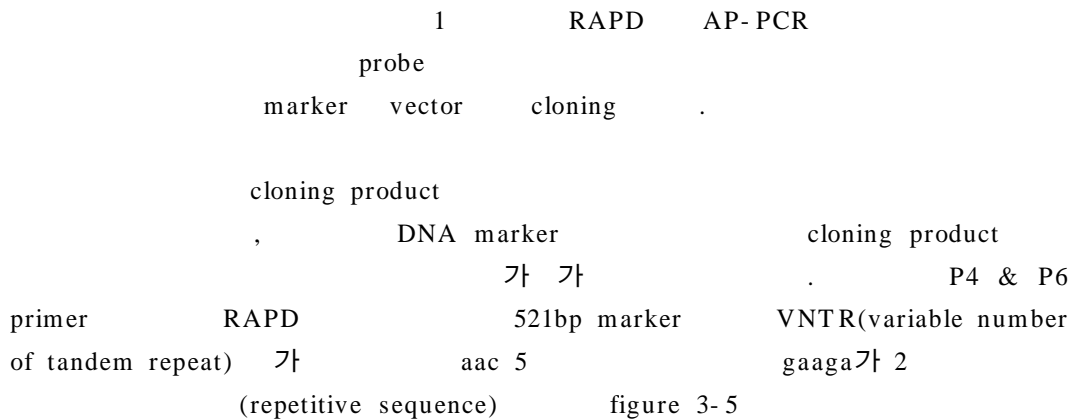
. Cloning DNA

Insert가	clone	dideoxynucleotide	(Sanger's
method) sequencing		DNA sequencing	insert
.	primer	vector	bind
T7	SP6 promoter primer	,	DNA
3-6	. Sequencing	RAPD No.10 marker	296 , P4&P6 marker
521bp	,	AP-PCR KPN- X	sequencing 284
.		RAPD AP-PCR	band 가

Table 3-6. The sequence of specific markers in Hanwoo(Korean Cattle).

(■ : PCR primer site)

Primer	Marker	Sequence
A RAPD No.10	296bp	gtccacacgggggaaggaccatggtgtcccaagtggggcagggtcattctttctcagaaaagg aggacaaggagagaaaaagcttctagtttaagtctctccagcagaacagactgtagaatgaggctgct acatgccaacgagcgagaggaaccagtgcggttggtgggtatcccaggactttataaccctgaca ctaccaccacacgtgtgtgctgaacctgctcattggaggatgaaaaatgaaacgaagaaaaatgtcc tcgtaacttagtgccgtgtggac
B RAPD P4&P6	521bp	agccagcgaaccagcctccacagctaattccagcacagtaaaataatacattgtattttcgaagct aaaaaagtaacaaaatcatgccttggcgtcacagctgaaaagaacteccagatctagtacaatcc tgatggaaatggtgagaaagatggtcctttcaaggtcacatagctagtggctctatttattaaaaaca acaacaacaacgttctcctcaaaataaagagataggaagagaagaagcaatgaatgggttattatt ctaattttatgagaagaacaaattcactgaattaagtaactgggccattacctatctaatctgtgttt taagtatttaaaacatcgaagtaataaggtacatgaatgataatttaaaaatcacatcatagcagac agaaggacttatcatgaatagcattctttctgtgctgttcttaagtctcagttgtgtccgactcttgcaa ccctatggactatgccga
C AP-PCR KPN-X	284bp	cttgcgcgcatadgcacaaccaaatacccttgacaccaaccactccaagcagagacagccagag atgatgtgagccagagtcacaaaaaattttgttttaaatattcaatctctagtctatgtaggaatagcaa cctcctgtgctggaggactctggatcaggccttttatccagactaataagcaaatgagccaggatctg ctttaagtctgctggcacatccactgatgaccattatgaactctaaaactggagttgtgcgtatgc



```

agccagcgaaccagcctccacagctaatactccagcacagtaaaataatacattgtattttcgaagctaaaaaggtaacaaaatatca
tgccttgccgtcacagctgaaaagaactcccagatctagtacaatcctgatggaaatgggtgagaaagatggcttttcaaggtcacata
gctagtggtcctatttattaaaaacaacaacaacaacgttctcctctaaaataagagataggaagagaagaagcaatgaatggg
gttatttctaattttatgagaagaacaattcactgaattaagtaactgggccattacctcatatctaatactgtgttttaagtatttaaac
atcgaagtaatgaagggtacatgaatgataatttaaaaaatcacatcatagcagacagaaggacttatcatgaatagcattcattctgtgct
gttctaagtctcagttgtgtccgactcttgcaccctatggactatcgccga

```

Figure 3-5. DNA sequence and designed DNA probe at 521bp of RAPD in Hanwoo(Korean Cattle). (**bold** : designed DNA probe)

RAPD DNA marker가 repetitive sequence  
 6 ( , , , Aberdeen Angus, Charolais  
 Holstein) . *Pst*  
 (aac)n (gaaga)n probe , (aac)n probe  
 가 marker .

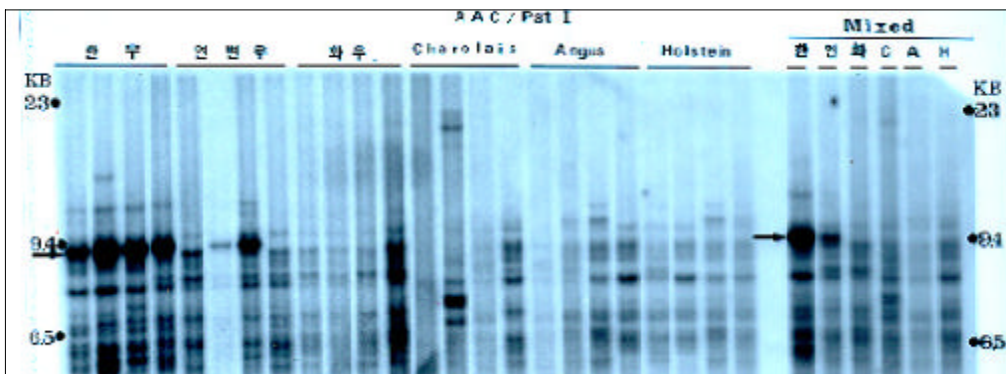


Figure 3-6. Differentiated DNA marker of Hanwoo(Korean Cattle) by specific probe (AAC)n/*Pst* . (➔ : specific marker)

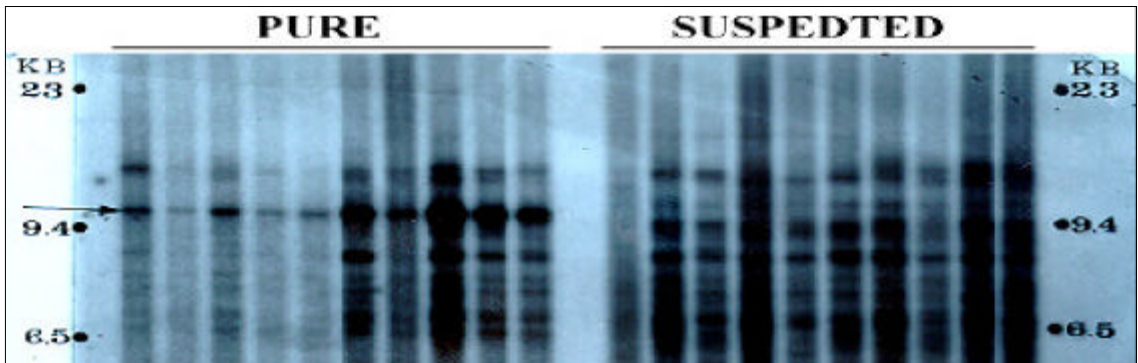


Figure 3-7. Screen of pure(left) and suspected(right) Hanwoo(Korean Cattle) individuals by (AAC)*n*/*Pst* . (➡:specific marker)

marker가  
 marker가  
 (AAC)*n* probe  
 DNA marker probe primer 가  
 가 DNA marker 가

**3. DNA marker primer**

Vos (1996) AFLP (amplified fragment length  
 polymorphism) RFLP PCR power 가  
 DNA marker polymorphism,  
 cloning advanced

(low) group (high) group 10 ,  
 가 (low) group (high) group 10 40 genomic

DNA 가 AFLP Figure 3-8  
 DNA DNA band polymorphism

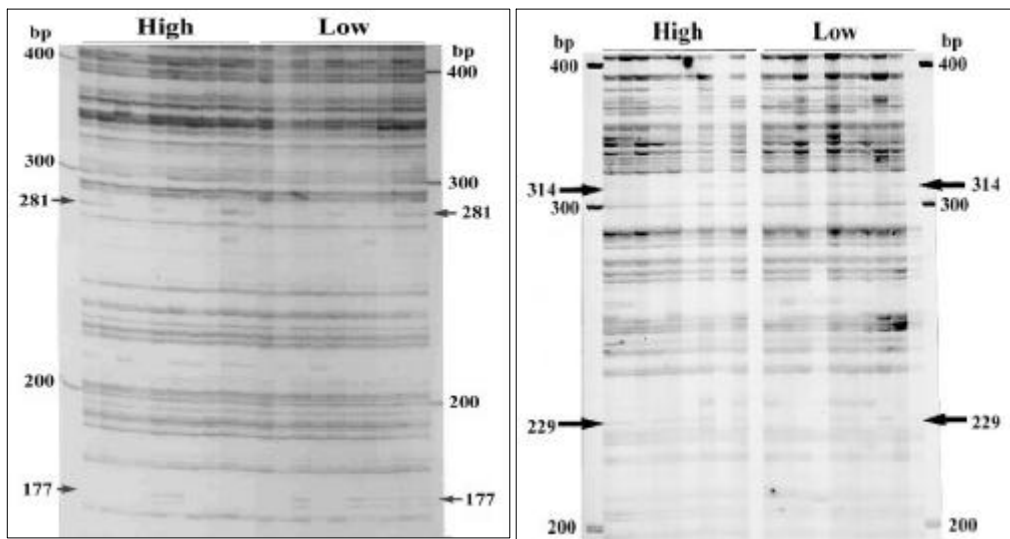


Figure 3-8. Patterns of DNA polymorphism between low and high groups of daily gain(left, E7T4 primers) and backfat thickness(right, E4T4 primers) in Hanwoo(Korean Cattle). (➡ specific marker)

Silver stained gel film expose	band	
E7T4 primer 281bp	high group , 177bp	
low group specific	.	
E4T4 primer 314bp	low group , 223bp	high
group specific	.	

	DNA marker	Table 3-7
marker	가	가
가	marker 281bp	가
marker 177bp	2	.





Table 3-9. Distribution of DNA markers related with daily gain in KPN bull and registered cow of Hanwoo(Korean Cattle).

Cattle	Marker		E7T4		Total
	281bp	177bp	281bp/177bp	None	
KPN bull	19	23	13	33	88
(%)	(21.59)	(26.14)	(14.77)	(37.50)	(100)
Registered cow	38	6	38	10	92
(%)	(41.30)	(6.52)	(41.30)	(10.87)	(100)

AFLP DNA marker가 Table 3-9  
 index marker 281bp 가  
 가 가 281bp 가  
 DNA marker Table  
 3- 10 marker 314bp  
 가

Table 3-10. Distribution of DNA markers related with backfat thickness in KPN bull and Registered cow of Hanwoo(Korean Cattle).

