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FecB

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ABRII

(// : // :)

PCR-RFLP

DNA

FecB

MCMA26

(I)

PIC-Value

(D)

0.67 (SD=0.08)

PIC

0.72 (SD=0.07)

3.128E-13

AvaII

PCR

FecBB

FecB

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New South

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Wales

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FecB

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²FecB

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PCR-RFLP

(> %)

%

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FecB

FecB

EDTA

cc

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ml DNA

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Miller *et al* (1998)

6. Donor
7. Strain

-
1. Bone morphogenetic receptor type 1 B gene
 2. Fecundity Booroola
 3. Gene Introgression
 4. Foreground Selection
 5. Background selection

.... :
MgCl₂ PCR
: PCR
/ dNTP DNA
Taq
MgCl₂
PCR
%
) TBE 0.5X
(SCAN ANALYTICS One-D-Scan

FecB
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PCR-RFLP FecB^B
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DNA
(Accession no. AF298885)
Primer F; 5-CCAGAGGACAATAGCAAAGCAAA-3
PrimerR;5- GAAGATGTTTTTCATGCCTCATCAACACGGTC-3
PCR
DNA :
/ dNTP
MgCl₂ / Taq

: PCR
°C °C °C
°C
PCR
AvaII

(Nei, 1978) (H_E)
(H_O)
(Botstein *et al*, 1980) (PIC)
PIC
(Yeh *et al* HET (Ott, 1997)
PopGene32 *al* 1999)
(Paetkau *et al*; 1995) (I)

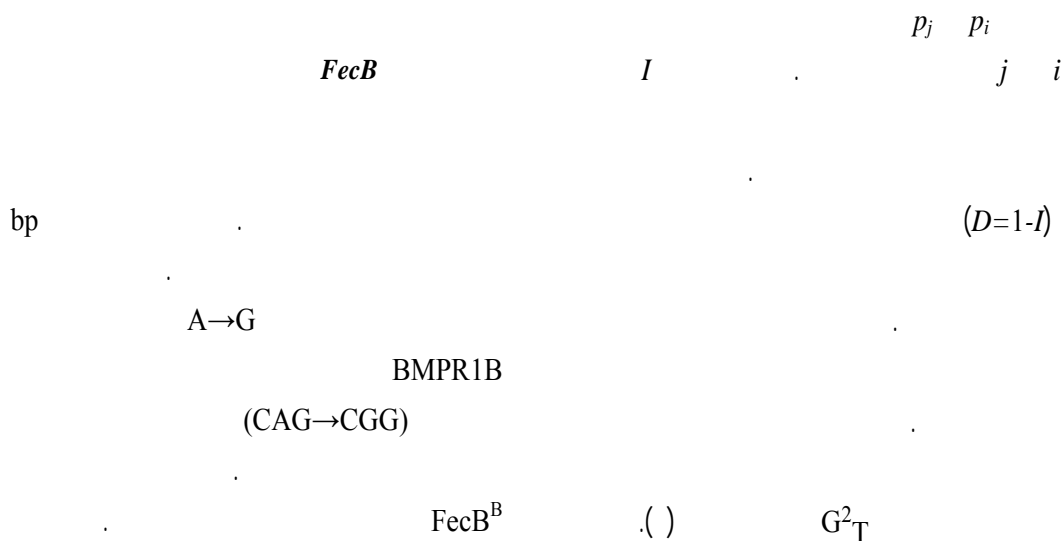
%
MAI¹
)
(FecB

$$I = \sum_i p_i^4 + \sum_i \sum_{j>i} (2p_i p_j)^2$$

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<http://rubens.its.unimelb.edu.au/~jillm/jill.htm>

- 2. Polymorphism Information Content
- 3. Probability of Identity
- 4. Individual Identification

