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(54) Title: OVINE IDENTIFICATION METHOD

(57) Abstract: The invention relates to method for identifying an ovine with a genotype indicative of one or more altered perfor-
mance traits, the method including the step of detecting, in a sample derived from the ovine, the presence of at least one allele of the
CP34 simple sequence repeat (SSR) marker, or at least one allele of a marker in linkage disequilibrium (LD) with CP34, wherein the
presence of the allele is indicative of the altered performance traits in the ovine.

WO 2009/011602 A1

OVINE IDENTIFICATION METHOD

5 FIELD OF THE INVENTION

The present invention relates to a method for identification of ovine with a genotype indicative of one or more altered performance traits.

10 BACKGROUND

Marker assisted selection (MAS) is an approach that is often used to identify animals that possess alteration in a particular trait using a genetic marker, or markers, associated with that trait. The alteration in the trait may be desirable and be advantageously selected for, or non-
15 desirable and advantageously selected against, in selective breeding programs. MAS allows breeders to identify and select animals at a young age and is particularly valuable for hard to measure and sex limited traits. The best markers for MAS are the causal mutations, but where these are not available, a haplotype that is in strong linkage disequilibrium with the causal mutation can also be used. Such information can be used to accelerate genetic gain, or reduce
20 trait measurement costs, and thereby has utility in commercial breeding programs.

Often in MAS, a particular marker is used for identification of animals with alteration in a particular trait, and different markers are used for different traits. For example, in sheep, the Inverdale marker is used to identify sheep with altered prolificacy (Galloway et al. 2000) and a
25 GDF8 marker haplotype can be used to identify sheep with a variant causing increased muscling (Johnson et al. 2005).

It would however be beneficial to have available individual markers that could be used to identify animals with alteration in one or multiple performance traits.

30 It is therefore an object of the invention to provide a method for identifying an ovine with a genotype indicative of one or more altered performance traits, and/or at least to provide the public with a useful choice.

SUMMARY OF THE INVENTION

In the first aspect the invention provides a method for identifying an ovine with a genotype indicative of at least two altered performance traits, the method including the step of detecting, in a sample derived from the ovine, the presence of at least one allele of the CP34 simple sequence repeat (SSR) marker, or at least one allele of a marker in linkage disequilibrium (LD) with CP34, wherein the presence of the allele is indicative of the altered performance traits in the ovine.

Preferably the performance trait is selected from the group comprising of: weaning weight (WWT), body weight at 8 months (LW8), body weight at 12 months (LW12), carcass weight (CW), adult ewe weight (EWT), eye muscle width (EMW), eye muscle depth (EMD), eye muscle area (EMA), fat depth (FD), carcass fat weight (FAT), carcass lean muscle weight (LEAN), number of lambs born (NLB), lamb fleece weight (LFW), hogget fleece weight (FW12), ewe (adult) fleece weight (EFW), hogget fibre diameter (FDIAM), and resistance to gastrointestinal parasitic nematode infection.

Preferably the performance trait is selected from the group consisting of: weaning weight (WWT), body weight at 8 months (LW8), body weight at 12 months (LW12), carcass weight (CW), adult ewe weight (EWT), eye muscle width (EMW), eye muscle depth (EMD), eye muscle area (EMA), fat depth (FD), carcass fat weight (FAT), carcass lean muscle weight (LEAN), number of lambs born (NLB), lamb fleece weight (LFW), hogget fleece weight (FW12), ewe (adult) fleece weight (EFW), hogget fibre diameter (FDIAM), and resistance to gastrointestinal parasitic nematode infection.

In one embodiment the performance trait is weaning weight (WWT).

Alternatively the performance trait is body weight at 8 months (LW8).

Alternatively the performance trait is body weight at 12 months (LW12).

Alternatively the performance trait is carcass weight (CW).

Alternatively the performance trait is adult ewe weight (EWT).

Alternatively the performance trait is eye muscle width (EMW).

5 Alternatively the performance trait is eye muscle depth (EMD).

Alternatively the performance trait is eye muscle area (EMA).

Alternatively the performance trait is fat depth (FD).

10

Alternatively the performance trait is carcass fat weight (FAT).

Alternatively the performance trait is carcass lean muscle weight (LEAN).

15 Alternatively the performance trait is number of lambs born (NLB).

Alternatively the performance trait is lamb fleece weight (LFW).

Alternatively the performance trait is hogget fleece weight (FW12).

