

Secondary Guidelines

for Development of National
Farm Animal Genetic Resources Management Plans

Measurement of
Domestic Animal Diversity (MoDAD):
Recommended Microsatellite Markers

New Microsatellite marker sets - Recommendations
of joint ISAG/FAO Standing Committee
(to be presented at ISAG 2004)



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*Iniciativa para
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▶ 1. Introduction

The task of the Advisory Group was to compile a list of microsatellites for the analysis of genetic distances within each domestic animal species, based on the recommendations of a working group (Report "An integrated global programme to establish the genetic relationships among the breeds of each domestic animal species" of Animal Production and Health Division, FAO, 1993, ISBN No. 1 86389 060 2). The Working Group recommended the use of twenty-five microsatellite loci. The following criteria to select appropriate microsatellites were issued by the Working Group:

1. The microsatellite markers should be in the public domain,
2. Where possible, microsatellite loci that have been identified in mapping studies should be used, and those selected should preferably be known to be unlinked,
3. The microsatellite variants should be shown to exhibit Mendelian inheritance (highly mutable microsatellite loci may show departures from the Mendelian segregation, and would not be suitable for genetic distance analysis),
4. Each microsatellite locus should exhibit at least four alleles,
5. There should be information on the microsatellites in a published report,
6. Microsatellite loci that can be used on several related species such as cattle, sheep and goats are preferable.

The microsatellite lists below were compiled according to these recommendations whenever possible. Sufficient microsatellite markers are presently available for cattle, chicken, sheep and swine. A list of microsatellites loci for horse and donkey will follow.

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▶ 2. Microsatellite Lists

▶• 2.1. Cattle

(compiled by D. Bradley)

The recommendation of a group of markers for universal use in cattle poses a particular problem which is not yet encountered in the other domestic species. Cattle are already the focus of much research activity and large bodies of data pertaining to genetic variation in different breeds already exist or are in preparation. Sadly, there is little overlap in marker choice between laboratories and consequently joint analyses of data produced will be difficult. Here we seek to list a set of 30 markers which may be recommended for use in such work such that joint analysis of future data will be possible with as much incorporation of previous work as possible.

The following criteria (complementary with those of the above mentioned Working Group), have been employed, but not absolutely, in marker choice.

1. Existence of prior population data
2. Readability of marker
3. Number of alleles
4. Suitability for use in an automated sequencer
5. Possibility of multiplexing
6. Cross-species utility.

These criteria were agreed in a meeting of the EU AIR Concerted Action Group "Analysis of genetic diversity in cattle to preserve future breeding options" which was held in Dublin, 1995. The first 11 markers in the list below were also agreed at that meeting and consequently should be regarded as the most secure inclusions in the following list. Markers 12-16 were recommended by Barbara Harlizius having proved useful in her studies of German cattle breeds, markers 17-24 all feature in a set of multiplex reactions which were communicated to me by Jan de Ruiter and markers 25-30 feature in a subset of the ILSTS loci which have been selected for their suitability for a population study of African breeds by ILRI (communicated by Olivier Hannotte). It was not possible to meet the requirement of cross-species utility, mainly because preference was given to microsatellites for which there were already population data available.

Cattle:

No.	Markers	Chr	Primer sequences (5' - 3')	Reference
1	ETH225 (D9S1)	9	GATCACCTTGCCACTATTTCT ACATGACAGCCAGCTGCTACT	Steffen et al. (1993)
2	ETH152 (D5S1)	5	TACTCGTAGGGCAGGCTGCCTG GAGACCTCAGGGTTGGTGATCAG	Steffen et al. (1993)
3	HEL1 (D15S10)	15	CAACAGCTATTTAACAAGGA AGGCTACAGTCCATGGGATT	Kaukinen & Varvio (1993)
4	ILSTS005 (D10S25)	10	GGAAGCAATGAAATCTATAGCC TGTTCTGTGAGTTTGTAAGC	Brezinsky et al. (1993a)
5	HEL5 ¹ (D21S15)	21	GCAGGATCACTTGTTAGGGA AGACGTTAGTGACATTAAC	Kaukinen & Varvio (1993)
6	INRA005 ² (D12S4)	12	CAATCTGCATGAAGTATAAATAT CTTCAGGCATACCCTACACC	Vaiman et al. (1992)
7	INRA035 (D16S11)	16	ATCCTTTGCAGCCTCCACATTG TTGTGCTTTATGACACTATCCG	Vaiman et al. (1994)
8	INRA063 (D18S5)	18	ATTTGCACAAGCTAAATCTAACC AAACCACAGAAATGCTTGGAAG	Vaiman et al. (1994)
9	MM8 (D2S29)	2	CCCAAGGACAGAAAAGACT CTCAAGATAAGACCACACC	Mommens et al. (1994)
10	MM12 (D9S20)	9	CAAGACAGGTGTTTCAATCT ATCGACTCTGGGGATGATGT	Mommens et al. (1994)
11	HEL9 (D8S4)	8	CCCATTCACTTTCAGAGGT CACATCCATGTTCTCACCAC	Kaukinen & Varvio (1993)
12	CSRM60 (D10S5)	10	AAGATGTGATCCAAGAGAGAGGCA AGGACCAGATCGTGAAAGGCATAG	Moore et al. (1994)
13	CSSM66 ³ (D14S31)	14	ACACAAATCCTTTCTGCCAGCTGA AATTTAATGCACTGAGGAGCTTGG	Barendse et al. (1994)
14	ETH185 (D17S1)	17	TGCATGGACAGAGCAGCCTGGC GCACCCCAACGAAAGCTCCCAG	Steffen et al. (1993)
15	HAUT24 (D22S26)	22	CTCTCTGCCTTTGTCCCTGT AATACACTTTAGGAGAAAAATA	Harlizius (comm. pers.)
16	HAUT27 (D26S21)	26	TTTTATGTTCATTTTTGTACTGG AACTGCTGAAATCTCCATCTTA	Harlizius (comm. pers.)
17	ETH3 (D19S2)	19	GAACCTGCCTCTCCTGCATTGG ACTCTGCCTGTGGCCAAGTAGG	Solinas Toldo et al. (1993)

^{1,2,3,4,5} The genetic distance between the marker pairs on the same chromosomes is not known

Cattle: Continued

No.	Markers	Chr	Primer sequences (5' - 3')	Reference
18	ETH10 ⁴ (D5S3)	5	G TTCAGGACTGGCCCTGCTAACA CCTCCAGCCCCTTTCTCTTCTC	Solinas Toldo et al. (1993)
19	INRA032 ⁵ (D11S9)	11	AAACTGTATTCTCTAATAGCAC GCAAGACATATCTCCATTCTTT	Vaiman et al. (1994)
20	INRA023 (D3S10)	3	GAGTAGAGCTACAAGATAAACTTC TAACTACAGGGTGTTAGATGAACTCA	Vaiman et al. (1994)
21	BM2113 (D2S26)	2	GCTGCCTTCTACCAAATACCC CTTAGACAACAGGGGTTTGG	Bishop et al. (1994)
22	BM1818 (D23S21)	23	AGCTGGGAATATAACCAAAGG AGTGCTTTCAAGTCCATGC	Bishop et al. (1994)
23	BM1824 (D1S34)	1	GAGCAAGGTGTTTTTCCAATC CATTCTCCAAGTCTTCTTGG	Bishop et al. (1994)
24	HEL13 ⁵ (D11S15)	11	TAAGGACTTGAGATAAGGAG CCATCTACCTCCATCTTAAC	Kaukinen & Varvio (1993)
25	ILSTS006 (D7S8)	7	TGTCTGATTTCTGCTGTGG ACACGGAAGCGATCTAAACG	Brezinsky et al. (1993b)
26	ILSTS030 (D2S44)	2	CTGCAGTTCTGCATATGTGG CTTAGACAACAGGGGTTTGG	Kemp et al. (1995)
27	ILSTS034 ⁴ (D5S54)	5	AAGGGTCTAAGTCCACTGGC GACCTGGTTTAGCAGAGAGC	Kemp et al. (1995)
28	ILSTS033 ² (D12S31)	12	TATTAGAGTGGCTCAGTGCC ATGCAGACAGTTTTAGAGGG	Kemp et al. (1995)
29	ILSTS011 ³ (D14S16)	14	GCTTGCTACATGGAAAGTGC CTAAAATGCAGAGCCCTACC	Brezinsky et al. (1993c)
30	ILSTS054 ¹ (D21S44)	21	GAGGATCTTGATTTTGATGTCC AGGGCCACTATGGTACTTCC	Kemp et al. (1995)

^{1,2,3,4,5} The genetic distance between the marker pairs on the same chromosomes is not known

Cattle: Additional information: Four multiplex reactions which include markers above are:

Marker	Approx. size range
ETH10 (D5S3)	210-226 bp
ETH225 (D9S1)	140-156 bp
ETH3 (D19S2)	117-129 bp
INRA005 (D12S4)	119-123 bp
INRA023 (D3S10)	197-223 bp
INRA063 (D18S5)	176-186 bp
HEL13 (D11S5)	198 bp
HEL5 (D21S15)	161 bp
HEL1 (D15S10)	110 bp
BM1818 (D23S21)	270-258 bp
BM1824 (D1S34)	178-190 bp
BM2113 (D2S26)	125-143 bp

Not all criteria have been fulfilled in the case of each marker, primarily in an effort to tie this list in with existing screening efforts. In some cases more than one marker has been selected from a chromosome. This will not be a complication in population genetic study unless linkage is close. However, the relative map positions of some pairs are unknown to the author at present.

Additional and possibly important information is that a set of markers are available commercially from Applied Biosystems and these may assume importance in population study if a wide number of laboratories use them. Several have indicated that they are already in use. The following information was forwarded by Stephen Bates, Perkin Elmer, Applied Biosystems Division, who also indicated that, despite these markers being patented, there should be no problem with researchers who wanted to manufacture their own primers for non-commercial use.

STRs that are optimized for fluorescent multiplexing; two quadruplexes and one triplex.

Cattle

Marker	Fluorochrome	Size Range	Chromosome
TGLA48(D7S26)	Tet (green)	68 – 86	7
TGLA263 (D3S34)	Tet (green)	110 – 130	3
TGLA53(D16S3)	Tet (green)	144 – 178	16
MGTG7(D23S5)	Tet (green)	273 – 300	23
TGLA57 (D1S8)	Fam (blue)	70 – 100	1
TGLA73 (D9S3)	Fam (blue)	102 – 128	9
MGTG4B (D4S5)	Fam (blue)	129 – 164	4
AGLA293 (D5S13)	Fam (blue)	196 – 260	5
TGLA227 (D18S1)	Hex (yellow)	80 – 100	18
TGLA126 (D20S1)	Hex (yellow)	108- 129	20
TGLA122 (D21S6)	Hex (yellow)	130 - 164	21

These primers are included in two published maps (Bishop et al. 1994; Barendse et al 1994) The original reference is: Georges M. Massey J. 1992. Polymorphic DNA markers in Bovidae (World Intellectual PropertyOrg., Geneva) WO Publ. No. 92/ 13102.

An additional development which may influence marker choice is the results from The Cattle Blood Typing Group of ISAG, which is chaired by Jerry Caldwell. This is evaluating 30 microsatellite markers in an attempt to standardize a set that can be used by parentage testing laboratories world-wide.