Cattle	Marker		E4T4		Total
	314bp	229bp	314bp/229bp	None	
KPN bull	38	12	16	22	88
(%)	(43.18)	(13.64)	(18.18)	(25.00)	(100)
Registered cow	25	16	25	26	92
(%)	(27.17)	(17.40)	(27.17)	(28.26)	(100)

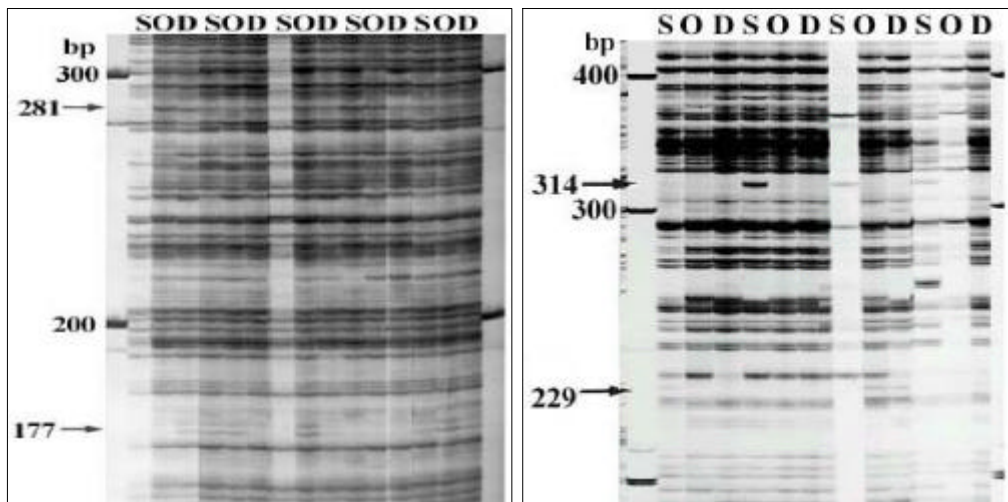


Figure 3-9. Inheritance of specific marker related with daily gain(left, E7T4 primer) and backfat thickness(right, E4T4 primer).  
(S : sire, D : dam, O : offspring)

E7T4 primer marker 281bp 177bp  
, E4T4 primer marker 314bp 229bp 314bp  
, 229bp marker  
(Figure 3-9)

Table 3-11. Inheritance of specific marker related with daily gain and backfat thickness in Hanwoo (Korean Cattle) using E7T4 and E4T4 primers.

Trait	Primer	Marker(bp)	Inheritance from	
			Sire	Dam
Daily gain	E7T4	281		
		177		
Backfat thickness	E4T4	229	×	
		314		

AFLP DNA marker  
 281bp, 177bp DNA marker E7T4 primer ,  
 314bp, 229bp DNA marker E4T4 primer . marker  
 cloning AFLP marker DNA acrylamide gel  
 gel slice template , AFLP  
 primer PCR cloning  
 (Figure 3-10), Invitrogen TA cloning kit pCR®  
 2.1 Vector ligation . 14 ligation 5μl  
 IVF competent cell . X-gal indicator plate 50%  
 white colony vector polycloning site  
 double digestion 281bp 177bp marker,  
 314bp 229bp marker insert 가 positive clone  
 ABI PRISM 377 automatic sequencer sequencing Table  
 3-12 .

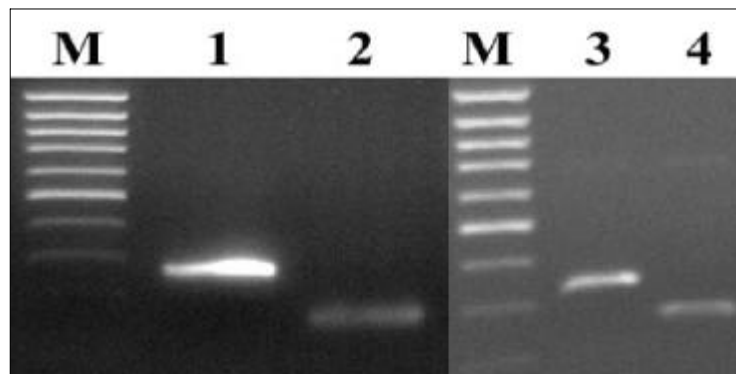


Figure 3-10. Bands of acrylamide gel slice PCR from specific marker related with daily gain(E7T4 primer) and backfat thickness(E4T4 primer) in Hanwoo(Korean Cattle).

- Lane M : 100bp ladder size marker
- Lane 1 : E7T4 primer 281bp marker
- Lane 2 : E7T4 primer 177bp marker
- Lane 3 : E4T4 primer 314bp marker
- Lane 4 : E4T4 primer 229bp marker

Table 3-12. The sequence of specific marker related with marbling and backfat thickness in Hanwoo(Korean Cattle)

Traits (primer)	Marker (bp)	Sequence
Daily gain (E7T4)	281	<b><i>gactgggtaccaattcagtc</i></b> cctgggcccccccgatgaagacacaatgacccaaaagagtctaggattgtaagaaatctacatgggcttctatgaggaaccacagtaggaaccaggctggatgaaactcaaaaggaggacttatgaaaaaacggatgtggcagtgactttaaggctttcacacagactggggagcagacgggactaaggacagctctggggttactactcagagggtcacagaggggcagggt <b><i>ttcggtcaggactcat</i></b>
	177	<b><i>gactgggtaccaattcagt</i></b> accaccaaacagctttacaacaaatgctaaaggacttatatagtcagaaatacaagagaagaaaaagatctacaaaatcaaacccaaaacaattaagaaaatgcaatcagttcagttcagttgctcagtc <b><i>gttcggtcaggactcatca</i></b>
Backfat thickness (E4T4)	314	<b><i>gactgcgtaccaattcacac</i></b> ctcaaaactaccttttcagattagagacatcactgtttttatgacattatattgtatcttgtatccaagcgaggacttagtattcatctggtagtcactgcaataatatcaatcttaccaaattcctctgtattaatgtagatgttctgatttaatatatttgtagtagaatttcattgtaattgagcactaaatgataccacttatggtaaagtgttcagaatTTTTgtaataatggattgtagtggaaataga <b><i>agttcggtcaggactcatc</i></b>
	229	<b><i>actgcgtaccaattcacag</i></b> gagaggggaggacggtcaccaggaatcatggagtcctctcctctgggtcatctgtacaaatacccccaaacataactaagtgaagtacatgcaacagagaagacaaataacacatgatattgtttatgcagattctaaagaaatgatgaaaagtgaaggttcagttcagttcagttgctcagtc <b><i>gttcggtcaggactcatc</i></b>

sequence  
Primer design  
, PRIMER program primer  
Table 3-13 ( , ) design primer .

Table 3-13. DNA sequence and primer synthesis related to daily gain of AFLP in Hanwoo(Korean Cattle)

Trait (primer)	Marker (bp)	Design primer sequence
Daily gain (E7T4)	281bp	E7 primer TGACTGCGTACCAATTCAGTCTGGGCCCCCCCCCGATG AAAGACACAATGACCCAAAAGAGTCTAGGATTGTAAGA AATCTACATGGGCTTCCT< ATGAGGAACACAGTAGG AACC>AGGCTGGATGAAACTATCAAAGGAGGACTTATG AAAAAACGGATGTGGCAGTGACTTTAAGGGCTTTCAC ACAGACTGGGGAGCAGACGGGACTAAGGGACAGCTCTG GGT< TACTACTCAGAGGTCACAGAGG>GGCAGGGCT TGTTCGGTCAGGACTCATCA T4 primer
	177bp	E7 primer TGACTGCGTACCAATTCAGT< ACCACCAAACCAGCTTT ACAAC>AAATGCTAAAGGGACTTATATAGTCAAGAAAT ACAAGAGAAGAAAAAGATCTACAAAATCAAACCCAAA ACAATTAAGAAAATGTCAATCA< GTTCAGTTCAGTTG CTCAGTCG>TGTTCGGTCAGGACTCATCA T4 primer

primer  
 281bp DNA marker primer(5'- ATGAGGAACACAGTA  
 GGAACC- 3') random primer(5'- GACATGATGAGAAGAG- 3')  
 ± 1.5SD 10 high  
 group low group design primer figure 3- 11  
 high group low group polymorphism  
 1% agarose gel marker 가  
 DNA marker 314bp  
 219bp primer design

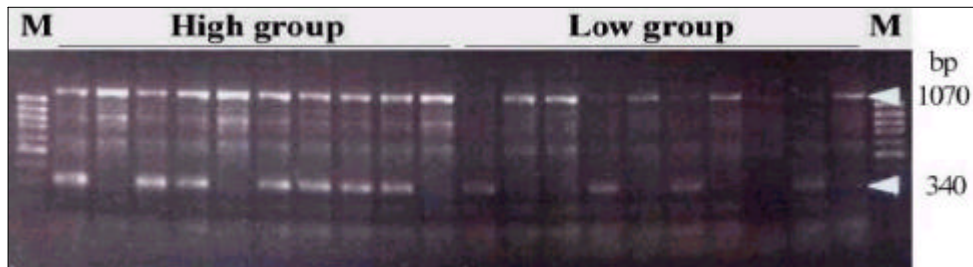


Figure 3-11. Patterns of DNA polymorphism between low and high groups of daily gains in the steer of Hanwoo(Korean Cattle) using design primers ( : specific markers).

**4. DNA marker primer**

high group DNA , AFLP template low group  
 DNA marker 154 , 184 , 88  
 , 92 (481 ) marker .  
 40 genomic DNA 가 AFLP (low) group (high) group 10  
 3- 12 figure  
 DNA DNA band polymorphism .

primer marker  
 E9T 2 primers 402bp, 179bp 139bp  
 229bp, 232bp, 314bp marker .  
 154 E9T2 marker  
 Table 3- 14 1 71.5%  
 5 52.6% . low 179bp 139bp  
 marker 가 1 22.2%, 3 11.1% 가  
 high 402bp marker 가 1 90.5% ,  
 3 0% 가  
 5 76.2% .  
 402bp marker 1 .

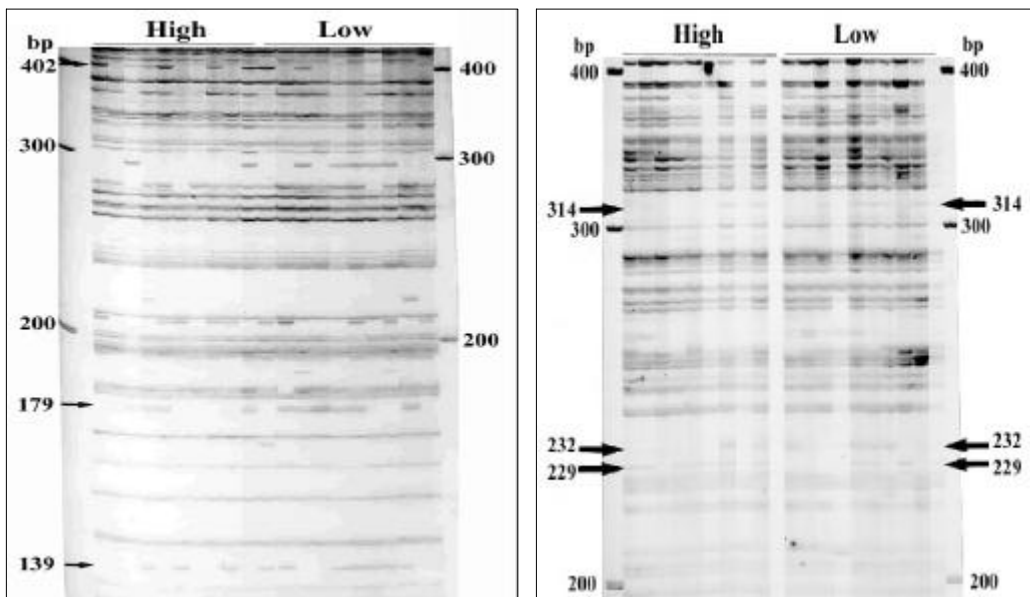


Figure 3- 12. Patterns of DNA polymorphism between low and high groups of marbling scores (left, E9T2 primers) and *M. longissimus dorsi* area(right, E4T4 primers) in the Korean Cattle. (➔ specific marker)



