

( )

**FecB**

\*

**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**

New South

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Wales

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( )

( ) BMPRIB<sup>1</sup> A → G

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( )

FecB

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<sup>2</sup>FecB

PCR-RFLP

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(> %)

%

( )

Archive of SID

FecB

FecB

EDTA

cc

( )

ml DNA

( )

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

...

MgCl<sub>2</sub> PCR

PCR ( )

( )

/ dNTP DNA PCR-RFLP FecB<sup>B</sup>

Taq ( )

MgCl<sub>2</sub> DNA

PCR (Accession no. AF298885)

Primer F; 5-CCAGAGGACAATAGCAAAGCAAA-3

PrimerR;5- GAAGATGTTTTTCATGCCTCATCAACACGGTC-3

PCR

DNA : / dNTP

MgCl<sub>2</sub> / Taq

SCAN ANALYTICS One-D-Scan

PCR °C °C °C

PCR

AvaII

%

(Nei, 1978) (H<sub>E</sub>)

(H<sub>O</sub>)

(Botstein *et al*, 1980) (PIC)

PIC MAI<sup>1</sup>

(Yeh *et al* HET (Ott, 1997) )

PopGene32 *al* 1999) ( )

(Paetkau *et al*; 1995) (I) FecB

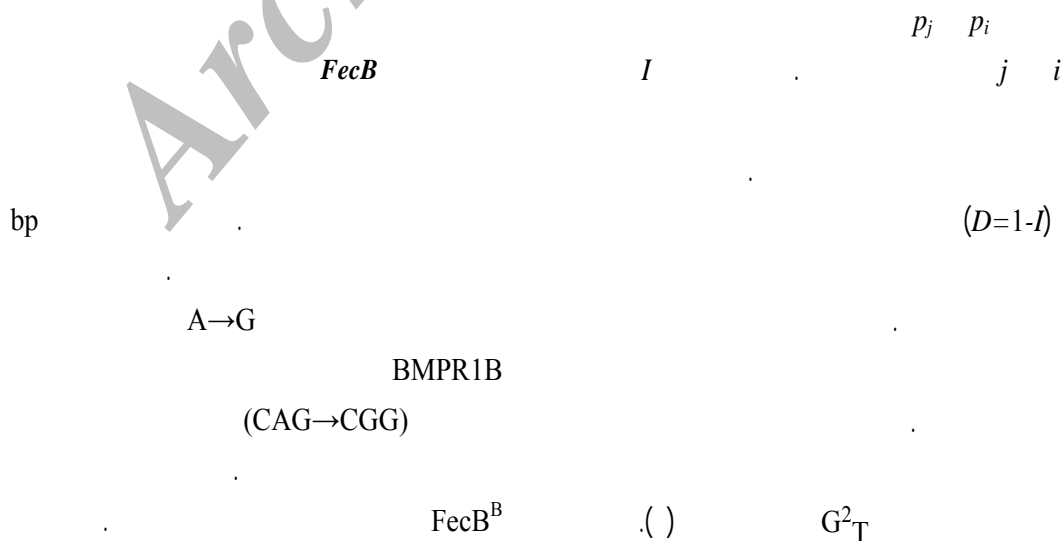
$$I = \sum_i p_i^4 + \sum_i \sum_{j>i} (2p_i p_j)^2$$

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

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

1. Marker Assisted Introgression

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

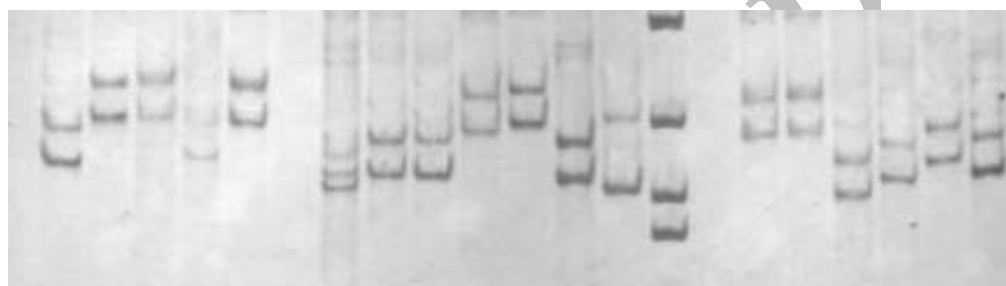


MCMA2 OarJMP58  
 CSSM18, OarAE64,

MCMA26

BM8125

( )



OarJMP29

(H <sub>o</sub> )	(ne)	(n)	(H <sub>E</sub> )				
(D)	(I)	(I)	H <sub>O</sub>	H <sub>E</sub>	PIC	I	D
Locus	n	ne	H <sub>O</sub>	H <sub>E</sub>	PIC	I	D
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

PIC

%

D I

MCMA26

( )

Caroux-Esplnouse mouflon

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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