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►• **2.2. Chicken**

Chicken: (compiled by N. Bumstead)

Marker	Chr.	Primer sequences (5'-3')	Ann. T.	Reference
MCW41	C3	CCCAATGTGCTTGAATAACTTGGG CCAGATTCTCAATAACAATGGCAG	55	Crooijmans et al. (1995)
MCW43	E1	TGACTACTTTGATACGCATGGAGA CACCAAGTAGACGAAAACACATTT	55	Crooijmans et al. (1995)
MCW44	?	AGTCCGAGCTCTGCTCGCCTCATA ACAGTGGCTCAGTGGGAAGTGACC	50	Crooijmans et al. (1995)
MCW48	C4	CGTATAGGAGGGTTTCTGCAGGGA AAGGAGGAACGCACCGCACCTTCT	55	Crooijmans et al. (1995)
MCW49	C6E1	AGCGGCGTTGAGTGAGAGGAGCGA TCCCAACCCGCGGAGAGCGCTAT	55	Crooijmans et al. (1995)
MCW50	?	GGTGTCCGCACCCCGGAGCTTCTT GCAGCATCGCGCAGCACCGCGGAT	55	Crooijmans et al. (1995)
MCW51	C3E6	GGAACAAGCTCTTTCTTCTTCCCG TCATGGAGGTGCTGGTACAAAGAC	50	Crooijmans et al. (1995)
MCW59	C1E2	AAGTGCCTTTGCTATCCTGATTGG AACTCCTATTGTGCAGCAGCTTAT	55	Crooijmans et al. (1995)
MCW71	?	TGGCGTTATTTCAAACGACCGTA GCGGTTCGTTTCGGTCTTATTTAA	55	Crooijmans et al. (1995)
MCW73	C33E46	TATTTACCCACGGGGACGAATAC AGGGTGCTGAGAGCTGCCAATGTC	55	Crooijmans et al. (1995)
MCW75	E unlinked	CGTCAAGCCAGATGCTGATGAGTG ATTCCAACCAGAAGTTTGAAGTCGC	55	Crooijmans et al. (1995)
MCW1	C4E28	ACTGTCACAGTGGGGTTCATGGACA ACACGTCCTGTGTACATGCCTGT	50	Crooijmans et al. (1995)
MCW2	C4	TCCAGAGACAGTTGCTCCACATTC GCAAGTTAGTTATTGTAGGGGCTC	50	Crooijmans et al. (1994)
MCW4	E2	GGATTACAGCACCTGAAGCCACTA AAACCAGCCATGGGTGCAGATTGG	55	Crooijmans et al. (1995)
MCW5	C11E5	ACCTCCTGCTGGCAAATAAATTGC TCACTTTAGCTCCATCAGGATTCA	55	Crooijmans et al. (1994)

Continued

Chicken: Continued

Marker	Chr.	Primer sequences (5'-3')	Ann. T.	Reference
MCW14	E11	AAAATATTGGCTCTAGGAACTGTC ACCGGAAATGAAGGTAAGACTAGC	55	Crooijmans et al. (1994)
MCW16	E2	ATGGCGCAGAAGGCAAAGCGATAT TGGCTTCTGAAGCAGTTGCTATGG	50	Crooijmans et al. (1994)
ADL102	C30E29	TTCCACCTTTCTTTTTTATT GCTCCACTCCCTTCTAACCC	47	Cheng et al. (1995)
ADL136	E5C10	TGTCAAGCCCATCGTATCAC CCACCTCCTTCTCCTGTTCA	52	Cheng et al. (1995)
ADL158	C30E29	TGGCATGGTTGAGGAATACA TAGGTGCTGCACTGGAAATC	52	Cheng et al. (1995)
ADL171	E43	ACAGGATTCTTGAGATTTTT GGTCTTAGCAGTGTTTGT	46	Cheng et al. (1995)
ADL172	E42	CCCTACAACAAAGAGCAGTG CTATGGAATAAAATGGAAAT	49	Cheng et al. (1995)
ADL176	E6	TTGTGGATTCTGGTGGTAGC TTCTCCCGTAACACTCGTCA	52	Cheng et al. (1995)
ADL210	E30	ACAGGAGGATAGTCACACAT GCCAAAAAGATGAATGAGTA	46	Cheng et al. (1995)
ADL267	C3E6	AAACCTCGATCAGGAAGCAT GTTATTCAAAGCCCCACCAC	50	Cheng et al. (1995)

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▶• 2.3. Sheep

(compiled by A. Crawford)

The marker had to have the following criteria to be included on the list:

1. Be amplified by a common PCR program. The following "Touchdown" programme is used:

3 cycles	95 C	45 secs
	60 C	1 min
3 cycles	95 C	45 secs
	57 C	1 min
3cycles	95 C	45 secs
	54 C	1 min
3 cycles	95 C	45 secs
	51 C	1 min
20 cycles	92 C	45secs
	48 C	1 min

There is no extension step. The buffer is published with the marker reports (e.g., Ede et al., 1994b). To detect the PCR product one of the primers is end labeled with either P33 or P32.

2. Have a minimum of five alleles and a PIC greater than 0.6,
3. Most importantly have clean, easily read and scored PCR products.

Sheep:

Marker	Chr	Primer sequences (5' - 3')*	Reference
BM1314*	22	TTCCTCCTCTTCTCTCCAAAC ATCTCAAACGCCAGTGTGG	Bishop et al. (1994)
BM6506*	1	GCACGTGGTAAAGAGATGGC AGCAACTTGAGCATGGCAC	Bishop et al. (1994)
BM6526*	26	CATGCCAAACAATATCCAGC TGAAGGTAGAGAGCAAGCAGC	Bishop et al. (1994)
BM757*	9	TGGAAACAATGTAAACCTGGG TTGAGCCACCAAGGAACC	Bishop et al. (1994)
BM8125*	17	CTCTATCTGTGGAAAAGGTGGG GGGGGTTAGACTTCAACATACG	Bishop et al. (1994)
BM827*	3	GGGCTGGTCGTATGCTGAG GTTGGACTTGCTGAAGTGACC	Bishop et al. (1994)
CSSM31*	23	CCAAGTTTAGTACTTGTAAAGTAGA GACTCTCTAGCACTTTATCTGTGT	Moore et al. (1994)
CSSM47*	2	TCTCTGTCTCTATCACTATATGGC CTGGGCACCTGAAACTATCATCAT	Moore et al. (1994)
HUJ616*	13	TTCAAACACTACACATTGACAGGG GGACCTTTGGCAATGGAAGG	Barendse et al. (1994)
ILSTS002*	14	TCTATACACATGTGCTGTGC CTTAGGGGTGAAGTGACACG	Kemp et al. (1992)
OarAE129	5	AATCCAGTGTGTGAAAGACTAATCCAG GTAGATCAAGATATAGAATATTTTTCAACACC	Penty et al. (1993)
OarCP20	21	GATCCCCTGGAGGAGGAAACGG GGCATTTCATGGCTTTAGCAGG	Ede et al. (1994a)
OarCP34	3	GCTGAACAATGTGATATGTTTCAGG GGGACAATACTGTCTTAGATGCTGC	Ede et al. (1994b)
OarCP38	10	CAACTTTGGTGCATATTCAAGGTTGC GCAGTCGCAGCAGGCTGAAGAGG	Ede et al. (1994b)
OarFCB128	2	CAGCTGAGCAACTAAGACATACATGCG ATTAAAGCATCTTCTCTTTATTTCTCGC	Buchanan & Crawford (1993)
OarFCB20	2	AAATGTGTTTAAGATTCCATACA GTG GGAAAACCCCATATATACCTATAC	Buchanan et al (1994)
OarFCB48	17	GAGTTAGTACAAGGATGACAAGAGGCAC GACTCTAGAGGATCGCAAAGAACCAG	Buchanan et al. (1994)

Continued

Sheep: Continued

Marker	Chr	Primer sequences (5' - 3')*	Reference
OarHH35	4	AATTGCATTCAGTATCTTTAACATCTGGC ATGAAAATATAAAGAGAATGAACCACACGG	Henry et al. (1993)
OarHH41	10	TCCACAGGCTTAAATCTATATAGCAACC CCAGCTAAAGATAAAAGATGATGTGGGAG	Henry et al. (1993)
OarHH47	18	TTTATTGACAAACTCTCTTCTAACTCCACC GTAGTTATTTAAAAAATATCATACCTCTTAAGG	Henry et al. (1993)
OarHH64	4	CGTTCCTCACTATGGAAAGTTATATATGC CACTCTATTGTAAGAATTTGAATGAGAGC	Henry et al. (1993)
OarJMP29	24	GTATACACGTGGACACCGCTTTGTAC GAAGTGGCAAGATTCAGAGGGGAAG	Penty et al. (in prep.)
OarJMP8	6	CGGGATGATCTTCTGTCCAAATATGC CATTTGCTTTGGCTTCAGAACCAGAG	Penty et al. (in prep.)
OarVH72	25	CTCTAGAGGATCTGGAATGCAAAGCTC GGCCTCTCAAGGGGCAAGAGCAGG	Pierson et al.(1993)
OMHC1	20	ATCTGGTGGGCTACAGTCCATG GCAATGCTTTCTAAATTCTGAGGAA	Groth & Wetherall (1994)
RM4*	15	CAGCAAATATCAGCAAACCT CCACCTGGGAAGGCCTTTA	Kossarek et al. (1993)
TGLA137*/**	5	GTTGACTTGTTAATCACTGACAGCC CCTTAGACACACGTGAAGTCCAC	Georges & Massey (1992)

* Bovine microsatellite

** The primer sequences for the TGLA markers were designed from the sequence provided in the patent (Georges & Massey, 1992) so they may be different from the published bovine primer sequences for the same marker.

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►• 2.4. Swine

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1. Twenty-seven *** (high quality) or ** (medium quality) markers were selected. There are 2 additional markers to the requested 25, which will allow 2 markers to be discarded if necessary. Preference was given to highly polymorphic markers.
2. One marker was selected on each chromosome (except chromosome 18), and if possible one marker on each arm of the longer chromosomes. No markers are found at a distance of less than 35 cm.
3. Markers for which null alleles have been reported and markers which yielded patterns which could not be unambiguously interpreted were avoided.
4. Preference was given to markers that can be analysed on automatic sequencers (tested on ABI sequencer in at least one laboratory). It means that no artifactual bands are amplified and that the markers can be multiloaded (this should be possible either using manual or automatic sequencers).
5. All markers have been grouped in 9 sets of markers analysable on 3 gels on ABI sequencers. The difference in size between two adjacent markers is at least 30 bp (in order to allow the identification of new alleles outside of the fragment minimum-maximum size range).

6. Control DNA for correct sizing of alleles may be obtained through D. Milan.

Swine: Sorted by set:

Marker	Set	Chr.	Proposed by		Quality		Size		Difference
			T	W	T	W	Min	Max	
CGA	1	1p		X		***	250	320	
S0101	1	7		X	***	***	197	216	34
S0215	1	13	X		***		135	169	28
S0355	2	15	X		***		243	277	
SW911	2	9	X	X	***	***	153	177	66
SW936	2	15	X		***		80	117	36
S0068	3	13		X		***	211	260	
SW632	3	7	X		***		159	180	31
SW24	3	17	X		***		96	121	38
S0227	4	4	X	X	**	**	231	256	
S0225	4	8	X	X	***	***	170	196	35
SW122	4	6		X		***	110	122	48
S0090	5	12	X	X	***	***	244	251	
S0226	5	2q	X		***		181	205	45
SW951	5	10	X		**		125	133	48
S0228	6	6	X		**		222	249	
S0218	6	X	X		***		164	184	38
S0178	6	8	X		***		110	124	
S0005	7	5	X	X	***	***	205	248	
S0386	7	11	X		**		156	174	31
SW72	7	3p		X	***	***	100	116	40
S0002	8	3q	X		***		190	216	
SW857	8	14	X	X	***	***	144	160	30
S0026	8	16		X		**	92	106	38
IGF1	9	5	X	X	***	***	197	209	35
S0155	9	1q	X		***		150	166	31
SW240	9	2p	X	X	***	***	96	115	35

T : Toulouse; W : Wageningen.

Difference: Difference in bp between two adjacent markers belonging to the same set.