Locus	Motif	Accession number	Chr No	Tm °C	Reported Allele Size (bp)	Observed Allele Size (bp)	Primer Sequence
OarHH55	(AC) ₂₄	<u>L13693</u>	6	62	117-155	111-127	F: GTTATTCCATATTCTTTCTCCATCATAAGC R: CCACACAGAGCAACTAAAACCCAGC
OarAE101	(GT) ₂₂	L13692	6	63	99-123	106-128	F: TAAGAAATATATTTGAAAAAACTGTATCTCCCC R: TTCTTATAGATGCACTCAAGCTAG
BM143	(GT) ₁₆	G18387	6	61	102-128	107-117	F: ACCTGGGAAGCCTCCATATC R: CTGCAGGCAGATTCTTTATCG
BMS2508	(TG) ₁₅	<u>AF394449</u>	6	58	158	154-188	F: AGGTTGACTTCTGTGTCTTTTC R: GTT TCTTAGGGGAGTGTGAT T
LSCV43	-	-	6	52	110-130	101-119	F: CCAGAATATAGAGTTTTG TCAAG R: GCCTGATTTGTATTTGTATGAG
CSSM18	(AC) ₁₇	<u>U03798</u>	18	58	116-134	112-118	F: TGTGCATAATTTGTGTCCGTCCGGA R: AGGAATTCCTCTAGAAAAGCAGGC
OY3	-	-	18	57	160	118-185	F: TTTTGGTTTCACCTATTGTTTGAG R: CTCTGTCTAAAGAAGCTTTTCCC
MCMA26	(GT) ₃₂	<u>AF098961</u>	18	52	188-212	192	F: TCTCTGCTTCCAGCTTATTC R: AGAGCTTTTAGGACAGCCACC
DYMS1	-	AJ621046	20	59	159-211	147-210	F: AACAAATCAAACAGTAAGAG R: CATAGTAACAGATCTTCCTACA
OarFCB304	(TC) ₂₂ (AC) ₁₅	<u>L01535</u>	19	63	150-188	118-148	F: CCCTAGGAGCTTTCAATAAAGAATCGG R: CGCTGCTGTCAACTGGGTCAGGG
OarAE64	(AC) ₂₅	<u>L13869</u>	7	55	122-158	116-148	F: TGCAAGAAGGGCAGACCTTGGAG R: CAGACCACTCTCTCCCTCCACG
OarCP26	(GT) ₂₇	<u>U15698</u>	4	55	120-170	145-201	F: GGCCTAACAGAATTCAGATGATGTTGC R: GTCACCATACTGACGGCTGGTCC
MCMA2	(GT) ₂₅	<u>AF098773</u>	13	52	157-201	160-195	F: TCCAGGATTCATTATGTAGTAGAGCG R: TTTCAAGTGACTTCTCCAGAGAC
MAF64	(GT) ₁₅	<u>M62993</u>	1	63	109-141	113-147	F: AATAGACCATTAGAGAAAACGTTGAC R: CTCATGGAATCAGACAAAAGGTAGG
OarJMP58	(TG) ₂₀	<u>U35058</u>	26	52	133-159	143-178	F- GAAGTCATTGAGGGGTCGCTAACCC R- CTTCATGTTACAGGACTTCTCTG
OarJMP29	(AC) ₂₃	<u>U30893</u>	24	58	96-150	90-141	F- GTATACACGTGGACCCGCTTTGTAC R- GAAGTGGCAAGATTCAGAGGGGAAG
MAF65	(AC) ₂₂	<u>M67437</u>	15	60	123-135	129-145	F: AAAGGCCAGAGTATGCAATTAGGAG R: CCACTCCTCCTGAGAATATAACATG
BM8125	(AC) ₁₈	<u>G18475</u>	17	55	116-122	112-123	F: CTCTATCTGTGGAAAAGGTGGG R: GGGGGTTAGACTTCAACATACG



MCMA2 OarJMP58
 CSSM18, OarAE64,

MCMA26

BM8125

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OarJMP29

(H _o)	(ne)	(n)	(H _E)					
	(D)	(I)						
	Locus	<i>n</i>	<i>ne</i>	<i>H_O</i>	<i>H_E</i>	PIC	<i>I</i>	<i>D</i>
	OarHH55	5	2.71	0.63	0.65	0.58	0.18	0.92
	OarAE101	6	2.94	0.83	0.76	0.70	0.10	0.90
	BM143	5	2.43	0.65	0.68	0.61	0.16	0.94
	BMS2508	7	2.38	0.76	0.70	0.65	0.13	0.87
	LSCV43	7	3.22	0.90	0.76	0.71	0.09	0.91
	CSSM18	4	2.32	0.40	0.61	0.54	0.21	0.79
	OY3	6	2.22	0.66	0.68	0.67	0.11	0.89
	OarFCB304	5	2.43	0.71	0.68	0.62	0.16	0.84
	OarAE64	4	3.86	0.51	0.62	0.61	0.15	0.85
	OarCP26	6	2.56	0.82	0.71	0.65	0.14	0.86
	MCMA2	9	5.21	0.72	0.80	0.78	0.05	0.95
	MAF64	7	6.11	0.80	0.83	0.81	0.04	0.96
	OarJMP58	9	7.12	0.91	0.85	0.84	0.03	0.97
	OarJMP29	7	3.58	0.86	0.72	0.68	0.11	0.89
	MAF65	5	3.21	0.85	0.69	0.64	0.15	0.85
	BM8125	4	3.36	0.82	0.70	0.58	0.19	0.81
	DYMS1	6	5.52	0.74	0.81	0.80	0.05	0.95
	Mean	6	3.48	0.74	0.71	0.66	0.12	0.88
	SD	1.59	1.45	0.14	0.07	0.08	0.05	0.05

DNA

(%)

OarJMP58
CSSM18

0.74 (SD= 0.13) 0.72 (SD=0.07)

PIC

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PIC

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D I

MCMA26

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Caroux-Esplnouse mouflon

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St. Kilda Soay

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3.128E-13

FecB

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(P < /)

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(RIPB)

FecB

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