Table 3- 14. Distribution of specific DNA markers for marbling score in the steer of Hanwoo(Korean Cattle) with E9T2 primer

Grade		Marker	402/ ×/ ×	×/179/ ×	×/ ×/139	402/179/ ×	402/ ×/139	×/179/139	All	None	Total
No.3	1	㉠	0	0	0	0	0	0	0	0	0
		㉡	0	0	1	0	0	0	0	0	1
		㉢	0	0	1	1	0	1	0	1	4
		No.3	0 (0%)	0 (0%)	2 (10.0%)	1 (5.9%)	0 (0%)	1 (11.1%)	0 (0%)	1 (1.9%)	5 (3.2%)
No.2	2	㉣	0	2	1	0	1	2	0	3	9
		㉤	0	0	0	0	0	0	0	1	1
		㉥	2	1	1	0	0	2	1	2	9
		㉣-㉥ (%)	2 (9.5%)	3 (13.6%)	2 (10.0%)	0 (0%)	1 (20.0%)	4 (44.4%)	1 (14.3%)	6 (11.3%)	19 (12.3%)
	3	㉦	0	3	0	1	0	2	0	2	8
		㉧	0	2	0	0	0	0	1	3	6
		㉨	0	0	0	1	0	0	0	5	6
		㉦-㉨ (%)	0 (0%)	5 (22.7%)	0 (0%)	2 (11.8%)	0 (0%)	2 (22.2%)	1 (14.3%)	10 (18.9%)	20 (13.0%)
		No.2	2 (9.5%)	8 (36.4%)	2 (10.0%)	2 (11.8%)	1 (20.0%)	6 (66.7%)	2 (28.6%)	16 (30.2%)	39 (25.3%)
		No.1	1	2	0	2	0	0	2	4	11
	No.1	4		0	3	2	1	1	0	2	10
				2	2	1	0	1	0	2	8
- (%)			3 (14.3%)	7 (31.8%)	3 (15.0%)	3 (17.6%)	2 (40.0%)	1 (11.1%)	2 (28.6%)	8 (15.1%)	29 (18.8%)
			5	0	1	2	0	0	0	2	10
5			3	5	0	2	2	0	0	4	16
			1	1	4	1	0	0	1	4	12
		?	3	0	3	1	0	0	1	5	13
		?	1	0	3	0	0	0	0	4	8
		?	1	0	0	3	0	0	0	5	9
		?	2	1	2	2	0	1	1	4	13
		-? (%)	16 (76.2%)	7 (31.8%)	13 (65.0%)	11 (64.7%)	2 (40.0%)	1 (11.1%)	3 (42.9%)	28 (52.8%)	81 (52.6%)
		No.1	19 (90.5%)	14 (63.6%)	16 (80.0%)	14 (82.3%)	4 (80.0%)	2 (22.2%)	5 (71.4%)	36 (67.9%)	110 (71.5%)
Total		21 (100%)	22 (100%)	20 (100%)	17 (100%)	5 (100%)	9 (100%)	7 (100%)	53 (100%)	154 (100%)	

KPN 88

92

DNA marker

402bp marker

가 9.78%, 11.37%

.(Table 3- 15)

Table 3- 15. Distribution of DNA markers related with marbling in KPN bull and registered cow of Hanwoo(Korean Cattle).

Marker Cattle	E9T2								Total
	402bp	179bp	139bp	402/179bp	179/139bp	402/139bp	402/179/139bp	None	
KPN bull (%)	10 (11.37)	2 (2.27)	43 (48.86)	2 (2.27)	14 (15.91)	6 (6.82)	7 (7.95)	4 (4.55)	88 (100)
Registered cow (%)	9 (9.78)	3 (3.26)	42 (45.65)	2 (2.17)	6 (6.52)	18 (19.57)	7 (7.61)	5 (5.44)	92 (100)

Table 3- 16 E4T4 primer DNA  
 marker 115 184  
 232bp/229bp group non-marker group 77.22cm<sup>2</sup>  
 79.13cm<sup>2</sup> 가 , 314bp/232bp group  
 84.58cm<sup>2</sup>  
 DNA marker 가  
 DNA marker 가  
 가 .

Table 3- 16. Distribution of specific DNA markers for *M. Longissimus dorsi* area in the bull and steer of Hanwoo(Korean Cattle) with E4T4.

Marker(bp) Cattle & trait	E4T4								Total
	314	232	229	314/232	314/229	232/229	314/232/229	None	
Steer (%)	19 (16.6)	15 (13.0)	17 (14.8)	12 (10.4)	8 (7.0)	9 (7.8)	12 (10.4)	23 (20.0)	115 (100)
<i>M. Longissimus dorsi</i> area (cm <sup>2</sup> )	81.11b	82.40ab	80.53b	84.58a	82.38ab	77.22b	81.50b	79.13bc	80.98
Bull (%)	24 (13.0)	12 (6.5)	36 (19.6)	13 (7.1)	35 (19.0)	22 (20.0)	7 (3.8)	35 (19.0)	184 (100)
<i>M. Longissimus dorsi</i> area (cm <sup>2</sup> )	85.0	87.0	85.4	85.8	82.9	85.0	86.7	86.7	85.3

E4T4 marker  
 (KPN) 314bp 232bp marker 가 33% 가  
 , 314bp, 232bp 229bp 가 , 232bp  
 marker . 314bp 232bp  
 가 가 , 232bp marker , 314bp, 232bp 229bp  
 marker 가 .(Table 3- 17)

314bp/232bp 가 가 DNA marker  
 , marker 18.5%  
 , marker 33%

Table 3- 17. Distribution of DNA markers related with *M. Longissimus dorsi* area in KPN bull and registered cow of Hanwoo(Korean Cattle).

Cattle	Marker(bp)								
	E4T4							None	Total
	314	232	229	314/232	314/229	232/229	314/232/229		
KPN bull (%)	9 (10.2)	13 (14.8)	2 (2.3)	29 (33.0)	1 (1.1)	10 (11.4)	15 (17.0)	9 (10.2)	88 (100)
Registered cow (%)	8 (8.7)	14 (15.2)	10 (10.9)	17 (18.5)	13 (14.2)	6 (6.5)	12 (13.0)	12 (13.0)	92 (100)

Figure 3-13 AFLP E9T2 primer DNA marker  
 E4T4 primer DNA marker  
 mechanism , full-sib 가 DNA marker  
 가 .

E9T2 primer specific marker 402bp, 179bp 139bp  
 , 402bp marker 가  
 가 가 AFLP  
 DNA marker 가  
 , E4T4 primer marker 314bp, 232bp  
 229bp 314bp 232bp , 229bp  
 marker .

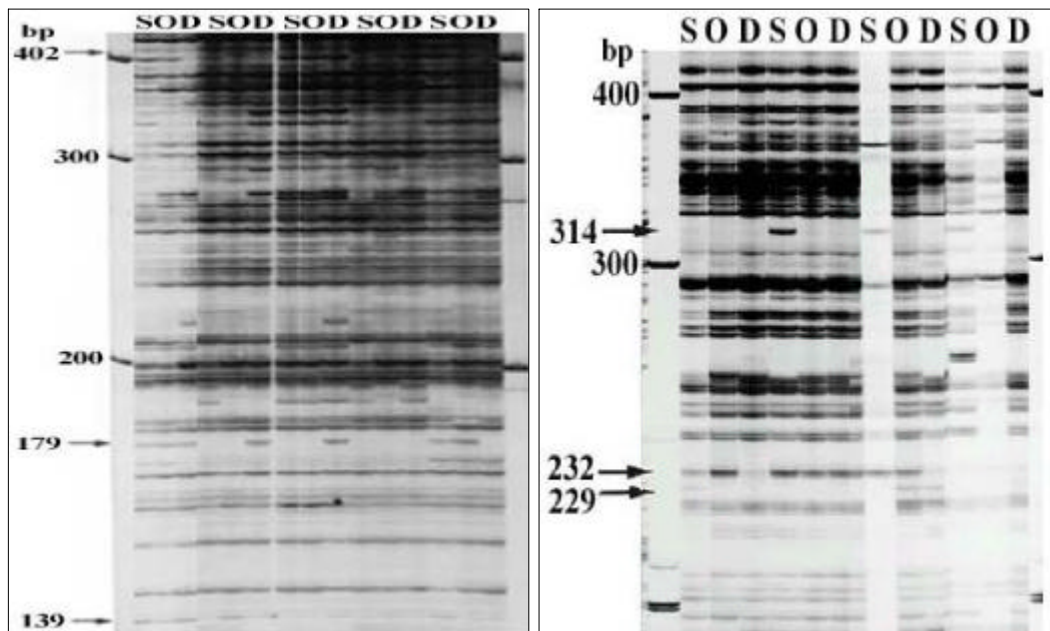


Figure 3-13. Inheritance of specific marker related with marbling scores and *M. Longissimus dorsi* area with E9T2(left) and E4T4(right). (S : sire, D : dam, O : offspring)

Table 3-18. Inheritance of specific marker related with marbling score and *M. Longissimus dorsi* area in Hanwoo(Korean Cattle) using E9T2 and E4T4 primers.

Trait	Primer	Marker(bp)	Inheritance from	
			Sire	Dam
Marbling score	E9T2	402		
		179		
		139		
<i>M. Longissimus dorsi</i> area(cm <sup>2</sup> )	E4T4	229	×	
		232		
		314		



Table 3-19. The sequence of specific marker related with marbling and *M. Longissimus dorsi* area in Hanwoo(Korean Cattle).

Traits (primer)	marker (bp)	Sequence
Marbling (E9T2)	402	<b><i>gactgcgtaccaattcat</i></b> ggaaataataggactgtagaccaaggaaaacccttctgaggtaatgctaattttcgccttgcttgcccttctctcaccatagctccagagcagattggggagggtccactgccctcccgtagccatggcactttctggaatttgcaaaaggaggctgagggtctccatggacttaaatgatttagcaaaagccttctagtctttgtgtgctgataagtcaaaacttagccctgccccgccccaaatagccttatgaggaatccaaagagctcaggtccttggtaagacagtactcttgattcacctcgtcactcaaacacctaagacaataatcttcccaaatgct <b><i>gttcggcaggactcatc</i></b>
	179	<b><i>gactgcgtaccaattcat</i></b> gacatgatgagaagagaagatattggttagctatccataatgtatctatgcaagtattattctacaagtgttcacatgacatgacatgattatgtgatttctttagaattaacagcaacatataggatatttct <b><i>gttcggcaggactcatc</i></b>
	139	<b><i>gactgcgtaccaattcat</i></b> ggtgtgaccgaaagtaaccatacctccaaagtgtggcgggtggaccacagagaagcaccacgccttgacctctcggacggacactgtgcttctgtttc <b><i>gttcggtcaggaactcatc</i></b>
<i>M. longissimus dorsi</i> area (E4T4)	229	<b><i>actgcgtaccaattcaca</i></b> ggagaggaggacggcaccaggaatcatggagtccttccctctgggtcatctgctacaaatacccccaaacatactaagtgaagtacatgcaacagagaaagacaataacacatgatattgttatatgcagattctaaagaaatgatgaaaagtgaaagtgtcagttcagttcagttgctcagtcg <b><i>gttcggtcaggactcatc</i></b>
	232	<b><i>gatgagtcctgaccgaacac</i></b> gactgagcaactgaactgaactgaactttcacttttcatcctcctgctgagtcctatattagactcttatgctctaategtcattgactgtctttactgtattatttcgagagttcaataatccccgtgctgaacaaatgatgattgtgagtgaaagtaagagagtgctggattatgcagtgccactgcattttt <b><i>atgtaattggtacgcagtc</i></b>
	314	<b><i>gactgcgtaccaattcac</i></b> acctcaaaacttacctttcagattagagacatcactgtttttatgacatttatattgttactctgtatccaagcgaggtagtattcatctggtagtcactgcaataataatcaatcttaccaaattcctggtattaatgtagatgttctgcatttaatatatttgcagtagaattcattgtaattgagcactaaatgataccacttatggtaaagtggtccagaatttttgaataaatggattgtagtggatagaag <b><i>gttcggtcaggactcatc</i></b>

sequence primer primer DNA marker  
 Table 3-20 ( ) design primer primer

Table 3-20. DNA sequence and primer synthesis related to daily gain and marbling score of AFLP in Hanwoo(Korean Cattle)