Swine: Sorted by chromosome:

Marker	Chr.	Set	Proposed by		Quality		Size		Distance cM
			T	W	T	W	Min	Max	
CGA	1p	1		X		***	250	320	-
S0155	1q	9	X		***		150	166	50
SW240	2p	9	X	X	***	***	96	115	-
S0226	2q	5	X			***	181	205	50
SW72	3p	7		X	***	***	100	116	-
S0002	3q	8	X		***		190	216	105
S0227	4	4	X	X	**	**	231	256	-
IGF1	5	9	X	X	***	***	197	209	-
S0005	5	7	X	X	***	***	205	248	40
SW122	6	4		X		***	110	122	35
S0228	6	6	X		**		222	249	-
S0101	7	1		X	***	***	197	216	-
SW632	7	3	X		***		159	180	60
S0225	8	4	X	X	***	***	170	196	-
S0178	8	6	X		***		110	124	>50
SW911	9	2	X	X	***	***	153	177	-
Sw951	10	5	X		**		125	133	-
S0386	11	7	X		**		156	174	-
S0090	12	5	X	X	***	***	244	251	-
S0215	13	1	X		***		135	169	-
S0068	13	3		X		***	211	260	55
SW857	14	8	X	X	***	***	144	160	-
S0355	15	2	X		***		243	277	-
SW936	15	2	X		***		80	117	70
S0026	16	8		X		**	92	106	-
SW24	17	3	X		***		96	121	-
S0218	X	6	X		***		164	184	-

T: Toulouse W: Wageningen

Swine:

Marker	Sequence of primers (5'-3')	Fluorochrome labelling	Ann. Temp./ MgC12(mM)	Reference
CGA	ATAGACATTATGTCCGTTGCTGAT GAACTTTCACATCCCTAAGGTCGT	X	62 / 1.5	(1, 2)
IGF1	GCTTGGATGGACCATGTTG CATATTTTTCTGCATAACTTGAACCT	X	58 / 1.5	(3, 1, 2, 4)
S0002	GAAGCCCAAAGAGACAACCTGC GTTCTTTACCCACTGAGCCA	X	62 / 1.5	(5, 4, 2, 6)
S0005	TCCTTCCCTCCTGGTAACTA GCACTTCCCTGATTCTGGGTA	X	58 / 1.5	(5, 1, 4, 2)
S0026	AACCTTCCCTTCCCAATCAC CACAGACTGCTTTTTACTCC	X	55 / 1.5	(2, 7)
S0068	AGTGGTCTCTCTCCCTCTTGCT CCTTCAACCTTTGAGCAAGAAC	X	62 / 1.5	(5, 1, 4, 2)
S0090	CCAAGACTGCCTTGTAGGTGAATA GCTATCAAGTATTGTACCATTAGG	X	58 / 1.5	(8, 4, 2)
S0101	GAATGCAAAGAGTTCAGTGTAGG GTCTCCCTCACACTTACCGCAG	X	60 / 1.5	(1)
S0155	TGTTCTCTGTTTCTCCTCTGTTG AAAGTGGAAAGAGTCAATGGCTAT	X	55 / 1.5	(1, 2)
S0178	TAGCCTGGGAACCTCCACACGCTG GGCACCAGGAATCTGCAATCCAGT	X	58 / 1.5	(1)
S0215	TAGGCTCAGACCCTGCTGCAT TGGGAGGCTGAAGGATTGGGT	X	55 / 4.0	(9, 2)
S0218	GTGTAGGCTGGCGGTTGT CCCTGAAACCTAAAGCAAAG	X	55 / 2.0	(9, 2)
S0225	GCTAATGCCAGAGAAATGCAGA CAGGTGGAAAGAATGGAATGAA	X	55 / 4.0	(9, 2)
S0226	GCACTTTTAACTTTTCATGATACTCC GGTTAACTTTTNCCCCAATACA	X	55 / 4.0	(9, 2)
S0227	GATCCATTTATAATTTTAGCACAAAGT GCATGGTGTGATGCTATGTCAAGC	X	55 / 4.0	(9, 2)
S0228	GGCATAGGCTGGCAGCAACA AGCCCACCTCATCTTATCTACT	X	55 / 4.0	(9, 2)
S0355	TCTGGCTCCTACACTCCTTCTTGATG TTGGGTGGGTGCTGAAAAATAGGA	X	55 / 4.0	(10)

Continued

Swine: Continued

Marker	Sequence of primers (5'-3')	Fluorochrome labelling	Ann. Temp./ MgC12(mM)	Reference
S0386	TCCTGGGTCTTATTTTCTA TTTTATCTCCAACAGTAT	X	48 / 3.0	(11)
SW24	CTTTGGGTGGAGTGTGTGC ATCCAAATGCTGCAAGCG	X	58 / 1.5	(4)
SW122	TTGTCTTTTTATTTTGCTTTTGG CAAAAAAGGCAAAAGATTGACA		58 / 1.5	(4)
SW857	AGAAATTAGTGCCTCAAATTGG AAACCATTAAGTCCCTAGCAAA	X	58 / 1.5	(4)
SW240	TGGGTTGAAAGATTTCCCAA GGAGTCAGTACTTTGGCTTGA	X	58 / 1.5	(4)
SW632	ATCAGAACAGTGCGCCGT TTTGAAAATGGGGTGTTTCC	X	58 / 1.5	(4)
SW72	TGAGAGGTCAGTTACAGAAGACC GATCCTCCTCCAAATCCCAT	X	58 / 1.5	(4)
SW911	CTCAGTTCTTTGGGACTGAACC CATCTGTGGAAAAAAAAAAGCC	X	60 / 1.5	(4)
SW936	TCTGGAGCTAGCATAAGTGCC GTGCAAGTACACATGCAGGG	X	58 / 1.5	(4, 10)
SW951	TTTCACAACTCTGGCACCAG GATCGTGCCCAAATGGAC	X	58 / 1.5	(4)

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Buffalos

Donkeys

Horses

Goats

Pigs

Sheep

Chicken

Ducks

Camelids

Cattle

<i>Nr</i>	<i>Name</i>	<i>Chr*</i>	<i>Map</i>	<i>Primer sequence (5' -> 3') ForwardReverse</i>	<i>Annealing temperature</i>	<i>GenBank (Accession Number</i>	<i>Multiplex</i>	<i>No. of known alleles, and allele range</i>	<i>Diversity studies</i>
1.	CSSM033	17 (17)		CAC TGT GAA TGC ATG TGT GTG AGC CCC ATG ATA AGA GTG CAG ATG ACT	65	U03805		11 154- 175	R1,R2 R3,
2.	CSSM038	11 (10)		TTC ATA TAA GCA GTT TAT AAA CGC ATA GGA TCT GGT AAC TTA CAG ATG	55	U03817		13 163- 187	R1,R2 R3,
3.	CSSM043	1p (27)		AAA ACT CTG GGA ACT TGA AAA CTA GTT ACA AAT TTA AGA GAC AGA GTT	55	U03824		12 222- 258	R1,R2 R3,
4.	CSSM047	3q (8)		TCT CTG TCT CTA TCA CTA TAT GGC CTG GGC ACC TGA AAC TAT CAT CAT	55	U03821		20 127- 162	R1,R2 R3,

5.	CSSM036	1p (27)		GGA TAA CTC AAC CAC ACG TCT CTG AAG AAG TAC TGG TTG CCA ATC GTG	55	U03827		7 162- 176	R1,R2 R3,
6.	CSSM019	1q (1)		TTG TCA GCA ACT TCT TGT ATC TTT TGT TTT AAG CCA CCC AAT TAT TTG	55	U03794		15 131- 161	R1, R3,
7.	CSRM060	11 (10)		AAG ATG TGA TCC AAG AGA GAG GCA AGG ACC AGA TCG TGA AAG GCA TAG	60	AF232758		15 95-135	R1,R2
8.	CSSM029	9(7)		CGT GAG AAC CGA AAG TCA CAC ATT C GCT CCA TTA TGC ACA TGC CAT GCT	55	U03807		11 174- 196	R1, R3,
9.	CSSM041	21 (22)		AAT TTC AAA GAA CCG TTA CAC AGC AAG GGA CTT GCA GGG ACT AAA ACA	55	U03816		11 129- 147	R1, R3,

10.	CSSM057	9(7)		GTC GCT GGA TAA ACA ATT TAA AGT TGT GGT GTT TAA CCC TTG TAA TCT	60	U03840		11 102- 130	R1, R3,
11.	BRN	11 (10)		CCT CCA CAC AGG CTT CTC TGA CTT CCT AAC TTG CTT GAG TTA TTG CCC	60	X59767		10 121- 147	R1, R3,
12.	CSSM032	1q (1)		TTA TTT TCA GTG TTT CTA GAA AAC TAT AAT ATT GCT ATC TGG AAA TCC	55	U03811		9 208- 224	R1, R3,
13.	CSSM008	-		CTT GGT GTT ACT AGC CCT GGG GAT ATA TTT GCC AGA GAT TCT GCA	55	U03796		7 179- 193	R1, R3,
14.	CSSM045	2q (2)		TAG AGG CAC AAG CAA ACC TAA CAC TTG GAA AGA TGC AGT AGA ACT CAT	60	U03830		7 102- 122	R1, R3,
15.	CSSM022	4q (5)		TCT CTC TAA TGG AGT TGG TTT TTG ATA TCC CAC TGA GGA TAA GAA TTC	55-60	U03806		6 203- 213	R1, R3,

16.	CSSM046	11 (10)		GGC TAT TAA CTG TTT TCT AGG AAT TGC ACA ATC GGA ACC TAG AAT ATT	55	U03834		6 152- 160	R1 , R3 ,
17.	CSSM013	5p (29)		ATA AGA GAT TAC CCT TCC TGA CTG AGG TAA ATG TTC CTA TTT GCT AAC	55	U03841		5 162- 172	R1 , R3 ,
18.	ETH003	3p (19)		GAA CCT GCC TCT CCT GCA TTG G ACT CTG CCT GTG GCC AAG TAG G	65	Z22744		19 96-192	R2 R4 ,
19.	CSSM061	-		AGG CCA TAT AGG AGG CAA GCT TAC TTC AGA AGA GGG CAG AGA ATA CAC	60	-		12 100- 126	R1 ,
20.	BMC1013	3p (19)		AAA AAT GAT GCC AAC CAA ATT TAG GTA GTG TTC CTT ATT TCT CTG G	54	G18560		10 217- 239	R2

21.	DRB3	2p (23)		GAG AGT TTC ACT GTG CAG CGC GAA TTC CCA GAG TGA GTG AAG TAT CT	50-55	M30012		9 142- 198	R2
22.	CSSM062	-		GTT TAA ACC CCA GAT TCT CCC TTG AGA TGT AAC AGC ATC ATG ACT GAA	55	-		8 124- 136	R1,
23.	CSSME070	3p (19)		TTC TAA CAG CTG TCA CTC AGG C ATA CAG ATT AAA TAC CCA CCT G	50-55	Af004364		8 119- 139	R2
24.	ETH121	2q (2)		CCA ACT CCT TAC AGG AAA TGT C ATT TAG AGC TGG CTG GTA AGT G	59	Z14037		7 182- 198	R2
25.	ILSTSO33	13 (12)		TAT TAG AGT GGC TCA GTG CC ATG CAG ACA GTT TTA GAG GG	55	L37213		6 126- 138	R3,

26.	ILSTS005	11 (10)		GGA AGC AAT GAA ATC TAT AGC C TGT TCT GTG AGT TTG TAA GC	55	L23481		5 173- 186	R2 R3 , R4 ,
27.	ILSTS030	2q (2)		CTG CAG TTC TGC ATA TGT GG CTT AGA CAA CAG GGG TTT GG	55	L37212		5 146- 158	R3 ,
28.	ILSTS008	15 (14)		GAA TCA TGG ATT TTC TGG GG TAG CAG TGA GTG AGG TTG GC	58	L23483		4 168- 176	R3 ,
29.	RM099	3p (19)		CCA AAG AGT CTA ACA CAA CTG AG ATC CGA ACC AAA ATC CCA TCA AG	60	G29087		4 87-119	R2 ,
30.	HMH1R	21 (22)		GGC TTC AAC TCA CTG TAA CAC ATT TTC TTC AAG TAT CAC CTC TGT GGC C	60	D10197		3 169- 187	R1 ,

* Cattle chromosome assignments (in parentheses) - as given at

www.thearkdb.org and www.cgd.csiro.au/cgi-bin/cgdlose , and converted to River Buffalo chromosome assignments

according to Di Berardino and Iannuzzi (1984) and El Nahas et al. 2001. NOTE: For Swamp Buffalo, 2n = 48, due to translocation of chromosome 9 to chromosome 4.

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Egyptian buffalo populations. *Livestock Production Science* 70: 203-211

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Multiplex:

none developed.