20

Alternatively the performance trait is ewe (adult) fleece weight (EFW).

Alternatively the performance trait is hogget fibre diameter (FDIAM).

25 Alternatively the performance trait is resistance to gastrointestinal parasitic nematode infection.

Preferably the ovine is altered for at least three, more preferably at least four and most preferably at least five performance traits.

30 In a further aspect the invention provides a method for identifying an ovine with a genotype indicative of at least one altered performance traits selected from the group consisting of: weaning weight (WWT), body weight at 8 months (LW8), body weight at 12 months (LW12), carcass weight (CW), adult ewe weight (EWT), eye muscle width (EMW), eye muscle depth

(EMD), eye muscle area (EMA), fat depth (FD), carcass fat weight (FAT), carcass lean muscle weight (LEAN), number of lambs born (NLB), lamb fleece weight (LFW), hogget fleece weight (FW12), ewe (adult) fleece weight (EFW), hogget fibre diameter (FDIAM), and resistance to gastrointestinal parasitic nematode infection, the method including the step of detecting, in a sample derived from the ovine, the presence of at least one allele of the CP34 simple sequence repeat (SSR) marker, or at least one allele of a marker in linkage disequilibrium (LD) with CP34, wherein the presence of the allele is indicative of the altered performance traits in the ovine.

In one embodiment the performance trait is weaning weight (WWT).

Alternatively the performance trait is body weight at 8 months (LW8).

Alternatively the performance trait is body weight at 12 months (LW12).

Alternatively the performance trait is carcass weight (CW).

Alternatively the performance trait is adult ewe weight (EWT).

Alternatively the performance trait is eye muscle width (EMW)

Alternatively the performance trait is eye muscle depth (EMD).

Alternatively the performance trait is eye muscle area (EMA).

Alternatively the performance trait is fat depth (FD).

Alternatively the performance trait is carcass fat weight (FAT).

Alternatively the performance trait is carcass lean muscle weight (LEAN).

Alternatively the performance trait is number of lambs born (NLB).

Alternatively the performance trait is lamb fleece weight (LFW).

Alternatively the performance trait is hogget fleece weight (FW12).

Alternatively the performance trait is ewe (adult) fleece weight (EFW).

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Alternatively the performance trait is hogget fibre diameter (FDIAM).

Alternatively the performance trait is resistance to gastrointestinal parasitic nematode infection.

- 10 Preferably the ovine is altered for at least two, more preferably at least three, more preferably at least four and most preferably at least five performance traits.

In a further aspect the invention provides a method for identifying an ovine with a genotype indicative of at least one altered performance traits selected from the group consisting of:
15 weaning weight (WWT), body weight at 8 months (LW8), body weight at 12 months (LW12), carcass weight (CW), adult ewe weight (EWT), eye muscle width (EMW), eye muscle depth (EMD), eye muscle area (EMA), fat depth (FD), carcass fat weight (FAT), carcass lean muscle weight (LEAN), number of lambs born (NLB), lamb fleece weight (LFW), hogget fleece weight (FW12), ewe (adult) fleece weight (EFW), and hogget fibre diameter (FDIAM, the method
20 including the step of detecting, in a sample derived from the ovine, the presence of at least one allele of the CP34 simple sequence repeat (SSR) marker, or at least one allele of a marker in linkage disequilibrium (LD) with CP34, wherein the presence of the allele is indicative of the altered performance traits in the ovine.

- 25 In one embodiment the performance trait is weaning weight (WWT).

Alternatively the performance trait is body weight at 8 months (LW8).

Alternatively the performance trait is body weight at 12 months (LW12).

30

Alternatively the performance trait is carcass weight (CW).

Alternatively the performance trait is adult ewe weight (EWT).

Alternatively the performance trait is eye muscle width (EMW)

Alternatively the performance trait is eye muscle depth (EMD).

5

Alternatively the performance trait is eye muscle area (EMA).

Alternatively the performance trait is fat depth (FD).

10 Alternatively the performance trait is carcass fat weight (FAT).

Alternatively the performance trait is carcass lean muscle weight (LEAN).

Alternatively the performance trait is number of lambs born (NLB).

15

Alternatively the performance trait is lamb fleece weight (LFW).

Alternatively the performance trait is hogget fleece weight (FW12).

20 Alternatively the performance trait is ewe (adult) fleece weight (EFW).

Alternatively the performance trait is hogget fibre diameter (FDIAM).