Trait(primer)	Marker	Design primer sequence
Marbling score (E9T2)	402bp	E9 primer tgactgcgtaccaatt <b>catg</b> gaaataataggactgtagaccaaggaaaacccttctgaggtaat gctaatttttcgcttgcttgc< cttctcttcaccatagctccaga>gcagattggggagggt ccactgccctcccgtagccatggtgcactttctggaattgcaaaggaggctgagggtctccat ggacttaaatgatttagcaaagccttctagtctttgtgttgctgataagtcaaacttagcccctgcc ccgccccaaataggcttatgaggaatccaaagagctcaggtccttgttgtaagacagtta< c tcttgattcacctcgtcacttc>aaacacctaagacaataatctccccaaatg <b>gtt</b> cggtcag gactcatca T2 primer
	179bp	E9 primer tgactgcgtaccaatt <b>catg</b> < _gacatgatgagaagag>aaagatattggttagctatccataa tgatctatgcaagtattatctacaagtgtgacatgtacctaggatttatgtgtattctttagaatta a< _cagcaacatatagga>ttttct <b>gtt</b> cggtcaggactcatca T2 primer
	139bp	E9 primer tgactgcgtaccaatt <b>catg</b> gtgtgaccgaaagtaaccatactcca< aagtgtggcgggtgga >ccacagagaagcaccacgccttgaccttctcgga< cggacactgtgcttc>tgttttc <b>gtt</b> cggtcaggactcatca T2 primer

primer 가 , primer  
 , 139bp DNA marker  
 primer (5'- AAGTGTGGCGGTGGA- 3', 5'- CGGACACTGTGCTTC- 3')  
 , ± 1.5SD 10  
 high group low group design primer figure  
 3- 15 . high group low group polymorphism  
 agarose gel 가  
 marker 가 .

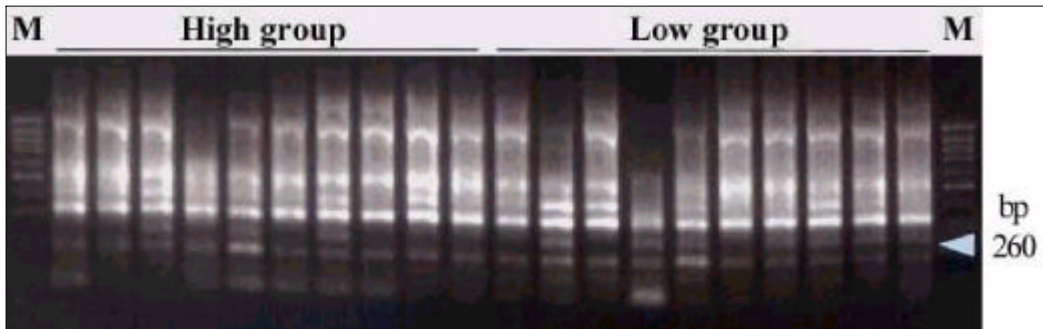


Figure 3-15. Patterns of DNA polymorphism between low and high groups of marbling score in the steer of Hanwoo(Korean Cattle) using design primers(Arrows : specific markers).

### 5. primer

design primer	281bp DNA marker	DNA marker 281bp	162	AFLP
marker	design primer	band	가	DNA band

Table 3-21. Distribution of specific DNA markers for daily gain of Hanwoo(Korean Cattle) with design primer (DG281L- random primer combination)

Items	Markers				Total
	1070bp	340bp	1070/340bp	None	
No. of head	41	33	50	38	162
Daily gain(g)	0.738	0.734	0.746	0.728	0.734
SD	0.064	0.062	0.066	0.062	0.063



AFLP	139bp DNA marker	168	Table 3-22	Table
3-23	primer	DNA marker	band	
가	1	79.4%	62.5%	marker가
	1	primer	17%	

Table 3-22. Least square means for marbling score related with specific DNA markers in the steer of Hanwoo using Design 139L-R primer

Items	Specific marker (260bp)	None	Total
Marbling score	11.38b	12.63a	12.39
No. of head	32	136	168
SD	5.085	3.759	4.058

ab : Means within a row with no common superscripts differ significantly(P<0.05)

DNA probe	DNA marker	가	electro elution probe	가
	band		probe	

Table 3-23. Distribution of specific DNA markers for marbling score of Hanwoo(Korean Cattle) with design primer(MS139L- R)

Grade Korea	marker		260bp	None	Total
	Japan				
3	1	㉠	0	0	0
		㉡	0	0	0
		㉢	1	1	2
		No.3(%)	1(3.1%)	1(0.7%)	2(1.2%)
2	2	㉣	3	1	4
		㉤	0	1	1
		㉥	2	6	8
	㉣- ㉥(%)	5(15.6%)	8(5.9%)	13(7.7%)	
	3	㉦	4	5	9
		㉧	2	5	7
		㉨	0	9	9
		㉦- ㉨(%)	6(18.8%)	19(14.0%)	25(14.9%)
	No.2(%)	11(34.4%)	27(19.9%)	38(22.6%)	
	1	4		2	14
			3	15	18
			2	8	10
- (%)			7(21.9%)	37(27.2%)	44(26.2%)
5			2	8	10
			0	15	15
			1	12	13
		?	2	14	16
		?	4	8	12
		?	1	7	8
		?	3	7	10
		- ? (%)	13(40.6%)	71(52.2%)	84(50.0%)
No.1(%)		20(62.5%)	108(79.4%)	128(76.2%)	
Total			32(100%)	136(100%)	168(100%)



DNA marker

DNA

DNA marker  
가

model

## 2

### 1.

가.

( )  
213

173

DNA

,

. AFLP

( )  
, 1999

4

1997

3

가

168

, 1999

26

가

213

가

26

138

### 2.

.

가(phenotypic value)

가

, band

.

가(genotypic value)

가(breeding value)

band

가.

. DNA  
 DNA marker group .  
 DNA marker 289 marker

1)

SAS  
 GLM

$$Y_{ijk} = \mu + Sex_i + BM_j + BT_k + E_{ijkl}$$

$$Y_{ijkl} = \mu + Sex_i + BM_j + BT_k + E_{ijkl} \quad , k \text{ genetic marker}$$

$$\mu =$$

$$Sex_i = i$$

$$BM_j = j$$

$$BT_k = k \quad \text{genetic marker}$$

$$E_{ijkl} =$$

2) Step-wise analysis

DNA marker  
 DNA marker group . DNA marker  
 group(X1, X2, X3, ....., Xi) multiple regression (Y) DNA marker  
 Y SS

group

step-wise

.

### 3

#### 1. Specific DNA markers

1, 2 *Pst* I probe M13

5 DNA

specific DNA marker 6 (8.6, 7.4, 7.1, 5.3, 2.4, 2.2kb), AP-PCR(284bp with KPN-X primer CTTGCGCGCATACG CACAAC), RAPD 2 RAPD-1(296bp with primer GTCCACACGG) RAPD-2 (521bp with primer TCGGCGATAG+AGCCAGCGAA) Table 4-1 . DNA marker

가 가 homozygote marker(7.1, 2.4 2.2kb)가 3 , heterozygote marker(8.6, 7.4 5.3kb) 3 . DNA marker homozygote marker 가 heterozygote marker 가 .

specific DNA marker heterozygote band 8.6, 7.4, 5.3kb 153 Table 4-1 . 3 marker 가 8.6 5.3kb 7.4 5.3kb 가 .

AP-PCR DNA marker band 가 가 80% , RAPD RAPD-1(296bp with primer GTCCACACGG) specific marker 85% , RAPD-2 (521bp with primer TCGGCGATAG +AGCCAGCGAA) specific marker 85% , 79% .

Table 4- 1. Distribution of DNA specific markers in registered Hanwoo

Markers(kb)	Sex	DNA Fingerprint								AP-PCR		RAPD-1		RAPD-2	
		1(8.6)	2(7.4)	3(5.3)	1-2	1-3	2-3	1-2-3	None	yes	no	yes	no	yes	no
Male ( )	No. of heads	7	9	9	11	20	4	22	3	69	16	0	85	73	12
	%	8.2	10.6	10.6	12.9	23.5	4.7	25.9	3.5	81.2	18.8	0	100	85.9	14.1
Female ( )	No. of heads	4	8	6	3	5	21	13	7	54	14	58	10	54	14
	%	6.0	11.9	9.0	4.5	7.5	31.3	19.4	10.4	79.4	20.6	85.3	14.7	79.4	20.6
Total	No. of heads	11	17	15	14	25	25	35	10	123	30	58	95	127	26
	%	7.2	11.2	9.9	9.2	16.4	16.4	23.0	6.6	80.4	19.6	37.9	62.1	83.0	17.0

\* AP-PCR : 284bp with KX primer(CTTGCGCGCATACGCACAAC)  
 RAPD- 1 : 296bp with primer #10(GTCCACACGG)  
 RAPD- 2 : 521bp with primer #4(TCGGCGATAG) + #6(AGCCAGCGAA)

2. DNA

specific DNA markers 가 .

가.

가 heterozygote marker (8.6, 7.4 5.3kb)

Table 4-2 . 8.6kb, 8.6

7.4kb DNA marker 가 가 .

marker , 8.6kb DNA marker

가 가 .