	Marker List for the Donkey								
	Name	HorseChr.	HorseMap	Primer sequence (5' -> 3') Forward Reverse	Annealing temperature	Genbank (Accession Number)	Multiplex	Allele range	Diversity studies
1.	HMS07	1	M1	CAGGAAACTCATGTTGATACCATC TGTTGTTGAAACATACCTTGACTGT	58°C	X74636	X1	165 – 183	R1, R3
2.	HMS06	4	M4	GAAGCTGCCAGTATTCAACCATTG CTCCATCTTGTGAAGTGAACTCA	58°C	X74635	X1	153 – 169	R1, R3
3.	HTG07	4	M4	CCTGAAGCAGAACATCCCTCCTTG ATAAAGTGTCTGGGCAGAGCTGCT	58°C	AF142607	X4	272 – 297	R1, R3
4.	AHT05	8	M8	ACGGACACATCCCTGCCTGC GCAGGCTAAGGGGGCTCAGC	58°C	None	X1	130 – 146	R1, R3
5.	HMS03	9	M9	CCAACCTCTTTGTCCACATAACAAGA CCATCCTCACTTTTTCACTTTGTT	58°C	X74632	X2	150 – 170	R1, R3
6.	HMS02	10	M10	ACGGTGGCAACTGCCAAGGAAG CTTGACAGTCGAATGTGATATAAATG	58°C	X74631		218 – 238	R1, R3
7.	HTG06	15	M15	CCTGCTTGGAGGCTGTGATAAGAT GTTCACTGAATGTCAAATCTGCT	58°C	None		84 – 106	R1, R3
8.	HTG10	21	M21	CAATTCGCCGCCACCCCGGCA TTTTTATTCTGATCTGCACATTT	54°C	AF169294	X2	93 – 113	R1, R3
9.	AHT04	24	M24	AACCGCCTGAGCAAGGAAGT CCCAGAGAGTTTACCCT	58°C	None	X1	148 – 164	R1, R3
10.	ASB17	2	M2	GAGGGCGGTACCTTTGTACC ACCAGTCAGGATCTCCACCG	58°C	X93531	X1	91 – 109	R1, R3
11.	ASB23	3	M3	GAGGTTTGTAAATTGGAATG GAGAAGTCATTTTTAACACCT	58°C	X93537	X1	128 – 154	
12.	LEX33	4	M4	TTTAATCAAAGGATTCAGTTG TTTCTCTCAGGTGTCCTC	58°C	AF075635	X2	203 – 217	
13.	LEX34	5	M5	GCGGAGGTAAGAAGTGCTAG GGCCTAAGATGAGGGTGAA	54°C	AF075636	X3	245 – 255	
14.	SGCV28	7	M7	CTGTGGCAGCTGTCACTTTGG CCCAATTCAGCCAGCTTGC	60°C	U90604		151 – 163	
15.	LEX68	11	M11	AAATCCCGAGCTAAAAATGTA TAGGAAGATAGGATCACAAGG	54°C	None		162 – 174	
16.	COR058	12	M12	GGGAAGGACGATGAGTGAC CACCAGGCTAAGTAGCCAAAAG	56°C	AF108375	X4	210 – 230	
17.	COR069	13	M13	AGCCACCAGTCTGTTCTCTG AATGTCCTTTGGTGGATGAAC	56°C	AF142606	X3	273 – 279	
18.	VHL209	14	M14	TCTTACATCCTTCCATTACAATA TGATACATATGTACGTGAAAAGGAT	56°C	Y08451	X5	84 – 96	
19.	ASB02	15	M15	CCTTCCGTAGTTTAAAGCTTCTG CACAACCTGAGTTCTCTGATAGG	54°C	X93516	X2	222 – 254	R1, R2, R3
20.	HMS20	16	M16	TGGGAGAGGTACCTGAAATGTAC GTTGCTATAAAAAATTGCTCCCTAC	58°C	None		116 – 140	
21.	COR007	17	M17	GTGTTGGATGAAGCGAATGA GACTTGCCTGGCTTTGAGTC	56°C	AF083450		156 – 170	
22.	LEX54	18	M18	TGCATGAGCCAATTCCTTAT TGGACAGATGACAGCAGTTC	55°C	AF075656	X5	165 – 177	

23.	LEX73	19	M19	CCCTAGAGCCATCTCTTTACA CAGATCCAGACTCAGGACAG	54°C	AF213359	234 – 264
24.	COR022	22	M22	AAGACGTGATGGGAAATCAA AGAAAGTTTTCAAATGTGCCA	56°C	AF101391	254 – 264
25.	LEX63	23	M23	CGGGGTGTGCATCTCTTAGG TGGCGAATGCTGAATCTGG	54°C	AF075663	241 – 249
26.	COR018	25	M25	AGTCTGGCAATATTGAGGATGT AGCAGCTACCCTTTGAATACTG	56°C	AF083461	X6 249 – 271
27.	COR071	26	M26	CTTGGGCTACAACAGGAATA CTGCTATTTCAAACACTTGGA	56°C	AF142608	X6 190 – 202
28.	HMS45	27	M27	TGTTACAGGTATTGGTAAACTGTGC GGAACAAGAAGAAATCACTAATGTC	58°C	U89813	185 – 197
29.	NVHEQ054	28	M28	AGATGTCCACCTTCTCGCTG CGGGGCTTTTAGGAGGTAATA	62°C	AJ245763	172 – 186
30.	COR082	29	M29	GCTTTTGTCTCAATCCTAGC TGAAGTCAAATCCCTGCTTC	58°C	AF154935	192 – 226

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Multiplexes:

1. Multiplex Master Mix : AHT04+AHT05+ASB17+ASB23+HMS06+HMS07
2. Multiplex Master Mix : ASB02+HTG10+HMS03+LEX33
3. Multiplex Master Mix : LEX34+COR069
4. Multiplex Master Mix : COR070+COR058
5. Multiplex Master Mix : VHL209+LEX54
6. Multiplex Master Mix : COR018+COR071

	Marker List for the Horse								
	Name	Chr.	Map	Primer sequence (5' -> 3')	Annealing temperature	Genbank (Accession Number)	Multiplex	Allele range	Diversity studies
				Forward					
				Reverse					
1.	HMS07	1	M1	CAGGAAACTCATGTTGATACCATC TGTTGTTGAAACATACCTTGACTGT	60°C	X74636 [SW1]	X1	165 – 183	R1,R2,R3, R4,R5,R6, R7,R8
2.	HMS06	4	M4	GAAGCTGCCAGTATTCAACCATTG CTCCATCTTGTGAAGTGTAACCTCA	60°C	X74635	X1	153 – 169	R1,R2,R3, R4,R5,R6,R7
3.	HTG07	4	M4	CCTGAAGCAGAACATCCCTCCTTG ATAAAGTGTCTGGGCAGAGCTGCT	60°C	None		120 – 130	R1,R2,R3, R4,R5,R6, R7,R8
4.	AHT05	8	M8	ACGGACACATCCCTGCCTGC GCAGGCTAAGGGGGCTCAGC	60°C	None	X1	130 – 146	R1,R2,R3, R4,R6,R7
5.	HTG04	9	M9	CTATCTCAGTCTTCATTGCAGGAC CTCCCTCCCTCCCTCTGTTCTC	55°C	None	X1	127 – 141	R1,R2,R3, R4,R5,R6, R7,R8
6.	HMS02	10	M10	ACGGTGGCAACTGCCAAGGAAG CTTGACAGTCGAATGTGTATTAAATG	60°C	X74631		218 – 238	R1,R2,R3, R4,R5,R6, R7,R8
7.	ASB02	15	M15	CCTTCCGTAGTTTAAGCTTCTG CACAACCTGAGTTCTCTGATAGG	55°C	X93516	X2	222 – 254	
8.	HMS03	9	M9	CCAACTCTTTGTACATAACAAGA CCATCCTCACTTTTTCACTTTGTT	60°C	X74632	X2	150 – 170	R4,R5,R6, R7,R8
9.	HTG06	15	M15	CCTGCTTGGAGGCTGTGATAAGAT GTTCACTGAATGTCAAATTCCTGCT	60°C	None			
10.	HTG10	21	M21	CAATTCCCGCCCCACCCCGGCA TTTTTATTCTGATCTGTCACATTT	55°C	AF169294	X2		
11.	AHT04	24	M24	AACCGCCTGAGCAAGGAAGT CCCAGAGAGTTTACCCT	60°C	None	X1		
12.	VHL20	30	M30	CAAGTCTCTTACTTGAAGACTAG AACTCAGGGAGAATCTTCCTCAG	60°C	None	X1		
13.	ASB17	2	M2	GAGGGCGGTACCTTTGTACC ACCAGTCAGGATCTCCACCG	60°C	X93531	X1	91 – 109	R1,R2, R3,R7
14.	ASB23	3	M3	GAGGTTTGTAAATGGAATG GAGAAGTCATTTTTAACACCT	60°C	X93537	X1	128 – 154	R7
15.	LEX33	4	M4	TTTAATCAAAGGATTCAGTTG TTTCTCTCAGGTGTCCTC	60°C	AF075635	X2	203 – 217	R7
16.	UCDEQ425	28	M28	AGCTGCCTCGTTAATTCA CTCATGTCCGCTTGTCTC	60°C	U67406			
17.	LEX34	5	M5	GCGGAGGTAAGAAGTGGTAG GGCCTAAGATGAGGGTGAA	55°C	AF075636	X3	245 – 255	
18.	SGCV28	7	M7	CTGTGGCAGCTGTCATCTTGG CCCAATTCCAGCCAGCTTGC	62°C	U90604		151 – 163	
19.	COR058	12	M12	GGGAAGGACGATGAGTGAC CACCAGGCTAAGTAGCCAAAG	58°C	AF108375	X4	210 – 230	
20.	COR069	13	M13	AGCCACCAGTCTGTTCTCTG AATGTCTTTGGTGGATGAAC	58°C	AF142606	X3	273 – 279	

21.	VHL209	14	M14	TCTTACATCCTTCCATTACA TGATACATATGTACGTGAAAGGAT	57°C	Y08451	X5	84 – 96
22.	COR007	17	M17	GTGTTGGATGAAGCGAATGA GACTTGCCTGGCTTTGAGTC	58°C	AF083450		156 – 170
23.	LEX54	18	M18	TGCATGAGCCAATTCCTTAT TGGACAGATGACAGCAGTTC	55°C	AF075656	X5	165 – 177
24.	LEX73	19	M19	CCCTAGAGCCATCTCTTTACA CAGATCCAGACTCAGGACAG	55°C	AF213359		234 – 264
25.	COR022	22	M22	AAGACGTGATGGGAAATCAA AGAAAGTTTTCAAATGTGCCA	58°C	AF101391		254 – 264
26.	LEX63	23	M23	CGGGGTGTGCATCTCTTAGG TGGCGAATGCTGAATCTGG	55°C	AF075663		241 – 249
27.	COR018	25	M25	AGTCTGGCAATATTGAGGATGT AGCAGCTACCCTTTGAATACTG	58°C	AF083461	X6	249 – 271
28.	COR071	26	M26	CTTGGGCTACAACAGGGAATA CTGCTATTTCAAACACTTGGGA	58°C	AF142608	X6	190 – 202
29.	HMS45	27	M27	TGTTACAGGTATTGGTAAACTGTGC GGAACAAGAAGAAATCACTAATGTC	60°C	U89813		185 – 197
30.	COR082	29	M29	GCTTTTGTFTTCTCAATCCTAGC TGAAGTCAAATCCCTGCTTC	59°C	AF154935		192 – 226

References:

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2. Bjornstad, G., N.O. Nilsen and K.H. Roed. 2003, Genetic relationship between Mongolian and Norwegian horses? *Animal Genetics* 34:55-58.
3. Bjornstad, G. and K.H. Roed. 2001. Breed demarcation and potential for breed allocation of horses assessed by microsatellite markers. *Animal Genetics.* 32:59-65.
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Multiplexes:

1. Multiplex Master Mix : AHT04+AHT05+ASB17+ASB23+HMS06+HMS07+HTG04+VHL20
2. Multiplex Master Mix : ASB02+HTG10+HMS03+LEX33
3. Multiplex Master Mix : LEX34+COR069
4. Multiplex Master Mix : COR070+COR058
5. Multiplex Master Mix : VHL209+LEX54
6. Multiplex Master Mix : COR018+COR071