25 Preferably the ovine is altered for at least two, more preferably at least three, more preferably at least four and most preferably at least five performance traits.

Resistance to gastrointestinal parasitic nematode infection can be assessed by measuring fecal egg count – summer lamb challenge (FEC1), fecal egg count – autumn lamb challenge (FEC2), and adult fecal egg count (AFEC). Preferably the nematode is of the genus: *Haemonchus*,
30 *Nematodirus*, *Teladorsagia* or *Trichostrongylus*. Preferably the nematode is of the species *Haemonchus contortus*, *Nematodirus spathiger*, *Nematodirus filicollis*, *Teladorsagia circumcincta*, *Trichostrongylus colubriformis* or *Trichostrongylus vitrinus*.

Preferably the marker in LD with CP34 is an SSR marker.

Preferably the SSR in LD with CP34 is selected from the group including but limited to BMS1084327, BMS1082942, BMS1082956, BMS1082961, BMS1083945, BMS1083008, BMS1082252, BMS1082669, BMS1082702, BMS1082722, BMS1082831, BMS1887400, BMS1887404, BMS1784528, BMS1600436, BMS1082043, BMS1082045, BMS1081952, BMS1081760, BMS1081860, BMS30480882, BMS30480889, BMS1081770, BMS1081774, RSAD2_1, BMS1081640, BMS1080704, and BMS1080870 as herein defined.

- 10 More preferably the SSR in LD with CP34 is selected from the group consisting of BMS1084327, BMS1082942, BMS1082956, BMS1082961, BMS1083945, BMS1083008, BMS1082252, BMS1082669, BMS1082702, BMS1082722, BMS1082831, BMS1887400, BMS1887404, BMS1784528, BMS1600436, BMS1082043, BMS1082045, BMS1081952, BMS1081760, BMS1081860, BMS30480882, BMS30480889, BMS1081770, BMS1081774, RSAD2_1, BMS1081640, BMS1080704, and BMS1080870 as herein defined.

In one embodiment the method, the allele of CP34 is selected from a group comprising: allele A, allele B, allele C, allele D, allele E, allele F, allele G and allele H as herein defined.

- 20 Preferably the allele of CP34 is allele A, G or H. More preferably the allele of CP34 is allele A. These alleles are particularly suitable to be selected for in sheep breeding programs.

Alternatively the allele of CP34 is allele C or E. Alternatively the allele of CP34 is allele E. These alleles are particularly suitable to be selected against in sheep breeding programs.

- 25 Preferably the allele of the marker in LD with CP34, is in LD with CP34 at a D' value of at least 0.1, more preferably at least 0.2, more preferably at least 0.3, more preferably at least 0.4, more preferably at least 0.5.

- 30 Preferably the allele of the marker in LD with CP34, is in LD with CP34 at a V^2 value of at least 0.05, more preferably at least 0.075, more preferably at least 0.1, more preferably at least 0.2, more preferably at least 0.3, more preferably at least 0.4, more preferably at least 0.5.

Preferably the allele of the marker is in LD with the traits at a D' value of at least 0.1, more preferably at least 0.2, more preferably at least 0.3, more preferably at least 0.4, more preferably at least 0.5.

- 5 Preferably the allele of the marker is in LD with the traits at a V^2 value of at least 0.05, more preferably at least 0.075, more preferably at least 0.1, more preferably at least 0.2, more preferably at least 0.3, more preferably at least 0.4, more preferably at least 0.5.

The allele may be detected by any suitable method. Preferably the allele is detected using a
10 polymerase chain reaction (PCR) step. PCR methods are well known to those skilled in the art and are described for example in Mullis *et al.*, Eds. 1994 The Polymerase Chain Reaction, Birkhauser, incorporated herein by reference. Preferably a PCR product is produced by amplifying the marker with primers comprising sequence complimentary to sequence of the ovine genome flanking the marker.

15 Any suitable primer pair may be used. Preferably the PCR is performed using at least one primer selected from those set forth in Table 2. Preferably the PCR is performed using at least one primer pair selected from those set forth in Table 2.

- 20 Preferably the allele is identified by the size of the PCR product amplified. Preferably size is estimated by running the PCR product through a gel. Preferably a size standard is also run in the gel for comparison with the PCR product.

Other methods for detecting the allele are also contemplated, such as but not limited to probe-
25 based methods, which are well known to those skilled in the art as described in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd Ed. Cold Spring Harbor Press, 1987, incorporated herein by reference.