Table 4-3 AP-PCR RAPD specific marker

AP-PCR specific marker

, RAPD marker , ,



Table 4- 2. Relative body measurements and specific DNA bands of DNA fingerprinting in Hanwoo female

Markers	Wither H	Hip H	Body L	Chest D	Chest W	Rump L	Hip W	Thurl W	Pin W	Chest G
1(8.6kb)	102.5a ± 0.53	102.7a ± 0.66	106.0a ± 1.44	106.50a ± 2.32	121.9b ± 20.18	112.8a ± 3.20	111.6a ± 11.34	113.9a ± 6.05	105.1ab ± 9.69	111.2b ± 6.33
2(7.4kb)	102.3a ± 3.37	101.7a ± 2.97	105.0a ± 3.56	106.1a ± 3.02	109.1ab ± 8.86	108.8a ± 5.21	111.4a ± 5.21	110.8a ± 6.97	108.6ab ± 7.73	109.4ab ± 5.14
3(5.3kb)	103.2a ± 2.88	102.6a ± 2.26	105.4a ± 2.73	108.3a ± 4.03	105.5a ± 11.27	108.8a ± 4.48	110.2a ± 4.38	110.6a ± 3.57	105.4ab ± 9.68	109.1ab ± 4.10
1- 2	101.8a ± 1.42	101.5a ± 0.93	107.9a ± 0.25	104.3a ± 2.66	105.8a ± 8.24	107.8a ± 7.07	111.7a ± 3.42	109.5a ± 1.07	115.4b ± 6.57	102.7a ± 8.71
1- 3	103.4a ± 4.06	102.7a ± 2.79	105.8a ± 4.29	107.1a ± 3.63	102.8a ± 9.54	109.2a ± 7.14	114.8a ± 6.26	111.3a ± 4.70	103.4a ± 9.48	103.6a ± 2.90
2- 3	102.7a ± 3.00	102.6a ± 2.70	104.9a ± 3.17	107.1a ± 3.65	116.1ab ± 8.98	111.0a ± 4.51	111.3a ± 6.57	110.8a ± 5.13	112.1ab ± 7.26	107.6ab ± 4.92
1- 2- 3	103.5a ± 2.93	103.3a ± 3.64	105.3a ± 3.36	107.3a ± 4.27	117.0ab ± 12.86	110.7a ± 4.96	113.6a ± 5.14	113.9a ± 6.06	112.7ab ± 6.14	108.8ab ± 5.72
None	101.2a ± 4.05	100.9a ± 3.41	105.7a ± 3.75	105.0a ± 3.34	111.9ab ± 4.81	111.1a ± 4.91	114.1a ± 3.71	114.1a ± 4.53	112.7ab ± 5.39	108.1ab ± 3.42

\* a,b means significant difference between two different alphabet in column( =0.05)

Table 4-3. Relative body measurements and specific DNA bands of AP-PCR and RAPD in Hanwoo female

Measurement	AP-PCR		R A P D		
	yes	no	296bp	521bp	296+521
Wither Height	102.92	101.95	103.72a $\pm$ 3.50	102.30t $\pm$ 2.47	106.67a $\pm$ 1.68
Hip Height	102.61	101.55	103.38a $\pm$ 3.15	101.95t $\pm$ 2.22	105.92a $\pm$ 2.71
Body Length	105.42	105.01	106.02 $\pm$ 3.15	105.73 $\pm$ 2.97	108.09 $\pm$ 3.56
Chest Depth	106.89	106.33	108.85a $\pm$ 3.95	105.72t $\pm$ 2.66	112.24a $\pm$ 3.20
Chest Width	113.27	110.27	120.01a $\pm$ 10.99	109.21t $\pm$ 8.43	125.21a $\pm$ 16.12
Rump Height	110.60	108.79	111.40a $\pm$ 4.41	108.49t $\pm$ 3.95	114.11a $\pm$ 6.22
Hip Width	112.33	112.18	115.65 $\pm$ 7.84	111.14 $\pm$ 3.82	114.68 $\pm$ 8.48
Thurl Width	112.05	110.64	103.38a $\pm$ 5.93	101.95t $\pm$ 4.30	105.92a $\pm$ 10.29
Pin Width	111.12a	106.15b	112.39 $\pm$ 8.60	109.68 $\pm$ 7.95	117.45 $\pm$ 7.74
Chest Girth	108.00	107.75	112.81a $\pm$ 3.91	107.38t $\pm$ 3.72	114.27a $\pm$ 6.77

\* a,b means significant difference between two different alphabet in row( =0.05)

가  
 7.4kb DNA marker  
 가 (Table 4-4)  
 가  
 Table 4-5  
 가  
 (p<0.01)  
 가  
 DNA marker homo hetero  
 가 가(genotypic value) 가(phenotypic value)

Table 4-4. Breeding value of body measurements related to DNA marker(7.4kb) in Hanwoo(Korean Cattle) males

T r a i t	Means $\mp$ SD	Minimum	Maximum
Rump height	0.107 $\mp$ 0.646	- 0,716	1.557
Thurl width	0.056 $\mp$ 0.617	- 0.969	1.461
Body length	0.572 $\mp$ 0.862	- 1.707	2.098
Chest girth	1.090 $\mp$ 3.020	- 3.108	8.199

Table 4-5. Relationship between DNA markers and breeding value of phenotypic traits in Hanwoo(Korean Cattle) males

Trait	Markers	7.4kb	
		Yes	No
Rump height		0.506	- 0.195
Thurl height		0.444	- 0.200
Body length		1.091	- 0.226
Chest girth		2.756	- 0.022

### 3. (Specific Genetic Marker)

DNA maker

DNA fingerprinting(VNTR) M13/Hae 4.6, 3.6,

2.8kb M13/Hinf 5.6 2.1kb ,

M13/Hae 12.4kb, 11.3kb 9.8kb Mo- 1/Hinf 2.3kb

functional gene action DNA

AFLP(amplified fragment length polymorphism) marker

E7T4 primer(281bp 177bp) E4T4(314bp 229bp)

primer marker ( )

114 173

MAS (marker assisted selection) 가

가.

287  
0.785kg, 581.00kg, 23.7  
0.84cm

Table 4- 6. General means and standard deviation of growth traits in Hanwoo (Korean Cattle)

Trait Hanwoo	No. head	Market days	Daily gain(kg)	Market body weight(kg)	Backfat thickness(cm)
Bull	173	703.88 ± 22.91	0.809 ± 0.071	592.84 ± 42.08	0.677 ± 0.383
Steer	114	720.29 ± 32.32	0.748 ± 0.077	563.04 ± 51.75	1.096 ± 0.465
Bull & Steer	287	710.40 ± 28.16	0.785 ± 0.079	581.00 ± 52.16	0.843 ± 0.464

. DNA fingerprinting(VNTR)

1)

Table 4- 7. Least square means for daily gain related with specific DNA markers in Hanwoo(Korean Cattle) using DNA fingerprinting with M13/Hae

Items	Markers(kb)								Total or Mean	
		None	4.6/ x/ x	x/3.6/ x	x/ x/2.8	4.6/3.6/ x	4.6/ x/2.8	x/3.6/2.8		
Bull	No. of head	5	2	12	17	26	22	42	47	173
	Daily gain(g)	830	788	847	825	833	830	828	837	832
	±SE	32.6	50.2	23.1	20.3	17.2	17.1	15.1	14.1	14.4
Steer	No. of head	13	6	37	17	10	5	17	9	114
	Daily gain(g)	685a	687ab	764c	745tc	724atc	790c	767c	759tc	746
	±SE	22.5	31.5	15.1	20.9	24.8	33.1	20.3	25.8	14.0
Bull & Steer	No. of head	18	8	49	34	36	27	59	56	287
	Daily gain(g)	735a	731a	794b	777ab	777ab	790b	785b	788b	781
	±SE	20.5	28.1	15.2	17.5	17.2	17.9	15.5	15.5	14.2

x : Means none band

atc : Means within a row with no common superscripts differ significantly(P<0.05)

Table 4-7 M13 probe/*Hae* , specific marker

4.6kb marker	3.6	2.6kb marker	
	,	3.6kb marker	1
60g	.	hormone	
mechanism	가	4.6kb marker	marker가 (685
687g), 3.6, 4.6/2.8	, 3.6/2.8kb	(764, 790,	767g)
	, 4.6/2.8kb marker	가	790g
100g	가	.	
	bull	steer	4.6kb
marker	none	marker	3.6kb marker
4.6/2.8, 3.6/2.8,	4.6/3.6/2.8kb	가	
	, 가		3.6kb
p<0.01	가	.	
	3.6kb	marker	가
	3.6kb	M13 probe	<i>Hae</i>
	major		DNA
,	4.6kb marker	negative	2.8kb marker
	가	focus	DNA marker
705		44g	31kg
가	.		

Table 4- 8. Least square means for daily gain related with specific DNA markers in Hanwoo (Korean Cattle) using M13 probe and *Hinf* .

Items	Markers(kb)	Markers(kb)				Total or Mean
		None	5.6/ ×	×/2.8	5.6/2.8	
	No. of head	31	37	53	52	173
Bull	Daily gain(g)	836 <sup>ab</sup>	851 <sup>b</sup>	819 <sup>a</sup>	829 <sup>a</sup>	832
	±SE	15.2	15.3	14.1	13.6	14.4
	<hr/>					
	No. of head	39	22	24	29	114
Steer	Daily gain(g)	720 <sup>a</sup>	749 <sup>ab</sup>	747 <sup>ab</sup>	770 <sup>b</sup>	746
	±SE	17.6	19.4	19.7	16.7	14.0
	<hr/>					
Bull & Steer	No. of head	70	59	77	81	287
	Daily gain(g)	771 <sup>a</sup>	797 <sup>b</sup>	775 <sup>ab</sup>	790 <sup>ab</sup>	781
	±SE	15.0	15.5	15.1	14.0	14.2

× : Means none band

ab : Means within a row with no common superscripts differ significantly(P<0.05)

Table 4- 8 M13 probe/ *Hinf* ,  
 5.6kb marker 2.8kb  
 p<0.05 가 2.8kb  
 marker marker .  
 5.6/2.8kb marker 가 None marker 가  
 5.6kb marker가 2.8kb  
 5.6kb marker가  
 marker

Table 4-9. Step-wise regression, forward selection for the genetic marker of the daily gain by M13/*Hae* .

Step	Genetic maker	Partial R <sup>2</sup>	Parameter Estimates
1	× / 3.6 / ×	0.6047	0.1858
2	4.6 / 3.6 / ×	0.1509	- 0.4885
3	4.6 / × / ×	0.0710	0.0907
Intercept			0.5420

Table 4-9 DNA marker 4.6, 3.6 2.8kb marker가 marker가 marker 3.6kb 가 marker 가 , marker 가 60% 가 4.6kb 3.6kb (4.6/3.6/ ×) 15% negative 가

2)

Table 4-10. Least square means for backfat thickness related with specific DNA markers in Hanwoo(Korean Cattle) using M13 probe and *Hae* .

Items	Markers(kb)	None	12.4/×/×	×/11.3/×	×/×/9.4	12.4/11.3/×	12.4/×/9.4	×/11.3/9.4	All
		No. of head	9	47	7	21	10	57	12
Bull	Backfat(cm)	.521 <sub>ab</sub>	.764 <sub>ab</sub>	.599 <sub>ab</sub>	.568 <sub>a</sub>	.579 <sub>a</sub>	.813 <sub>b</sub>	.576 <sub>ab</sub>	.698 <sub>ab</sub>
	±SE	.154	.101	.172	.119	.150	.097	.142	.130
Steer	Backfat(cm)	1.191	1.019	1.424	1.216	.848	1.114	1.065	1.069
	±SE	.255	.125	.253	.133	.204	.107	.172	.000
Bull & Steer	No. of head	13	74	11	43	17	95	23	11
	Backfat(cm)	801 <sub>ab</sub>	.907 <sub>ab</sub>	.960 <sub>ab</sub>	.887 <sub>ab</sub>	.736 <sub>a</sub>	.973 <sub>b</sub>	.828 <sub>ab</sub>	.897 <sub>ab</sub>
	±SE	.151	.102	.159	.111	.137	.097	.128	.149

× : Means none band

ab : Means within a row with no common superscripts differ significantly(P<0.05)





Table 4- 12. Step- wise regression, forward selection for the genetic marker of the backfat thickness by M13/*Hae*

Step	Genetic maker	Partial R <sup>2</sup>	Parameter Estimates
1	12.4/11.3/ ×	0.3501	- 2.2584
2	×/11.3/ ×	0.1481	1.1266
3	12.4/ ×/ ×	0.0446	0.4447
4	×/11.3/9.4	0.0951	- 0.5088
Intercept			1.8093

. AFLP

1)

Table 4- 13. Least square means for daily gain related with specific DNA markers in Hanwoo(Korean Cattle) using E7T4 primers

Items	Markers(bp)	281bp	177bp	281bp/177bp	None	Total
	No. of head	46	16	12	46	120
Bull	Daily gain(g) ± SE	848 ± 16	831 ± 24	843 ± 21	840 ± 12	837 ± 8
	No. of head	52	27	17	39	135
Steer	Daily gain(g) ± SE	743 ± 10	724 ± 14	731 ± 19	745 ± 11	738 ± 6
	No. of head	98	43	29	85	255
Bull & Steer	Daily gain(g) ± SE	773 ± 10	765 ± 14	770 ± 18	783 ± 10	775 ± 6

Table 4- 13

E7T4 primer

specific DNA marker

g 724g DNA marker marker 848g 831g 745

Table 4- 14. Forward selection procedure for the daily gain by the genetic marker.