Seite: 1

[\[SW1\]](#) Hatte hier falschen link geschickt. – Hier würde ich Genbank-Zugang angeben. Ich habe alle links geändert. <http://www.ebi.ac.uk/cgi-bin/emblfetch?G01593>

<i>Rank</i>	<i>Name</i>	<i>Origin</i>	<i>Map Info</i>	<i>Primer sequence (5' -> 3')</i> <i>ForwardReverse</i>	<i>Annealing temperature</i>	<i>Genbank (Accession Number)</i>	<i>Allele range</i>	<i>Multiplex</i>	<i>Diversity studies</i>
1	SRCRSP5	CHI21	M1	GGACTCTACCAACTGAGCTACAAG TGAAATGAAGCTAAAGCAATGC	55°C	L22197	156-178		D1,D2
2	MAF065	OAR15	M2	AAAGGCCAGAGTATGCAATTAGGAG CCACTCCTCCTGAGAATATAACATG	58°C	M67437	116-158	VIC 8mp	D1,D2
3	MAF70	BTA4	M3	CACGGAGTCACAAAGAGTCAGACC GCAGGACTCTACGGGGCCTTTGC	65°C	M77199	134-168		D1,D4
4	SRCRSP23	unknown	M4	TGAACGGGTAAAGATGTG TGTTTTTAATGGCTGAGTAG	58°C		81-119	FAM 8mp	D2
5	OarFCB48	OAR17	M5	GAGTTAGTACAAGGATGACAAGAGGCAC GACTCTAGAGGATCGCAAAGAACCAG	58°C	M82875	149-173	FAM 7mp	D2,D4,D5
6	INRA023	BTA3	M6	GAGTAGAGCTACAAGATAAACTTC TAACTACAGGGTGTTAGATGAACT	58°C	X80215	196-215	FAM 8mp	D1
7	SRCRSP9	CHI12	M7	AGAGGATCTGGAAATGGAATC GCACTCTTTTCAGCCCTAATG	58°C	L22200	99-135	NED 7mp	D2,D5
8	OarAE54	OAR25	M8	TACTAAAGAAACATGAAGCTCCCA GGAAACATTTATTCTTATTCCTCAGTG	58°C	L11048	115-138	VIC 7mp	D2,D5
9	SRCRSP8	Unknown	M9	TGCGGTCTGGTTCTGATTTAC GTTTCTTCCTGCATGAGAAAGTCGATGCTTAG	55°C	L22200	215-255		D1,D2,D5
10	SPS113	BTA10		CCTCCACACAGGCTTCTCTGACTT CCTAACTTGCTTGAGTTATTGCC	58°C		134-158	PET 7mp	
11	INRABERN172	BTA26		CCACTTCCCTGTATCCTCCT GGTGCTCCCATTTGTGTAGAC	58°C		234-256	FAM 7mp	
12	OarFCB20	OAR2	M12	GGAAAACCCCATATATACCTATAC AAATGTGTTTAAAGATTCCATACATGTG	58°C	L20004	93-112	NED 8mp	D1,D2
13	CSR247	OAR14	M13	GGACTTGCCAGAACTCTGCAAT CACTGTGGTTTGTATTAGTCAGG	58°C		220-247	PET 8mp	
14	McM527	OAR5	M14	GTCCATTGCCTCAAATCAATTC AAACCACTTGACTACTCCCCAA	58°C	L34277	165-187	PET 8mp	

15	ILSTS087	BTA6	M15	AGCAGACATGATGACTCAGC CTGCCTCTTTTCTTGAGAG	58°C	L37279	135- 155	FAM 8mp	
16	INRA063	CHI18	M16	GACCACAAAGGGATTGCACAAGC AAACCACAGAAATGCTTGGAAG	58°C	X71507	164- 186	VIC 8mp	D2,D3, D4
17	ILSTS011	BTA14	M17	GCTTGCTACATGGAAAGTGC	58°C	L23485	256- 294	FAM 7mp	D1,D2
18	SRCRSP7	CHI6	M18	TCTCAGCACCTTAATTGCTCT GGTCAACACTCCAATGGTGAG	55°C	L22199	117- 131		D2
19	ILSTS005	BTA10	M19	GGAAGCAATTGAAATCTATAGCC TGTTCTGTGAGTTTGTAAGC	55°C	L23481	172- 218		D1,D2; D3,D4
20	SRCRSP15	Unknown	M20	CTTTACTTCTGACATGGTATTTCC TGCCACTCAATTTAGCAAGC	55°C		172- 198		D2,D5
21	SRCRSP3	CHI10	M21	CGGGGATCTGTTCTATGAAC TGATTAGCTGGCTGAATGTCC	55°C	L22195	98- 122		D2
22	ILSTS029	BTA3	M22	TGTTTTGATGGAACACAG TGGATTTAGACCAGGGTTGG	55°C	L37252	148- 170		D2,D3, D5
23	TGLA53	BTA16	M23	GCTTTCAGAAATAGTTTGCATTCA ATCTTCACATGATATTACAGCAGA	55°C		126- 160		D1,D2
24	ETH10	CHI5	M24	GTTCAGGACTGGCCCTGCTAACA CCTCCAGCCCACTTTCTCTTCTC	55°C	Z22739	200- 210		D2,D3, D5
25	MAF209	CHI17	M25	GATCACAAAAGTTGGATACAACCGTG TCATGCACTTAAGTATGTAGGATGCTG	55°C	M80358	100- 104		D2
26	INRABERN185	CHI18	M26	CAATCTTGCTCCCCTATGC CTCCTAAAACACTCCCACACTA	55°C	X73937	261- 289		D2,D3, D5
27	BM6444	BTA2	M27	CTCTGGGTACAACACTGAGTCC TAGAGAGTTTCCCTGTCCATCC	65°C	G18444	118- 200		
28	P19 (DYA)	Unknown		AACACCATCAAACAGTAAGAG CATAGTAACAGATCTTCCTACA	55°C	AJ621046	160- 196		
29	TCRVB6	BTA10		GAGTCCTCAGCAAGCAGGTC CCAGGAATTGGATCACACCT	55	L18953	217- 255		

30	DRBP1	BTA23	ATGGTGCAGCAGCAAGGTGAGCA GGGACTCAGTCTCTCTATCTCTTTG	58°C	M55069	195- 229	FAM 7mp	D2
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Diversity studies

- D1. Li MH, Zhao SH, Bian C, Wang HS, Wei H, Liu B, Yu M, Fan B, Chen SL, Zhu MJ, Li SJ, Xiong TA, Li K. Genetic relationships among twelve Chinese indigenous goat populations based on microsatellite analysis. *Genet Sel Evol.* 2002 Nov-Dec; 34(6): 729-44.
- D2. Luikart G, Biju-Duval MP, Ertugrul O, Zagdsuren Y, Maudet C, Taberlet P. Power of 22 microsatellite markers in fluorescent multiplexes for parentage testing in goats (*Capra hircus*). *Anim Genet.* 1999 Dec; 30(6): 431-8.
- D3. Saitbekova N, Gaillard C, Obexer-Ruff G, Dolf G. Genetic diversity in Swiss goat breeds based on microsatellite analysis. *Anim Genet.* 1999 Feb; 30(1): 36-41.
- D4. Barker, Tan, Moore, Mukherjee, Matheson, Selvaraj Genetic variation within and relationships among populations of Asian goats (*Capra hircus*) *Journal of Animal Breeding and Genetics* Volume 118, Issue 4, Page 213-233, Aug 2001
- D5. C. Maudet C. Miller B. Bassano C. Breitenmoser-Würsten D. Gauthier G. Obexer-Ruff J. Michallet P. Taberlet and G. Luikart Microsatellite DNA and recent statistical methods in wildlife conservation management: applications in Alpine ibex [*Capra ibex (ibex)*] *Molecular Ecology* Volume 11 Issue 3 Page 421 - March 2002

<i>Rank</i>	<i>Name</i>	<i>Origin</i>	<i>Map</i>	<i>Primer sequence (5' -> 3')</i> <i>Forward</i> <i>Reverse</i>	<i>Annealing temperature</i>	<i>Genbank (Accession Number)</i>	<i>Allele range</i>	<i>Multiplex</i>	<i>Diversity studies</i>
1	MAF65	OAR15	M1	AAAGGCCAGAGTATGCAATTAGGAG CCACTCCTCCTGAGAATATAACATG	60°C	M67437	123-127 bp	4.1 6-FAM	D3,D4,D5
2	OarFCB193	OAR11	M2	TTCATCTCAGACTGGGATTCAGAAAGGC GCTTGAAATAACCCTCCTGCATCCC	54°C	L01533	96-136 bp	5.1 6-FAM	D5
3	OarJMP29	OAR24	M3	GTA TAC ACG TGG ACA CCG CTT TGT AC GAA GTG GCA AGA TTC AGA GGG GAA G	56°C	U30893	96-150 bp	4.2 NED	D5
4	OarJMP58	OAR26	M4	GAAGTCATTGAGGGGTCGCTAACC CTTCATGTTACAGGACTTTCTCTG	58°C	U35058	145-169 bp	4.3 HEX	
5	OarFCB304	OAR19	M5	CCCTAGGAGCTTTCAATAAAGAATCGG CGCTGCTGTCAACTGGGTCAGGG	56°C	L01535	150-188 bp	5.3 NED	D1,D2,D6
6	BM8125	OAR17	M6	CTCTATCTGTGGAAAAGGTGGG GGGGGTTAGACTTCAACATACG	50°C	G18475	110-130 bp	3.1 NED	D1
7	OarFCB128	OAR2	M7	ATTAAAGCATCTTCTCTTTATTTCTCGC CAGCTGAGCAACTAAGACATACATGCG	55°C	L01532	96-130 bp	1.1 6-FAM	D1,D5,D6
8	OarCP34	OAR3	M8	GCTGAACAATGTGATATGTTTCAGG GGGACAATACTGTCTTAGATGCTGC	50°C	U15699	112-130 bp	3.2 VIC	D1,D3,D4,D5,D6
9	OarVH72	OAR25	M9	GGCCTCTCAAGGGGCAAGAGCAGG CTCTAGAGGATCTGGAATGCAAAGCTC	57°C	L12548	121-145 bp	2.1 6-FAM	D1
10	OarHH47	OAR18	M10	TTTATTGACAACTCTCTTCCTAACTCCACC GTAGTTATTTAAAAAATATCATACCTCTTAAGG	58°C	L12557	130-152 bp	2.2 VIC	D2

11	DYMS1	OAR20	M11	AACAACATCAAACAGTAAGAG CATAGTAACAGATCTTCCTACA	59°C	AJ621046	159- 211 bp	2.3 NED	
12	SRCRSP1	CHI13	M12	TGC AAG AAG TTT TTC CAG AGC ACC CTG GTT TCA CAA AAG G	54°C	L22192	116- 148 bp	3.1 NED	
13	SRCRSP5	OAR18	M13	GGA CTC TAC CAA CTG AGC TAC AAG GTT TCT TTG AAA TGA AGC TAA AGC AAT GC	56°C	L22197	126- 158 bp	2.3 6- FAM	
14	SRCRSP9	CHI12	M14	AGA GGA TCT GGA AAT GGA ATC GCA CTC TTT TCA GCC CTA ATG	55°C	L22201	99- 135 bp	1.1 6- FAM	
15	MCM140	OAR6	M15	GTT CGT ACT TCT GGG TAC TGG TCT C GTC CAT GGA TTT GCA GAG TCA G	60°C	L38979	167- 193 bp	3.3 6- FAM	
16	MAF33	OAR9	M16	GAT CTT TGT TTC AAT CTA TTC CAA TTT C GAT CAT CTG AGT GTG AGT ATA TAC AG	60°C	M77200	121- 141 bp	3.2 HEX	D3,D4
17	MAF209	OAR17	M17	GAT CAC AAA AAG TTG GAT ACA ACC GTG G TCA TGC ACT TAA GTA TGT AGG ATG CTG	63°C	M80358	109- 135 bp	5.2 NED	D5,D6
18	INRA063	OAR14	M18	ATTTGCACAAGCTAAATCTAACC AAACCACAGAAATGCTTGGAAG	58°C	X71507	163- 199 bp	4.4 6- FAM	D7
19	OarFCB20	OAR2	M19	AAATGTGTTTAAGATTCCATACAGTG GGAAAACCCCATATATACCTATAC	56°C	L20004	95- 120 bp	4.5 HEX	D5,D6
20	BM1329	OAR6	M20	TTGTTTAGGCAAGTCCAAAGTC AACACCGCAGCTTCATCC	50°C	G18422	160- 182 bp	3.3 6- FAM	
21	MAF214	OAR16	M21	GGG TGA TCT TAG GGA GGT TTT GGA GG AAT GCA GGA GAT CTG AGG CAG GGA CG	58°C	M88160	174- 282 bp	2.1 HEX	D2,D5, D6

22	ILSTS11	OAR9	M22	GCT TGC TAC ATG GAA AGT GC CTA AAA TGC AGA GCC CTA CC	55°C	L23485	256- 294 bp	1.3 6- FAM	D2
23	MCM527	OAR5	M23	GTCCATTGCCTCAAATCAATTC AAACCACTTGACTACTCCCCAA	58°C	L34277	165- 187 bp	4.2 6- FAM	D2
24	OarFCB226	OAR2	M24	CTA TAT GTT GCC TTT CCC TTC CTG C GTG AGT CCC ATA GAG CAT AAG CTC	60°C	L20006	119- 153 bp	4.1 HEX	
25	ILSTS28	OAR3	M25	TCC AGA TTT TGT ACC AGA CC GTC ATG TCA TAC CTT TGA GC	53°C	L37211	105- 177 bp	2.2 NED	D2
26	MAF70	OAR4	M26	CACGGAGTCACAAAGAGTCAGACC GCAGGACTCTACGGGGCCTTTGC	60°C	M77199	124- 166 bp	5.4 HEX	D3,D4, D5
27	BM1824	OAR1	M27	GAGCAAGGTGTTTTTCCAATC CATTCTCCAAGTCTTCCTTG	58°C	G18394		5.5 FAM	D6,D7
28	OarAE129	OAR5	M28	AATCCAGTGTGTGAAAGACTAATCCAG GTAGATCAAGATATAGAATATTTTTCAACACC	54°C	L11051	133- 159 bp	1.2 NED	D1,D5
29	HUJ616	OAR13	M29	TTCAAACACTACACATTGACAGGG GGACCTTTGGCAATGGAAGG	54°C	M88250	114- 160 bp	1.3 VIC	
30	OarCP38	OAR10	M30	CAACTTTGGTGCATATTCAAGGTTGC GCAGTCGCAGCAGGCTGAAGAGG	52°C	U15700	117- 129 bp	6-FAM	D5
31	ILSTS5	OAR7	M31	GGA AGC AAT GAA ATC TAT AGC C TGT TCT GTG AGT TTG TAA GC	55°C	L23481	174- 218 bp	1.2 NED	D2,D7

Diversity studies

D1. Tapio M, Miceikiene I, Vilkki J, Kantanen J. Comparison of microsatellite and blood protein diversity in sheep: inconsistencies in fragmented

breeds. *Mol Ecol.* 2003 Aug; 12(8): 2045-56.

D2. Pariset L., Bavarese M.C., Cappuccio I., A. Valentini Use of microsatellites for genetic variation and inbreeding analysis in Sarda sheep flocks of central Italy. *J. Anim. Breed. Genet.* 2003 120: 425-432.

D3. Arranz JJ, Bayon Y, San Primitivo F. Genetic relationships among Spanish sheep using microsatellites. *Anim Genet.* 1998 Dec; 29(6): 435-40.

D4. Arranz JJ, Bayon Y, San Primitivo F. Differentiation among Spanish sheep breeds using microsatellites. *Genet Sel Evol.* 2001 Sep-Oct; 33(5): 529-42.

D5. Stahlberger-Saitbekova N., Shlapfer J., Dolf G., Gaillard C. Genetic relationships in Swiss sheep breeds based on microsatellite analysis. *J. Anim. Breed. Genet.* 2001, 118: 379-387.

D6. Diez-Tascon C, Littlejohn RP, Almeida PA, Crawford AM. Genetic variation within the Merino sheep breed: analysis of closely related populations using microsatellites. *Anim Genet.* 2000 Aug; 31(4): 243-51.

D7. Martin-Burriel I, Garcia-Muro E, Zaragoza P. Genetic diversity analysis of six Spanish native cattle breeds using microsatellites. *Anim Genet.* 1999 Jun; 30(3): 177-82.

Nr.	Name	Chr.	Origin	Map	Primer sequence (5' -> 3') D- indicates Dye labelled primer	Annealing temperature	Genbank (Accession Number)	Multiplex	Allele range	Diversity studies
1.	S0026	16	D1	M1	D-AACCTTCCCTTCCCAATCAC CACAGACTGCTTTTTACTCC	55°C	L30152	X1	87 - 105	R1, R2, R3, R4, R6
2.	S0155	1	D1	M2	D-TGTTCTCTGTTTCTCCTCTGTTTG AAAGTGAAAGAGTCAATGGCTAT	55°C	NA	X1	142 - 162	R1, R2, R3, R4, R6
3.	S0005	5	D1	M3	D-TCCTTCCCTCCTGGTAACTA GCACTTCCTGATTCTGGGTA	55°C	NA	X1	203 - 267	R1, R2, R3, R4, R6
4.	Sw2410	8	D2	M4	D-ATTTGCCCCAAGGTATTTTC CAGGGTGTGGAGGGTAGAAG	50°C	AF207836	X2	90 - 131	R5, R6
5.	Sw830	10	D2	M5	D-AAGTACCATGGAGAGGGAAATG ACATGGTTCCAAAGACCTGTG	50°C	AF235378	X2	168 - 203	R6
6.	S0355	15	D1	M6	D- TCTGGCTCCTACACTCCTTCTTGATG TTGGGTGGGTGCTGAAAAATAGGA	50°C	L29049	X2	244 - 271	R1, R2, R3, R4, R6
7.	Sw24	17	D1	M7	D-CTTTGGGTGGAGTGTGTGC ATCCAAATGCTGCAAGCG	55°C	AF235245	X3	95 - 124	R1, R2, R3, R4, R6
8.	Sw632	7	D1	M8	D-TGGGTTGAAAGATTTCCCAA GGAGTCAGTACTTTGGCTTGA	55°C	AF225099	X3	148 - 178	R1, R2, R3, R4, R6
9.	Swr1941	13	D2	M9	D-AGAAAGCAATTTGATTTGCATAATC ACAAGGACCTACTGTATAGCACAGG	55°C	AF253904	X3	202 - 224	R6
10.	Sw936	15	D1	M10	D-TCTGGAGCTAGCATAAGTGCC GTGCAAGTACACATGCAGGG	55°C	AF225107	X4	90 - 116	R1, R2, R3, R4, R6
11.	S0218	X	D1	M11	D-GTGTAGGCTGGCGGTTGT CCCTGAAACCTAAAGCAAAG	55°C	L29048	X4	158 - 205	R1, R2, R3, R4, R6
12.	S0228	6	D1	M12	D-GGCATAGGCTGGCAGCAACA AGCCACCTCATCTTATCTACTACT	55°C	L29195	X4	220 - 246	R1, R2, R3, R4, R6
13.	Sw122	6	D1	M13	D-CAAAAAGGCAAAAGATTGACA TTGTCTTTTTATTTTGCTTTTGG	55°C	AF235206	X5	106 - 128	R1, R2, R3, R4, R6
14.	Sw857	14	D1	M14	D-TGAGAGGTCAGTTACAGAAGACC GATCCTCCTCCAAATCCCAT	55°C	AF225105	X5	141 - 159	R1, R2, R3, R4, R6
15.	S0097	4	D2	M15	D-GACCTATCTAATGTCATTATAGT TTCCTCCTAGAGTTGACAAACTT	55°C	M95020	X5	209 - 250	R6
16.	sw240	2	D1	M16	D-AGAAATTAGTGCCCTCAAATTGG AAACCATTAAGTCCCTAGCAAA	55°C	AF235246	X6	92 - 124	R1, R2, R3, R4, R6
17.	IGF1	5	D1	M17	D-GCTTGGATGGACCATGTTG CATATTTTTCTGCATAACTTGAACCT	55°C	NA	X6	193 - 209	R1, R2, R3, R4, R6
18.	Sw2406	6	D2	M18	D-AATGTCACCTTTAAGACGTGGG AATGCGAAACTCCTGAATTAGC	55°C	AF225140	X6	222 - 262	R6
19.	Sw72	3	D1	M19	D-ATCAGAACAGTGCGCCGT TTTGAAAATGGGGTGTTTCC	55°C	AF235346	X7	97 - 114	R1, R2, R3, R4, R6
20.	S0226	2	D1	M20	D-GCACTTTTAACTTTTCATGATACTCC GGTTAAACTTTTNCCTCAATACA	55°C	L29230	X7	180 - 210	R1, R2, R3, R4, R6

21.	S0090	12	D1	M21	D -CCAAGACTGCCTTGTAGGTGAATA GCTATCAAGTATTGTACCATTAGG	55°C	M95002	X7	227 - 249	R1, R2, R3, R4, R6
22.	Sw2008	11	D2	M22	D -CAGGCCAGAGTAGCGTGC CAGTCCTCCCAAAAATAACATG	55°C	AF253773	X8	95 - 108	R5, R6
23.	Sw1067	6	D2	M23	D -TGCTGGCCAGTGA CTCTG CCGGGGGATTAAACAAAAG	55°C	AF235183	X8	136 - 176	R6
24.	S0101	7	D1	M24	D -GAATGCAAAGAGTTTCAGTGTAGG GTCTCCCTCACACTTACCGCAG	58°C	NA	X8	197 - 221	R1, R2, R3, R4, R6
25.	Sw1828	1	D2	M25	D -AATGCATTGTCTTCATTCAACC TTAACCGGGCACTTGTG	55°C	AF253712	X9	82 - 110	R6
26.	S0143	12	D2	M26	D -ACTCACAGCTTGTCTGGGTGT CAGTCAGCAGGCTGACAAAAC	55°C	NA	X9	150 - 167	R6
27.	S0068	13	D1	M27	D -CCTTCAACCTTTGAGCAAGAAC AGTGGTCTCTCTCCCTCTTGCT	55°C	NA	X9	211 - 262	R1, R2, R3, R4, R6
28.	S0178	8	D1	M28	D -TAGCCTGGGAACCTCCACACGCTG GGCACCAGGAATCTGCAATCCAGT	60°C	NA	X10	101 - 128	R1, R2, R3, R4, R6
29.	Sw911	9	D1	M29	D -CTCAGTTCTTTGGGACTGAACC CATCTGTGGAAAAAAAAGCC	60°C	AF225106	X10	149 - 173	R1, R2, R3, R4, R6
30.	S0002	3	D1	M30	D -GAAGCCAAAGAGACA ACTGC GTTCTTTACCCACTGAGCCA	60°C	NA	X10	186 - 216	R1, R2, R3, R4, R6

Before the use of this list we recommend to look at <http://www.toulouse.inra.fr/lgc/pig/panel/panel2004.htm> to check for the availability of possible additional or updated information

Multiplexes and annealing temperature:

Multiplex indicated here should only be considered as propositions of sets of markers compatible in size (which could thus be labelled with the same dye) which generally could be amplified in similar conditions. Most of these markers were also successfully amplified in very different conditions (annealing conditions differing of up to 10 °C), we however strongly recommend you to determine the annealing temperature optimal in your own PCR conditions. All selected markers have been successfully multiplexed with others, however multiplex PCR conditions have not been defined up to now for this updated list of markers (see also [how where selected diversity markers](#)). Multiplex conditions for first generation diversity markers have been successfully determined by [Yves Amigues](#) from [Labogena](#) and by [Martien Groenen team](#).

Diversity sets:

1Twenty one markers (indicated as D1) were from the original set of ISAG-FAO diversity markers originally set up in the frame of PiGMap II project. These markers were also analysed in the frame of the large scale PigBiodiv EU project.

2. Nine markers (indicated as D2) were analysed in the frame of the large scale PigBiodiv EU project.

Markers from current diversity set were selected among the markers analysed in the frame of the large scale PigBiodiv EU project (including ISAG-FAO first generation set of markers). Markers have been selected among markers that have been successfully analysed on a large number of breeds, for which the heterozygosity was of at least 64 % and for which on average 9 alleles have been observed.