Step	Variable	Partial R2	Parameter Estimate
1	281 / ×	0.7604	- 0.0080
2	× / 177	0.1101	- 0.0094
3	× / ×	0.0729	0.0243
Intercept			0.6028

Table 4- 14 AFLP E7T4 DNA  
 marker 281bp 177bp marker가  
 가 marker negative marker  
 281bp 가 marker negative 11% 가  
 177bp 가 marker negative 11% 가  
 DNA marker 가 DNA marker positive 가  
 DNA marker 가  
 DNA marker M13/Hae  
 4.6/2.8, 3.6/2.8, negative 4.6 3.6kb marker  
 M13/Hinf 5.6 2.8kb marker  
 M13/Hae  
 12.4/11.3kb negative 가  
 가 marker 가 . AFLP marker 281bp  
 negative 314/229bp negative  
 가 .

2)

Table 4- 15. Least square means for backfat thickness related with specific DNA markers in Hanwoo(Korean Cattle) using E4T4 primers

Items	Markers(bp)					
	314	229	314/229	None	Total	
Bull	No. of head	20	37	23	46	126
	Backfat thickness(mm) ± SE	7.52 <sup>b</sup> ± 0.57	8.84 <sup>c</sup> ± 0.69	8.40 <sup>c</sup> ± 0.72	6.00 <sup>a</sup> ± 0.76	7.76 ± 0.39
Steer	No. of head	25	19	15	21	80
	Backfat thickness(mm) ± SE	8.38 <sup>a</sup> ± 0.53	9.32 <sup>t</sup> ± 0.83	7.86 <sup>a</sup> ± 0.68	8.54 <sup>a</sup> ± 0.58	8.60 ± 0.33
Bull & Steer	No. of head	45	56	38	67	206
	Backfat thickness(mm) ± SE	9.9 <sup>t</sup> ± 0.63	10.4 <sup>t</sup> ± 0.72	9.1 <sup>c</sup> ± 0.85	8.4 <sup>a</sup> ± 0.69	9.5 ± 0.36

× : Means none band

abc : Means within a row with no common superscripts differ significantly(P<0.05)

Table 4- 15 AFLP E4T4 primer

		314	229bp marker	가
(6.00 ± 0.76mm)	marker	가		(7.52mm 8.84mm)
314bp	229bp	가		7.86mm 가
가	, 229bp	가		9.32mm 가
가		가	314bp 229bp marker	
		AFLP	314bp/229bp marker	

Table 4-16. Stepwise regression, forward selection for the genetic marker of the backfat thickness by AFLP(E4T4)

Step	Genetic maker	Partial R**2	Parameter Estimates
1	314/229	0.6673	- 0.6347
2	× / ×	0.0667	- 0.1455
3	314/ ×	0.0525	0.2278
Intercept			2.4552

regression DNA marker step wise  
 314bp marker positive  
 314/229 marker 가  
 negative 67%

#### 4. (Specific Genetic Marker)

marker VNTR AFLP ( ) DNA  
 142 147 289  
 MAS(marker assisted selection) 가  
 step- wise regression .

가.

Table 4-17 289  
 147 2.54 3  
 142 10.74 2 .  
 가 85.37cm<sup>2</sup> 80.30cm<sup>2</sup> .

Table 4- 17. General means of carcass traits in the Hanwoo(Korean Cattle)

Cattle \ Trait	No. of head	Market month	Marbling score (1- 19 degree)	<i>M. longissimus dorsi</i> area (cm <sup>2</sup> )
Bull	147	23.02 ± 0.81	2.54 ± 2.26	85.37 ± 9.01
Steer	142	23.60 ± 1.15	10.74 ± 4.71	80.30 ± 8.17
Total	289	23.32 ± 1.03	6.68 ± 5.52	82.81 ± 8.94

(Specific genetic marker)

1) DNA Fingerprinting

DNA probe enzyme polymorphism VNTR specific  
 marker model 289  
 Table 4- 18 M13/*Hae* 9.4  
 3.6kb marker 가 marker가 6.32  
 9.4kb 가 marker M13/*Hinf*  
 9.4kb marker marker  
 2.9kb 2  
 negative  
 marker가

Table 4-18. Least square means for marbling score related with specific DNA markers in the bull and steer of Hanwoo(Korean Cattle) using M13/Hae and M13/Hinf

Probe/enzyme	Specific markers(kb)	No. of head (%)	Marbling score
M13/Hae	9.4/ x	36 (12.5)	8.29 <sub>a</sub> ± 0.90
	x / 3.6	81 (28.0)	7.40 <sub>ab</sub> ± 0.76
	9.4/3.6	128 (44.3)	7.51 <sub>ab</sub> ± 0.71
	x / x	44 (15.2)	6.32 <sub>t</sub> ± 0.85
	Total	289 (100)	7.38 ± 0.81
M13/Hinf	9.4/ x	48 (16.6)	8.14 <sub>a</sub> ± 0.71
	x / 2.9	84 (29.1)	6.80 <sub>t</sub> ± 1.15
	9.4/2.9	98 (33.9)	8.11 <sub>ab</sub> ± 1.05
	x / x	59 (20.4)	6.90 <sub>t</sub> ± 0.70
	Total	289 (100)	7.49 ± 0.90

x : Means none band

ab : Means within a column with no common superscripts differ significantly(P<0.05)

Table 4-19. Step-wise regression, forward selection for the genetic marker of the marbling score by M13/Hae

Step	Genetic maker	Partial R2	Parameter Estimates
1	9.4 / x	0.6218	0.9085
2	x / 3.6	0.0546	0.5226
3	x / x	0.0276	- 0.3373
Intercept			4.2429

Table 4-19 M13/Hae  
DNA marker 9.4kb 3.6kb marker가  
. 3.6kb marker 가 9.4kb  
marker 가 가 marker  
, 9.4kb/ x marker 62%  
. DNA marker  
1 3 step marker 가 70%

30% 가 DNA marker 가

Table 4- 20. Step- wise regression, forward selection for the genetic marker of the marbling score by M13/Hinf

Step	Genetic maker	Partial R2	Parameter Estimates
1	9.4 / x	0.6871	1.3354
2	x / 2.9	0.0703	3.1097
3	9.4 / 2.9	0.0281	0.8054
Intercept			3.1696

Table 4- 20 M13/Hinf  
 DNA marker 9.4kb 2.9kb marker가  
 9.4kb marker 가  
 가 marker , 9.4kb/x marker  
 69%  
 DNA marker 1 3  
 step marker 가 79%  
 20% 가 DNA marker 가

Table 4- 21. Least square means for *M. longissimus dorsi* area related with specific DNA markers in Hanwoo(Korean Cattle) using M13/Hae and M13/Hinf

Probe/Enzyme	Specific markers(kb)	No. of head (%)	<i>M. longissimus dorsi</i> area
M13/Hae	5.6	121 (42.2)	81.67 ± 1.70
	x	166 (57.8)	81.68 ± 1.72
	Total	287 (100)	81.68 ± 1.71
M13/Hinf	5.6/ x	127 (45.0)	82.40 ± 1.74
	x /4.3	16 (5.7)	81.03 ± 2.80
	5.6/4.3	20 (7.1)	81.75 ± 2.57
	x / x	119 (42.2)	81.03 ± 1.71
	Total	282 (100)	81.55 ± 2.21

x: means none band

Table 4- 21

	marker	M13/ <i>Hae</i>	M13/ <i>Hinf</i>	
High group	5.6kb	Low group	marker 4.3kb	M13/ <i>Hinf</i> marker가

Table 4016

marker 가 DNA

Table 4- 22. Step- wise regression, forward selection for the genetic marker of the *M. longissimus dorsi* area by M13/*Hinf*

Step	Genetic maker	Partial R <sup>2</sup>	Parameter Estimates
1	5.6 / ×	0.9681	1.3640
2	× / ×	0.0103	1.7026
3	5.6 / 4.3	0.0140	- 2.3241
4	× / 4.3	0.0056	1.1174
Intercept			64.4486

Table 4- 22 M13/*Hinf*

DNA marker 5.6kb 4.3kb marker가  
 5.6kb marker 가  
 marker , 5.6kb/ × marker  
 97% positive  
 DNA marker Table 4- 22  
 1 4 step marker 가 99%  
 marker



Table 4- 23. Least square means for marbling score and *M. longissimus dorsi* area related with specific DNA markers in Hanwoo(Korean Cattle) using M13/*Hinf*

Probe/Enzyme	Specific markers(kb)	No. of head (%)	Marbling score	<i>M. longissimus dorsi</i> area
M13/ <i>Hinf</i>	9.4/ x / x	20 (6.9)	8.51 <sup>ab</sup> ± 1.13	83.79 <sup>ab</sup> ± 2.64
	x /5.6/ x	32 (11.1)	7.41 <sup>ab</sup> ± 0.96	82.72 <sup>ab</sup> ± 2.24
	x / x /2.9	39 (13.5)	6.83 <sup>bc</sup> ± 0.87	81.03 <sup>ab</sup> ± 2.03
	9.4/5.6/ x	31 (10.7)	8.12 <sup>ab</sup> ± 0.95	81.90 <sup>ab</sup> ± 2.23
	9.4/ x /2.9	56 (19.4)	6.73 <sup>bc</sup> ± 0.79	80.58 <sup>b</sup> ± 1.84
	x /5.6/2.9	52 (18.0)	8.19 <sup>ab</sup> ± 0.84	84.50 <sup>a</sup> ± 1.97
	9.4/5.6/2.9	45 (15.6)	8.49 <sup>a</sup> ± 0.83	81.25 <sup>ab</sup> ± 1.94
	x / x / x	14 (4.8)	6.29 <sup>bc</sup> ± 1.03	79.83 <sup>b</sup> ± 2.42
Total	289 (100)	7.57 ± 0.93	81.95 ± 2.16	

x : Means none band

ab : Means within a column with no common superscripts differ significantly(P<0.05)

Table 4- 23

DNA marker

M13/*Hinf* 9.4, 2.9kb  
 5.6kb marker marker 9.4, 5.6  
 2.9kb 가 9.4kb marker 가  
 marker  
 DNA marker MAS가

2) AFLP(amplified fragment length polymorphism)

Primer adapter polymorphism  
 AFLP marker Table 4- 24  
 E9T2 primer marker marker가  
 402bp marker 가 13.76 가  
 , 179bp 139bp marker 가 7.44 가  
 , marker 가

Table 4- 24. Least square means for marbling score related with specific DNA markers in Hanwoo(Korean Cattle) using E9T2 primers

Primers	Specific markers(bp)	No. of head (%)	Marbling score
E9T2	402 / × / ×	21 (13.6)	13.76 <sub>b</sub> ± 0.76
	× / 179 / ×	22 (14.3)	10.55 <sub>a</sub> ± 0.82
	× / × / 139	20 (13.9)	12.95 <sub>b</sub> ± 1.17
	402 / 179 / ×	17 (13.0)	13.35 <sub>b</sub> ± 1.11
	402 / × / 139	5 (27.8)	11.00 <sub>ab</sub> ± 1.84
	× / 179 / 139	9 (5.8)	7.44 <sub>a</sub> ± 1.64
	402 / 179 / 139	7 (4.5)	12.00 <sub>b</sub> ± 1.79
	× / × / ×	53 (34.4)	12.40 <sub>b</sub> ± 0.65
	Total	154 (100)	12.14 ± 0.38

× : Means none band

ab : Means within a column with no common superscripts differ significantly(P<0.05)

Table 4- 25. Forward selection procedure for the marbling score by the genetic marker.