Miscellaneous information

D- : indicates dye labelled primer

NA : not available

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R1 [Laval G, Iannuccelli N, Legault C, Milan D, Groenen MA, Giuffra E, Andersson L, Nissen PH, Jorgensen CB, Beeckmann P, Geldermann H, Foulley JL, Chevalet C, Ollivier L. Genetic diversity of eleven European pig breeds. *Genet Sel Evol.* 2000. 32\(2\):187-203.](#)

R2 . [Fan B., Wang Z.G., Li Y.J., Zhao X.L., Liu B., Zhao S.H., Yu M., Li M.H., Xiong T.A., Li K., Genetic variation analysis within and among Chinese indigenous swine population using microsatellite markers, *Anim. Genet.* 33\(2002\) 222-227.](#)

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[Yang SL, Wang ZG, Liu B, Zhang GX, Zhao SH, Yu M, Fan B, Li MH, Xiong TA, Li K. Genetic variation and relationships of eighteen Chinese indigenous pig breeds. *Genet Sel Evol.* 2003 35\(6\):657-71](#)

R3 [Martínez, A. M., Delgado, J. V., Rodero, A. & Vega-Pla, J. L. \(2000a\). Genetic structure of the Iberian pig breed using microsatellites. *Animal Genetics.* 31, 295-301.](#)

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Microsatellite list for biodiversity studies in chickens

<i>Nr</i>	<i>Name</i>	<i>Chr</i>	<i>Map</i>	<i>Primer sequence (5' -> 3')</i> <i>Forward Reverse</i>	<i>Annealing temperature</i>	<i>Genbank (Accession Number)</i>	<i>Multiplex</i>	<i>Allele range</i>	<i>Diversity studies</i>
1	ADL0268	1	M1	CTCCACCCCTCTCAGAACTA CAACTTCCCATCTACCTACT	60°C	G01688	X1	102- 116	R1,R2, R4,R5
2	MCW0206	2	M2	ACATCTAGAATTGACTGTTCAC CTTGACAGTGATGCATTAATG	60°C	AF030579	X7	221- 249	R2,R4, R5
3	LEI0166	3	M3	CTCCTGCCCTTAGCTACGCA TATCCCCTGGCTGGGAGTTT	60°C	X85531	X1	354- 370	R2,R4
4	MCW0295	4	M4	ATCACTACAGAACACCCTCTC TATGTATGCACGCAGATATCC	60°C	G32051	X3	88- 106	R1,R2, R4,R5
5	MCW0081	5	M6	GTTGCTGAGAGCCTGGTGCAG CCTGTATGTGGAATTACTTCTC	60°C	none	X2	112- 135	R1,R2, R4,R5
6	MCW0014	6	M7	TATTGGCTCTAGGAACTGTC GAAATGAAGGTAAGACTAGC	58°C	none	X4	164- 182	R1,R2, R4,R5
7	MCW0183	7	M8	ATCCAGTGTGAGTATCCGA TGAGATTTACTGGAGCCTGCC	58°C	G31974	X4	296- 326	R1,R2, R4,R5
8	ADL0278	8	M25	CCAGCAGTCTACCTTCCTAT TGTCATCCAAGAACAGTGTG	60°C	G01698	X1	114- 126	R1,R2, R4,R5
9	MCW0067	10	M9	GCACTACTGTGTGCTGCAGTTT GAGATGTAGTTGCCACATTCCGAC	60°C	G31945	X6	176- 186	R1,R2, R4,R5
10	MCW0104	13	M10	TAGCACAACCTCAAGCTGTGAG AGACTTGCACAGCTGTGTACC	60°C	none	X5	190- 234	R6
11	MCW0123	14	M11	CCACTAGAAAAGAACATCCTC GGCTGATGTAAGAAGGGATGA	60°C	none	X5	76- 100	R6
12	MCW0330	17	M12	TGGACCTCATCAGTCTGACAG AATGTTCTCATAGAGTTCTCTGC	60°C	G32085	X6	256- 300	R1,R2, R6
13	MCW0165	23	M13	CAGACATGCATGCCAGATGA GATCCAGTCCTGCAGGCTGC	60°C	none	X5	114- 118	R6
14	MCW0069	E60C04W23	M14	GCACTCGAGAAAACCTTCCTGCG ATTGCTTCAGCAAGCATGGGAGGA	60°C	none	X2	158- 176	R2,R4, R5
15	MCW0248	W29	M15	GTTGTTCAAAGAAGATGCATG TTGCATTAAGTGGCACTTTC	60°C	G32016	X1	205- 225	R1,R2, R4,R5
16	MCW0111	1	M16	GCTCCATGTGAAGTGGTTTA ATGTCCAATTGTCAATGATG	60°C	L48909	X3	96- 120	R1,R2, R4,R5
17	MCW0020	1	M17	TCTTCTTTGACATGAATTGGCA GCAAGGAAGATTTTGTACAAAATC	60°C	none	X5	179- 185	R6
18	MCW0034	2	M18	TGCACGCACTTACATACTTAGAGA TGTCCTTCCAATTACATTCATGGG	60°C	none	X2	212- 246	R4,R5
19	LEI0234	2	M27	ATGCATCAGATTGGTATTCAA CGTGGCTGTGAACAAATATG	60°C	Z94837	X3	216- 364	R4

20	MCW0103	3	M19	AACTGCGTTGAGAGTGAATGC TTTCCTAACTGGATGCTTCTG	64°C	G31956	X7	266- 270	R2,R4, R5
21	MCW0222	3	M20	GCAGTTACATTGAAATGATTCC TTCTCAAAACACCTAGAAGAC	60°C	G31997	X2	220- 226	R2,R4, R5
22	MCW0016	3	M28	ATGGCGCAGAAGGCAAAGCGATAT TGGCTTCTGAAGCAGTTGCTATGG	60°C	none	X3	162- 206	R6
23	MCW0037	3	M24	ACCGGTGCCATCAATTACCTATTA GAAAGCTCACATGACACTGCGAAA	64°C	none	X3	154- 160	R4,R5
24	MCW0098	4	M21	GGCTGCTTTGTGCTCTTCTCG CGATGGTCGTAATTCTCACGT	60°C	none	X6	261- 265	R2,R4, R5
25	LEI0094	4	M5	GATCTCACCAGTATGAGCTGC TCTCACACTGTAACACAGTGC	60°C	X83246	X1	247- 287	R4
26	MCW0284	4	M30	CAGAGCTGGATTGGTGTCAAG GCCTTAGGAAAACTCCTAAGG	60°C	G32043	X8	235- 243	R4
27	MCW0078	5	M22	CCACACGGAGAGGAGAAGGTCT TAGCATATGAGTGTACTGAGCTTC	60°C	none	X6	135- 147	R1,R2, R4,R5
28	LEI0192	6	M29	TGCCAGAGCTTCAGTCTGT GTCATTACTGTTATGTTTATTGC	60°C	Z83797	X8	244- 370	R4
29	ADL0112	10	M23	GGCTTAAGCTGACCCATTAT ATCTCAAATGTAATGCGTGC	58°C	G01725	X4	120- 134	R1,R2, R4,R5
30	MCW0216	13	M26	GGGTTTTACAGGATGGGACG AGTTTCACTCCAGGGCTCG	60°C	AF030586	X1	139- 149	R2,R4, R5

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Multiplexes

- Multiplex Master Mix Qiagen: ADL0278, ADL0268, LEI0094, MCW0248, MCW0216
- Multiplex Master Mix Qiagen: MCW0081+MCW0034+MCW0069+MCW0222+MCW0295
- Multiplex Master Mix Qiagen: MCW0111, MCW0037, MCW0016, LEI0166, LEI0234
- Multiplex Master Mix Qiagen: MCW0183, ADL0112, MCW0014
- Multiplex Master Mix Qiagen: MCW0165, MCW0020, MCW0123, MCW0104
- Multiplex Master Mix Qiagen: MCW0078+MCW0067+MCW0330+ MCW0098
- Hot Star Taq Master Mix Qiagen : MCW0206, MCW0103
- no information

Nr.	Name	Chr.*	Map	Primer sequence (5' -> 3')	Annealing temperature	Genbank (Accession Number)	Multiplex	Allele range**	Diversity studies
				Forward					
1.	CMS9			TGCTTTAGACGACTTTTACTTTAC ATTTCACTTTCTTCATACTTGTGAT	55 °C	AF329160		229–237 ^A 227–247 ^L 233–256 ^B 231–243 ^D	R1
2.	CMS13			TAGCCTGACTCTATCCATTTCTC ATTATTTGGAATTCAACTGTAAGG	55 °C	AF329158		246–265 ^A 242–261 ^L 248–265 ^B 238–254 ^D	R1
3.	CMS15			AAATACTTAAAGGTTCCCAGA TTGTAAACTAAAGCCAGAAAG	55 °C	AF329151		138–146 ^A 140–146 ^L 140–159 ^B 121–144 ^D	R1
4.	CMS17			TATAAAGGATCACTGCCTTC AAAATGAACCTCCATAAAGTTAG	55 °C	AF329147		140–161 ^A 135–147 ^L 144–149 ^B 149–167 ^D	R1
5.	CMS18			GAACGACCCTTGAAGACGAA AGCAGCTGGTTTTAGGTCCA	60 °C	AF329148		165–182 ^A 165–188 ^L 157–186 ^B 157–163 ^D	R1
6.	CMS25			GATCCTCCTGCGTTCTTATT CTAGCCTTTGATTGGAGCAT	58 °C	AF380345		93–118 ^A 93–95 ^L 118–128 ^B 93–102 ^D	R1
7.	CMS32			ACGGACAAGAAGCTGCTCATA ACAACCAATAAATCCCCATT	55 °C	AF329146		167–169 ^A 167–169 ^L 198–204 ^B 198–209 ^D	R1
8.	CMS50			TTTATAGTCAGAGAGAGTGCTG TGTAGGGTTCATTGTAACA	55 °C	AF329149		129–135 ^A 129–140 ^L 154–183 ^B 170–190 ^D	R1
9.	CMS121			CAAGAGAAGCTGGTGAGGATTTTC AGTTGATAAAAATACAGCTGGAAAG	60 °C	AF329159		128–157 ^A 128–151 ^L 151–159 ^B 147–166 ^D	R1
10.	CVRL01			GAAGAGGTTGGGGCACTAC CAGGCAGATATCCATTGAA	55 °C	AF217601		Polymorphic ^A 188–253 ^B 196–253 ^D	R5 , R6
11.	CVRL02			TGTCACAAATGGCAAGAT AGTGTACGTAGCAGCATTATTT	55 °C	AF217602		Polymorphic ^A 206–216 ^B 205–216 ^D	R3 , R5 , R6
12.	CVRL05			CCTTGGACCTCCTTGCTCTG GCCACTGGTCCCTGTCATT	60 °C	AF217602		Polymorphic ^A 148–174 ^B 155–176 ^D	R3 , R5 , R6
13.	CVRL06			TTTTAAAAATTCTGACCAGGAGTCTG CATAATAGCCAAAACATGGAAACAAC	60 °C	AF217606		Polymorphic ^A 185–205 ^B 196–203 ^D	R3 , R5 , R6