Step	Variable	Partial R <sup>2</sup>	Parameter Estimate
1	× / × / ×	0.7582	1.5258
2	402/ × / ×	0.1037	0.4657
3	402/ × / 139	0.0338	0.1561
4	402/179/139	0.0310	0.1175
5	402/179/ ×	0.0034	- 0.1505
Intercept			- 1.1302

Table 4- 25  
 Table  
 “402/ × / ×”, “402/ × / 139”, “402/179/139”  
 AFLP genetic marker  
 band가 “× / × / ×” 0.7582 가  
 “402/179/ ×”

marker VNTR DNA  
 marker 가 ,  
 DNA marker 가  
 Table 4- 26 . E4T4 primer (steer)

Table 4-26. Least square means for *M. longissimus dorsi* area related with specific DNA markers in the steer of Hanwoo(Korean Cattle) using E4T4 primers

Primers	Specific markers(bp)	No. of head (%)	<i>M. longissimus dorsi</i> area(cm <sup>2</sup> )
E4T4	314/ x / x	16 (16.7)	78.80 ± 2.64
	x /232/ x	13 (13.5)	80.29 ± 2.95
	x / x /229	14 (14.6)	79.57 ± 2.73
	314/232/ x	11 (11.4)	82.10 ± 2.98
	314/ x /229	8 (8.3)	79.88 ± 3.66
	x /232/229	7 (7.3)	75.71 ± 3.78
	314/232/229	6 (6.3)	82.38 ± 4.00
	x / x / x	21 (21.9)	76.56 ± 2.49
	Total	96 (100)	79.41 ± 3.15

x: means none band

Table 4-27. Forward selection procedure for the *M. longissimus dorsi* area by the genetic marker.

Step	Variable	Partial R2	Parameter estimate
1	314/ x / x	0.9009	- 0.2935
2	x /232/229	0.0231	- 0.3662
3	314/ x /229	0.0242	0.6152
4	314/232/ x	0.0518	0.7823
Intercept			65.0361

Step-wise regression

positive

“314/ x / x” marker

가 band negative 가

가

marker

DNA marker M13/Hae M13/Hinf

9.4kb marker

, M13/Hinf DNA marker

가

primer AFLP marker 402, 179 139bp VNTR . E9T2

. E4T4 primer

marker 가

5.

assisted selection) DNA marker MAS(marker  
 ,  
 DNA marker  
 step wise regression index 가  
 ,  
 ,  
 MAS 가 가 .  
 regression  
 marker 가  
 가 DNA marker DNA marker  
 economic weight ,  
 step wise regression index  
 marker model  
 가 .  
 가 marker  
 step wise regression  
 4- 28 가  
 DNA marker(9.4  
 3.6kb) maker  
 marker DNA marker . 3  
 DNA (RAPD, AP- PCR, RFLP) DNA marker  
 primer probe .  
 Table 4- 29 1997 1999 가  
 293 DNA marker  
 DNA marker가  
 11.3kb 9.4kb 3.6kb DNA marker  
 11.3kb 9.4kb가

Table 4-28. Least square means and standard error for economic traits related with specific DNA markers in Hanwoo(Korean Cattle) by M13/Hae

Marker	No. of head	<i>M. longissimus dorsi</i> area(cm <sup>2</sup> )	Marbling score	Backfat thickness(mm)	Daily gain(g)
9.4/3.6	90	80.84 <sub>c</sub> ± 1.25	12.247 <sub>t</sub> ± 0.672	9.414 ± 0.601	728 ± 12
9.4/ x	43	84.64 <sub>ab</sub> ± 1.52	15.689 <sub>a</sub> ± 0.821	9.393 ± 0.734	731 ± 15
x /3.6	41	84.58 <sub>a</sub> ± 1.60	13.974 <sub>bc</sub> ± 0.863	10.011 ± 0.772	725 ± 16
x / x	32	82.36 <sub>abc</sub> ± 1.73	10.107 <sub>bc</sub> ± 0.932	8.360 ± 0.832	722 ± 17
12.4/9.4/3.6	53	80.68 <sub>bc</sub> ± 1.38	11.975 <sub>t</sub> ± 0.746	9.915 ± 0.660	731 ± 14
12.4/9.4/ x	20	84.40 <sub>ab</sub> ± 1.92	15.790 <sub>a</sub> ± 1.035	8.733 ± 0.915	725 ± 19
12.4/ x /3.6	27	84.79 <sub>a</sub> ± 1.83	14.662 <sub>at</sub> ± 0.991	10.529 ± 0.876	735 ± 18
12.4/ x / x	16	80.28 <sub>c</sub> ± 2.19	10.087 <sub>t</sub> ± 1.181	8.963 ± 1.044	720 ± 22
x /9.4/3.6	37	81.48 <sub>ab</sub> ± 1.67	12.756 <sub>at</sub> ± 0.899	8.570 ± 0.795	724 ± 16
x /9.4/ x	23	85.21 <sub>a</sub> ± 1.96	15.692 <sub>a</sub> ± 1.057	9.755 ± 0.934	737 ± 19
x / x /3.6	14	84.72 <sub>ab</sub> ± 2.31	12.829 <sub>at</sub> ± 1.248	8.839 ± 1.103	708 ± 23
x / x / x	16	84.80 <sub>a</sub> ± 2.22	10.197 <sub>t</sub> ± 1.200	7.578 ± 1.061	724 ± 22
11.3/9.4/3.6	32	80.11 <sub>b</sub> ± 1.66	12.770 <sub>t</sub> ± 0.905	8.666 ± 0.808	711 ± 16
11.3/9.4/ x	17	84.56 <sub>ab</sub> ± 2.11	16.543 <sub>a</sub> ± 1.147	8.844 ± 1.024	741 ± 21
11.3/ x /3.6	15	85.24 <sub>a</sub> ± 2.22	14.267 <sub>at</sub> ± 1.207	9.397 ± 1.077	742 ± 22
11.3/ x / x	12	86.54 <sub>a</sub> ± 2.43	11.309 <sub>bc</sub> ± 1.320	7.493 ± 1.178	733 ± 24
x /9.4/3.6	58	81.33 <sub>b</sub> ± 1.37	12.023 <sub>t</sub> ± 0.743	9.764 ± 0.663	737 ± 13
x /9.4/ x	26	84.71 <sub>a</sub> ± 1.76	15.245 <sub>at</sub> ± 0.957	9.633 ± 0.855	724 ± 17
x / x /3.6	26	84.37 <sub>a</sub> ± 1.83	13.877 <sub>t</sub> ± 0.993	10.293 ± 0.886	715 ± 18
x / x / x	20	79.77 <sub>b</sub> ± 2.01	9.447 <sub>c</sub> ± 1.091	8.816 ± 0.974	715 ± 20
9.4/5.6/3.6	64	80.85 <sub>b</sub> ± 1.33	12.547 <sub>at</sub> ± 0.718	9.787 ± 0.637	734 ± 13
9.4/5.6/ x	19	85.93 <sub>a</sub> ± 2.02	15.887 <sub>a</sub> ± 1.090	8.868 ± 0.968	755 ± 20
9.4/ x /3.6	26	80.93 <sub>b</sub> ± 1.86	11.416 <sub>bc</sub> ± 1.003	8.184 ± 0.891	709 ± 18
9.4/ x / x	24	83.73 <sub>ab</sub> ± 1.84	15.508 <sub>a</sub> ± 0.992	9.633 ± 0.881	712 ± 18
x /5.6/3.6	19	83.80 <sub>ab</sub> ± 2.04	13.387 <sub>at</sub> ± 1.101	10.244 ± 0.978	723 ± 20
x /5.6/ x	14	83.88 <sub>ab</sub> ± 2.32	10.374 <sub>bc</sub> ± 1.252	7.907 ± 1.112	727 ± 23
x / x /3.6	22	85.26 <sub>a</sub> ± 1.99	14.353 <sub>a</sub> ± 1.071	9.585 ± 0.951	725 ± 19
x / x / x	18	81.24 <sub>ab</sub> ± 2.13	9.869 <sub>c</sub> ± 1.149	8.562 ± 1.020	717 ± 21

\* Continued next page

Marker	No. of head	<i>M. longissimus dorsi</i> area(cm <sup>2</sup> )	Marbling score	Backfat thickness(mm)	Daily gain(g)
11.3/3.6/2.8	32	79.42 <sub>c</sub> ± 1.65	13.531 ± 0.965	8.757 ± 0.791	705 <sub>t</sub> ± 16
11.3/3.6/ ×	15	86.90 <sub>a</sub> ± 2.29	12.648 ± 1.333	9.275 ± 1.094	760 <sub>a</sub> ± 22
11.3/ ×/2.8	19	85.93 <sub>ab</sub> ± 2.04	15.579 ± 1.187	8.520 ± 0.973	760 <sub>a</sub> ± 19
11.3/ ×/ ×	10	85.04 <sub>ab</sub> ± 2.62	12.430 ± 1.527	7.930 ± 1.253	700 <sub>t</sub> ± 25
×/3.6/2.8	52	81.87 <sub>bc</sub> ± 1.41	11.997 ± 0.821	10.119 ± 0.673	741 <sub>ab</sub> ± 13
×/3.6/ ×	32	82.88 <sub>ab</sub> ± 1.72	13.747 ± 1.006	9.781 ± 0.825	713 <sub>t</sub> ± 17
×/ ×/2.8	21	83.80 <sub>ab</sub> ± 1.91	12.847 ± 1.111	7.914 ± 0.911	718 <sub>ab</sub> ± 18
×/ ×/ ×	25	81.78 <sub>bc</sub> ± 1.85	12.962 ± 1.076	10.536 ± 0.883	722 <sub>ab</sub> ± 18
4.6/3.6/2.8	29	80.92 <sub>t</sub> ± 1.77	14.196 ± 1.017	9.458 ± 0.851	720 <sub>ab</sub> ± 17
4.6/3.6/ ×	20	82.02 <sub>ab</sub> ± 2.05	13.029 ± 1.176	9.684 ± 0.984	736 <sub>ab</sub> ± 20
4.6/ ×/2.8	22	84.68 <sub>ab</sub> ± 1.88	13.323 ± 1.079	7.632 ± 0.903	743 <sub>a</sub> ± 18
4.6/ ×/ ×	13	84.55 <sub>ab</sub> ± 2.39	14.363 ± 1.373	10.204 ± 1.149	744 <sub>ab</sub> ± 23
×/3.6/2.8	55	80.95 <sub>t</sub> ± 1.39	12.036 ± 0.797	9.833 ± 0.667	729 <sub>ab</sub> ± 13
×/3.6/ ×	27	85.80 <sub>a</sub> ± 1.86	14.164 ± 1.070	9.789 ± 0.895	721 <sub>ab</sub> ± 18
×/ ×/2.8	18	84.82 <sub>ab</sub> ± 2.14	15.563 ± 1.229	9.126 ± 1.029	729 <sub>ab</sub> ± 21
×/ ×/ ×	22	81.71 <sub>ab</sub> ± 1.96	12.181 ± 1.125	9.688 ± 0.941	697 <sub>t</sub> ± 19
12.4/9.4/2.8	51	81.61 ± 1.39	12.566 ± 0.797	8.883 <sub>bc</sub> ± 0.645	732 ± 14
12.4/9.4/ ×	22	81.83 ± 1.94	14.039 ± 1.111	11.133 <sub>a</sub> ± 0.899	719 ± 19
12.4/ ×/2.8	23	82.87 ± 1.90	13.444 ± 1.086	10.858 <sub>ab</sub> ± 0.879	728 ± 18
12.4/ ×/ ×	20	83.45 ± 2.08	12.476 ± 1.186	8.849 <sub>bcd</sub> ± 0.960	729 ± 20
×/9.4/2.8	42	83.24 ± 1.63	13.996 ± 0.932	8.750 <sub>cd</sub> ± 0.755	732 ± 16
×/9.4/ ×	18	82.18 ± 2.18	13.638 ± 1.245	9.523 <sub>abc</sub> ± 1.008	718 ± 21
×/ ×/2.8	8	79.76 ± 2.94	9.162 ± 1.677	6.075 <sub>c</sub> ± 1.358	703 ± 28
×/ ×/ ×	22	86.60 ± 2.00	12.267 ± 1.142	8.842 <sub>bcd</sub> ± 0.924	721 ± 19