14.	CVRL07	AATACCCTAGTTGAAGCTCTGTCCT GAGTGCCTTTATAAATATGGGTCTG	55 °C	AF217607	Polymorphic A 255-263 ^B 272-306 ^D	R3 , R5 , R6
15.	LCA66	GTGCAGCGTCCAAATAGTCA CCAGCATCGTCCAGTATTCA	50-58 °C	AF091125	220-262 ^{A+L} 212-242 ^B 240-244 ^D	R2 , R3 , R8
16.	VOLP03	AGACGGTTGGGAAGGTGGTA CGACAGCAAGGCACAGGA	55-60 °C	AF305228	129-169 ^A 145-206 ^B 145-176 ^D	R2 , R6 , R7 , R9
17.	VOLP08	CCATTCACCCCATCTCTC TCGCCAGTGACCTTATTTAGA	55 °C	AF305230	148-152 ^A 142-180 ^B 144-150 ^D	R2 , R3 , R6 , R7 , R9
18.	VOLP10	CTTTCTCCTTTCCTCCCTACT CGTCCACTTCCTTCATTTTC	55 °C	AF305231	231-235 ^A 232-260 ^B 250-268 ^D	R2 , R3 , R6 , R7 , R9
19.	VOLP32	GTGATCGGAATGGCTTGAAA CAGCGAGCACCTGAAAGAA	55 °C	AF305234	192-247 ^A 256-262 ^B 256-262 ^D	R2 , R3 , R6 , R7 , R9
20.	VOLP67	TTAGAGGGTCTATCCAGTTTC TGGACCTAAAAGAGTGGAG	55 °C	AF305237	158-170 ^A 142-172 ^B 150-203 ^D	R2 , R7 , R9
21.	YWLL 08	ATCAAGTTTGAGGTGCTTTCC CCATGGCATTGTGTTGAAGAC	55-60 °C		135-177 ^{A+L} 154-180 ^B 133-172 ^D	R2 , R3 , R4 , R6 , R9
22.	YWLL 09	AAGTCTAGGAACCGGAATGC AGTCAATCTACACTCCTTGC	50-58 °C		154-180 ^{A+L} 158-177 ^B 158-162 ^D	R2 , R4 , R6
23.	YWLL 38	GGCCTAAATCCTACTAGAC CCTCTCACTCTTGTTCTCCTC	55-60 °C		174-178 ^{A+L} 180-192 ^B 182-190 ^D	R2 , R3 , R4 , R6 , R9
24.	YWLL 44	CTCAACAATGCTAGACCTTGG GAGAACACAGGCTGGTGAATA	55-60 °C		86-120 ^{A+L} 101-117 ^B 90-114 ^D	R2 , R3 , R4 , R6 , R9
25.	YWLL 59	TGTGCAGGAGTTAGGTGTA CCATGTCTCTGAAGCTCTGGA	55-58 °C		96-136 ^{A+L} 109-135 ^B 109-111 ^D	R2 , R4 , R6

* Unassigned but believed to be all autosomal

** A: alpaca (*Lama pacos*), L: llama (*Lama glama*), B: Bactrian camel (*Camelus bactrianus*), D: dromedary camel (*Camelus dromedarius*).

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Multiplexes: None developed.

Nr.	Name	Chr.	Map	Primer sequence (5' -> 3')		Annealing temperature	Genbank (Accession Number)	Multiplex ¹	Allele range	Diversity studies
				Forward	Reverse					
1.	INRA063 (D18S5)	18	M1	ATTTGCACAAGCTAAATCTAACC AAACCACAGAAATGCTTGGAAAG		55-58°C	[SW1] X71507	1.1 HEX	167- 189	R1, R2, R3, R4, R5, R6, R7, R8, R9, R10, R11, R12, R13
2.	INRA005 (D12S4)	12	M2	CAATCTGCATGAAGTATAAATAT CTTCAGGCATACCCTACACC		55°C	X63793	1.2 FAM	135- 149	R1, R2, R3, R4, R5, R6, R7, R8, R9, R10, R11,
3.	ETH225 (D9S1)	9	M3	GATCACCTTGCCACTATTTCT ACATGACAGCCAGCTGCTACT		55-65°C	Z14043	4.7 HEX	131- 159	R1, R2 , R3, R4, R5, R6, R7, R8, R9, R10, R11, R12, R14, R15, R16, R17
4.	ILSTS005 (D10S25)	10	M4	GGAAGCAATGAAATCTATAGCC TGTTCTGTGAGTTTGTAAAGC		54-58°C	L23481	3.5 FAM	176- 194	R1, R2, R3, R4, R5, R6, R7, R8, R9, R10, R14, R15, R18, R20
5.	HEL5 (D21S15)	21	M5	GCAGGATCACTTGTTAGGGA AGACGTTAGTGACATTAAC		52-57°C	X65204	2.4 FAM	145- 171	R1, R2, R3, R4, R5, R6, R7, R8, R9, R10, R13, R14, R15, R16
6.	HEL1 (D15S10)	15	M6	CAACAGCTATTTAACAAGGA AGGCTACAGTCCATGGGATT		54-57°C	X65202	1.1 HEX	99-119	R1, R2, R3, R4, R5, R6, R7, R8, R9, R12
7.	INRA035 (D16S11)	16	M7	ATCCTTTGCAGCCTCCACATTG TTGTGCTTTATGACACTATCCG		55-60°C	X68049	3.5 FAM	100- 124	R1, R2, R3, R4, R5, R6, R7, R8, R9, R14
8.	ETH152 (D5S1)	5	M8	TACTCGTAGGGCAGGCTGCCTG GAGACCTCAGGGTTGGTGATCAG		55-60°C	Z14040, G18414	2.3 TET	181- 211	R1, R2, R3, R4, R5, R6, R7, R8, R9, R10, R11, R12, R14, R15, R16 , R17
9.	INRA023 (D3S10)	3	M9	GAGTAGAGCTACAAGATAAACTTC TAACTACAGGGTGTTAGATGAACTC		55°C	X67830	4.7 TET	195- 225	R1, R2, R3, R4, R5, R6, R7, R8, R9, R11, R12, R19

10.	ETH10 (D5S3)	5	M10	G TTCAGGACTGGCCCTGCTAACA CCTCCAGCCCACTTTCTCTTCTC	55-65°C	Z22739	4.7 FAM	207- 231	R1, R2, R3, R4, R5, R6, R7, R8, R9, R10, R12, R17, R19
11.	HEL9 (D8S4)	8	M11	C CCATTCAGTCTTCAGAGGT CACATCCATGTTCTCACCAC	52-57°C	X65214	2.3 TET	141- 173	R1, R2, R3, R4, R5, R6, R7, R8, R9, R10, R13
12.	CSSM66 (D14S31)	14	M12	A CACAAATCCTTTCTGCCAGCTGA AATTTAATGCACTGAGGAGCTTGG	55-65°C		1.1 FAM	171- 209	R1, R2, R3, R4, R5, R6, R7, R8, R10
13.	INRA032 (D11S9)	11	M13	A AACTGTATTCTCTAATAGCTAC GCAAGACATATCTCCATTCCTTT	55-58°C	X67823	3.4 TET	160- 204	R1, R2, R3, R4, R5, R6, R7, R8, R9, R11
14.	ETH3 (D19S2)	19	M14	G AACCTGCCTCTCCTGCATTGG ACTCTGCCTGTGGCCAAGTAGG	55-65°C	Z22744	2.3 FAM	103- 133	R1, R2, R3, R4, R5, R6, R7, R8, R9, R10, R12, R17, R19
15.	BM2113 (D2S26)	2	M15	G CTGCCTTCTACCAAATACCC CTTCCTGAGAGAAGCAACACC	55-60°C	M97162	4.7 FAM	122- 156	R1, R2, R3, R4, R5, R6, R9, R10, R12, R13, R17, R19
16.	BM1824 (D1S34)	1	M16	G AGCAAGGTGTTTTTCCAATC CATTCTCCAACCTGCTTCCTTG	55-60°C	G18394	1.2 TET 4.8 HEX	176- 197	R1, R2, R3, R4, R5, R6, R9, R10, R12, R17, R19
17.	HEL13 (D11S15)	11	M17	T AAGGACTTGAGATAAGGAG CCATCTACCTCCATCTTAAC	52-57°C	X65207	2.4 FAM	178- 200	R1, R2, R3, R4, R5, R6, R9, R10,
18.	INRA037 (D10S12)	10	M18	G ATCCTGCTTATATTTAACCAC AAAATTCCATGGAGAGAGAAAAC	57-58°C	X71551	1.1 TET	112- 148	R1, R2, R6, R7, R8, R9, R10, R11
19.	BM1818 (D23S21)	23	M19	A GCTGGGAATATAACCAAAGG AGTGCTTTCAAGGTCCATGC	56-60°C	G18391	2.3 HEX	248- 278	R1, R2, R3, R4, R5, R6, R10, R12, R17
20.	ILSTS006 (D7S8)	7	M20	T GTCTGTATTTCTGCTGTGG ACACGGAAGCGATCTAAACG	55°C	L23482	2.3 FAM	277- 309	R1, R2, R3, R4, R5, R6, R10, R18
21.	MM12 (D9S20)	9	M21	C AAGACAGGTGTTTCAATCT ATCGACTCTGGGGATGATGT	50-55°C	Z30343	3.5 TET	101- 145	R1, R2, R10
22.	CSRM60 (D10S5)	10	M22	A AGATGTGATCCAAGAGAGAGGCA AGGACCAGATCGTGAAGGCATAG	55-65°C		1.1 FAM	79-115	R1, R2, R3, R4, R5, R10,
23.	ETH185 (D17S1)	17	M23	T GCATGGACAGAGCAGCCTGGC GCACCCAACGAAAGCTCCCAG	58-67°C	Z14042	3.5 TET	214- 246	R1, R2,
24.	HAUT24 (D22S26)	22	M24	C TCTCTGCCTTTGTCCCTGT AATACACTTTAGGAGAAAAATA	52-55°C	X89250	3.6 HEX	104- 158	R1, R2, R10,
25.	HAUT27 (D26S21)	26	M27	T TTTATGTTTCATTTTTGGACTGG AACTGCTGAAATCTCCATCTTA	57°C	X89252	1.2 HEX	120- 158	R1, R2, R10,
26.	TGLA227 (D18S1)	18	M26	C GAATTCCAAATCTGTTAATTTGCT ACAGACAGAACTCAATGAAAGCA	55-56°C		1.2 TET/ 4.8 FAM	75-105	R1, R2, R10, R12, R17, R18

27.	TGLA126 (D20S1)	20	M27	CTAATTTAGAATGAGAGAGGCTTCT TTGGTCTCTATTCTCTGAATATTCC	55-58°C		4.8 TET	115- 131	R1, R2, R10, R12, R17, R18, R19
28.	TGLA122 (D21S6)	21	M28	CCCTCCTCCAGGTAATCAGC AATCACATGGCAAATAAGTACATAC	55-58°C		4.7 TET	136- 184	R1, R2, R10, R18, R17, R19
29.	TGLA53 (D16S3)	16	M29	GCTTTTCAGAAATAGTTTGCATTCA ATCTTCACATGATATTACAGCAGA	55°C		4.7 HEX	143- 191	R1, R2, R12, R17
30.	SPS115 (D15)	15	M30	AAAGTGACACAACAGCTTCTCCAG AACGAGTGTCTAGTTTGGCTGTG	55-60°C	X16451	4.8 HEX	234- 258	R1, R2, R17, R19

¹ The multiplexing has been developed by K. Moazami- Goudarzi, INRA, Jouy-en-Josas. Indicated are lane (from 1 to 4), reaction (from 1 to 8, 2 reactions loaded per lane), and label (FAM, HEX or TET), respectively. The annealing temperature for all reactions is 55°C. For markers TGLA227 and BM1824, two alternatives (systems 1 and 2, respectively) are shown. Summary of both systems:

lane	reaction	marker	range	label
1	1	CSRM60	79-115	FAM
		CSSM66	171-209	FAM
		HEL1	99-119	HEX
		INRA063	167-189	HEX
		INRA037	112-148	TET
1	2	INRA005	135-149	FAM
		HAUT27	120-158	HEX
		(System 1) TGLA227	75-105	TET
		(System 1) BM1824	176-197	TET
2	3	ETH3	103-133	FAM
		BM1818	248-278	HEX
		TGLA53	143-191	HEX
		ETH152	181-211	TET
		HEL9	141-173	TET
		ISLT006	277-309	FAM
2	4	HEL5	145-171	FAM
		HEL13	178-200	FAM
3	5	INRA035	100-124	FAM
		ILST005	176-194	FAM
		MM12	101-145	TET
		ETH185	214-246	TET

3	6	INRA032	160-204	TET
		HAUT24	104-158	HEX
4	7	INRA023	195-225	TET
		TGLA122	136-184	TET
		BM2113	122-156	FAM
		ETH225	131-159	HEX
		ETH10	207-231	FAM
4	8	SPS115	234-258	HEX
		TGLA126	115-131	TET
		(system 2) TGLA227	75-105	FAM
		(system 2) BM1824	176-197	HEX

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