× : Means none band

ab,c,d : Means within a column with no common superscripts differ significantly(P<0.05)

가 , M13 Hae 11.3 9.4kb  
5.5% 8.06mm  
10.16mm 2mm 748g  
701g 47g  
가 marbling 11.3/9.4kb marker  
15.63 1 9.35 6  
86.37cm<sup>2</sup> 79.7cm<sup>2</sup>

Table 4-29. Distribution of DNA markers related with backfat thickness, daily gain, marbling score, and *M. longissimus dorsi* area of Hanwoo(Korean Cattle)

Items	Traits and DNA marker(%)								
	113	94	34	11.89.4	11.38.4	948.4	11.38.4	None	Total
<b>Backfat thickness(mm)</b>									
No. of head	14	35	44	16	20	91	40	31	293
Mean	8.571 <sup>bc</sup>	9.481 <sup>ab</sup>	9.741 <sup>ab</sup>	8.063 <sup>c</sup>	8.900 <sup>b</sup>	10.115 <sup>a</sup>	8.625 <sup>bc</sup>	9.161 <sup>b</sup>	9.451
SE	0.945	0.712	0.594	0.793	0.440	0.445	0.474	0.539	0.230
<b>Daily gain(g)</b>									
No. of head	14	35	44	16	20	91	40	31	293
Mean	701 <sup>b</sup>	740 <sup>a</sup>	737 <sup>a</sup>	748 <sup>b</sup>	733 <sup>ab</sup>	745 <sup>a</sup>	737 <sup>a</sup>	744 <sup>a</sup>	739
SE	15	11	11	16	13	7	11	13	4
<b>Marbling score(19 degree)</b>									
No. of head	14	35	44	16	20	91	40	31	293
Mean	10.281 <sup>d</sup>	14.257 <sup>d</sup>	13.761 <sup>d</sup>	23.625 <sup>c</sup>	13.100 <sup>b</sup>	12.178 <sup>b</sup>	11.025 <sup>b</sup>	9.358 <sup>b</sup>	12.379
SE	1.019	0.659	0.608	0.953	0.915	0.518	0.832	0.815	0.282
<b><i>Mlongissimus dorsi</i>(cm<sup>2</sup>)</b>									
No. of head	14	35	44	16	20	91	40	31	293
Mean	80.714	82.600	82.800	86.375	82.900	80.365	79.750	81.000	81.515
SE	3.175	1.427	1.072	1.763	1.862	0.822	1.240	1.310	0.472

## 5

1. Barre-Dirie, A., M. Basedow, C. Looft, E. Kalm and B. Harlizius, 1996. Genetic distance between German cattle breeds. *25th International Conference on Animal Genetics*, France:27
2. Beever, J.E., P.D. George, R.L. Fernando, C.J. Stormont, and H.A. Lewin, 1990. Associations between genetic markers and growth and carcass traits in paternal half-sib family of Angus cattle. *J. of Animal Science* 68:337.
3. Buitkamp, J., H. Ammer and H. Geldermann, 1991. DNA fingerprinting in domestic animals. *Electrophoresis* 12:169.
4. Cockett, N.E., T.L. Shay, R.D. Green and D.L. Hancock, 1995. A *Taq-I* restriction fragment length polymorphism in the bovine calpastatin gene. *J. of Animal Science* 73:3790.
5. Falconer, D.S., 1960. *Introduction to Quantitative Genetics*. Oliver & Boyd, Edinburgh.
6. Gawakisa, P.S., S.J. Kemp and A.J. Teale, 1994. Characterization of Zebu cattle breeds in Tanzania using random amplified polymorphic DNA markers. *Animal Genetics* 25:89.
7. Georges, M., A.S. Lequarre, M. Castelli, R. Hanset and G. Vassart, 1988. DNA fingerprinting in domestic animals using four different minisatellite probes. *Cytogenet Cell Genet.* 47:127.
8. Glowatzki-Mullis, C. Gaillard, G. Wigger and R. Fries, 1995. Microsatellite based on parantage control in cattle. *Animal Genetics* 26:7.
9. Habersfeld, A., D. Kalay, D. Weisberger, O. Gal and J. Hillel, 1993. Application of multilocus molecular marker in cattle breeding. 1. Minisatellites and microsatellites. *J. of Dairy Science* 6:645.
10. Higgs, D.R., J.S. Wainscoat, J. Flint, A.V.S. Hill, S.L. Tein, R.D. Nicolls, H. Teal, H. Ayyub, T.E.A. Peto, A.G. Falusi, A.D. Jarman, J.B. Clegg and D.J. Weatherall, 1986. Analysis of the human alpha-globin gene cluster reveals a highly informative locus. *Proc. Natl. Acad. Sci. USA*, 83:5165- 5169.
11. Hillel, J., D. Kalay, O. Gal, Y. Plotsky, P. Weisberger and A. Habersfeld, 1993. Application of multilocus molecular markers in cattle breeding. 2. Use of blood mixes. *J. of Dairy Science* 76:653.
12. Hirano, T., S.N. Akane, K. Hara, S. Satoh, M. Inoue-Murayama, T. Kubokawa, A. Kvasz, W. Coppeters, M. Georges, and Y. Sugimoto, 1996. Linkage analysis of Wagyu meat quality. *25th International Conference on Animal Genetics*, France:163.
13. Huebscher, K.J., G. Dolf, J. Fery, G. Stranzinger and C. Gaillard, 1995. Features of the DNA Fingerprinting probe pITZ1. *Animal Genetics* 26:27- 30.



14. Ikeda, K., K.Tsutsumi, S. Ejiri and Y. Yasuda, 1992. DNA fingerprints applied to individual identification and paternity testing in bovines. *Animal Science Technology(Jpn.)* 64:129.
15. Inoue-Murayama, M., T. Hirano, T. Watanabe, K. Mizoshita, H. Yamakuchi, S. Nakane. and Y. Sugimoto, 1997. Individual identification and paternity control of Japanese Black cattle based on microsatellite polymorphism. *Animal Science Technology(Jpn.)* 68:443- 449.
16. Jayarao, B.M., J.J. Dore, and S.P. Oliver, 1992. Restriction fragment length polymorphism analysis of 16s ribosomal DNA of Streptococcus and Entrococcus species of bovine origin. *J. of Clini Microbiology* 30:2235.
17. Jeffreys, A.J., V. Wilson and S.L. Thein, 1985. Individual-specific fingerprints of human DNA. *Nature* 316:76.
18. Kashi,Y., F. Iraqi, Y. Tikoschinsky, B. Ruzinski, A. Nave, J.S. Beckmann, A. Friedman, M. Soller and Y. Gruenbaum, 1990. (TG)<sub>n</sub> uncovers a sex-specific hybridization pattern in cattle. *Genomics* 6:31- 36.
19. Kikkawa, Y., T. Amano and H. Suzuki, 1995. Analysis of genetic diversity of domestic cattle in East and Southeast Asia in terms of variations in restriction sites and sequences of mitochondrial DNA. *Biochemical Genetics* 33:51.
20. Kuhnlein, U., D. Zadworny, Y. Dawe, R.W. Fairfull and J.S. Gavora, 1990. Assessment of inbreeding by DNA fingerprinting : Development of a calibration curve using defined strains of chickens. *The Genetics Society of America* 125:161..
21. Mannen, H., S. Tsuji, F. Mukai, N. Goto and Ohtagaki, 1993. Genetic Similarity using DNA fingerprinting in cattle to determine relationship coefficient. *J. Hered.* 84:166.
22. Mannen, H. and S. Tsuji, 1993. DNA fingerprinting for individual identification and parentage test in Japanese Black cattle using five different mini- and one microsatellite probes. *J. of Animal Genetics* 21:62.
23. Meuwissen, T.H.E. and J.A.M. VanArendonik, 1992. Potential improvement in rate of genetic gain from marker-assisted selection in Dairy cattle breeding schemes. *J. of Dairy Science* 75:1651.
24. Mitani, K., Y. Takahashi and R. Kominami, 1990. A GGCAGG motif in minisatellite affecting their germ line instability. *J. of Bio. Chem.* 265: 15203- 15210.
25. Moody, D.E., D. Pomp and Barendse, 1995. Restriction fragment length polymorphism in amplification products of the bovine growth hormone-releasing hormone gene. *J. cf Animal Science* 73:3789

26. Nakamura, Y., P.O. Leppert, R. Wolff, T. Holm, M. Culver and R. White, 1987. Variable number of tandem repeat(VNTR) markers for human gene mapping. *Science* 25:1616- 1622.
27. Plotsky, Y., A. Cahner, A. Haberfeld, U. Lavi and J. Hillel, 1989. Analysis of genetic association between DNA fingerprints and quantitative traits using DNA mixes Proc. *4th World Congress on Genetics applied to Livestock Production* 13:133.
28. Ruane, J. and J.J. Colleau, 1996. Marker-assisted selection for sex-limited character in nucleus breeding population. *J. of Dairy Science* 79:1666- 1678.
29. Steffen, P., A. Eggen, B. Dietz, J.E. Womack, G. Stranzinger and R. Fries, 1993. Isolation and mapping of polymorphic microsatellites in cattle. *Animal Genetics* 24:121- 124.
30. Taylor, J.F., S.K. Davis, J.O. Sanders, J.W. Turner, R.K. Miller and S.B. Smith, 1998. Identification of QTLs for growth and carcass quality in a cross between *Bos indicus* and *Bos taurus*. *Plant-Animal Genome Conference*, San Diego, CA:W19.
31. Tsuji, S. 1995. Recent progress in the gene mapping of domestic animals. *Animal Science and Technology* 66:1047.
32. Vassart, G., M. Georges, R. Monsieur, A. Brocas, S. Lequarre and D. Christophe, 1987. Sequence in M13 phage detects hypervariable minisatellites in human and animal DNA. *Science* 235:683.
33. Vos, P., R. Hogers, M. Bleeker, M. Reijans, T. Van de Lee, M. Hornes, A. Frejters, J. pot, J. Peleman, M. Kuiper and M. Zabeau, 1995. AFLP : a new technique for DNA fingerprinting. *Nucleic Acids Research* 23(21):4407.
34. Yeo, J.S., E.J. Lee and J.W. Kim, 1996. Study for DNA polymorphism of DNA fingerprinting using several different restriction enzymes and probes in Korean Cattle. *Korean Journal of Animal Science* 38(6):555- 560.
35. Yeo, J.S., J.W. Kim E.J. Lee, M.Y. Lee and Y.H. Yang, 1997. Genetic analysis of cattle breeds using DNA fingerprinting. *Korean Journal of Animal Science* 39(6):641- 646.
36. Yeo, J.S., J.W. Kim T.K. Jang, N.H. Park and M.Y. Lee, 1999. Identification of DNA markers related to daily gain in Hanwoo. *Korean Journal of Animal Science* 41(4):419- 426.
37. Yeo, J.S., J.W. Kim, T.K. Jang, Y.A. Park and D.H. Nam, 2000. Utilization of DNA Marker-Assisted selection in Korean Native Animals. *Biotechnol. Bioprocess Eng.* 5:71- 78.

1.

2.

3. 가