Beneficially in the method of the invention, the presence of a combination of more than one
30 allele of the CP34 SSR marker, or more than one allele of a marker in linkage disequilibrium (LD) with CP34, may be detected to identify the ovine. Detection of various combinations of alleles of the CP34 SSR and/or alleles of a marker in LD with CP34, commonly known as haplotypes is contemplated.

In a further aspect the invention provides a method for selecting an ovine with at least two altered performance traits, the method comprising selecting an ovine identified by a method of the invention.

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In a further aspect the invention provides a method for identifying an ovine with a genotype indicative of at least one altered performance traits selected from the group consisting of: weaning weight (WWT), body weight at 8 months (LW8), body weight at 12 months (LW12), carcass weight (CW), adult ewe weight (EWT), eye muscle width (EMW), eye muscle depth
10 (EMD), eye muscle area (EMA), fat depth (FD), carcass fat weight (FAT), carcass lean muscle weight (LEAN), number of lambs born (NLB), lamb fleece weight (LFW), hogget fleece weight (FW12), ewe (adult) fleece weight (EFW), hogget fibre diameter (FDIAM), and resistance to gastrointestinal parasitic nematode infection, the method comprising selecting an ovine identified by a method of the invention.

15

In a further aspect the invention provides a method for identifying an ovine with a genotype indicative of at least one altered performance traits selected from the group consisting of: weaning weight (WWT), body weight at 8 months (LW8), body weight at 12 months (LW12), carcass weight (CW), adult ewe weight (EWT), eye muscle width (EMW), eye muscle depth
20 (EMD), eye muscle area (EMA), fat depth (FD), carcass fat weight (FAT), carcass lean muscle weight (LEAN), number of lambs born (NLB), lamb fleece weight (LFW), hogget fleece weight (FW12), ewe (adult) fleece weight (EFW), and hogget fibre diameter (FDIAM), the method comprising selecting an ovine identified by a method of the invention.

25 In a further aspect the invention provides an isolated polynucleotide comprising an SSR marker selected from the group consisting of BMS1084327, BMS1082942, BMS1082956, BMS1082961, BMS1083945, BMS1083008, BMS1082252, BMS1082669, BMS1082702, BMS1082722, BMS1082831, BMS1887400, BMS1887404, BMS1784528, BMS1600436, BMS1082043, BMS1082045, BMS1081952, BMS1081760, BMS1081860, BMS30480882,
30 BMS30480889, BMS1081770, BMS1081774, RSAD2_1, BMS1081640, BMS1080704, and BMS1080870 as herein defined.

In a further aspect the invention provides a primer suitable for amplifying a polynucleotide of the invention. Preferably the primer comprises sequence complimentary to sequence of the ovine genome flanking the marker. Preferably the primer comprises flanking sequence from the primers set forth in Table 2. Preferably the primer is selected from those set forth in Table 2.

5

In a further aspect combinations of the alleles of two or more of the above markers, commonly called a haplotype, could be used.

DETAILED DESCRIPTION OF THE INVENTION

10

Definitions

In this specification where reference has been made to patent specifications, other external documents, or other sources of information, this is generally for the purpose of providing a context for discussing the features of the invention. Unless specifically stated otherwise, reference to such external documents is not to be construed as an admission that such documents, or such sources of information, in any jurisdiction, are prior art, or form part of the common general knowledge in the art.

15

The term “comprising” as used in this specification means “consisting at least in part of”. When interpreting each statement in this specification that includes the term “comprising”, features other than that or those prefaced by the term may also be present. Related terms such as “comprise” and “comprises” are to be interpreted in the same manner.

20

The term “polynucleotide(s),” as used herein, means a single or double-stranded deoxyribonucleotide or ribonucleotide polymer of any length but preferably at least 15 nucleotides, and include as non-limiting examples, coding and non-coding sequences of a gene, sense and antisense sequences complements, exons, introns, genomic DNA, cDNA, pre-mRNA, mRNA, rRNA, siRNA, miRNA, tRNA, ribozymes, recombinant polynucleotides, isolated and purified naturally occurring DNA or RNA sequences, synthetic RNA and DNA sequences, nucleic acid probes or primers and fragments.

25
30

The term "primer" refers to a short polynucleotide, usually having a free 3'OH group, that is hybridized to a template and used for priming polymerization of a polynucleotide complementary to the target.

- 5 The term "probe" refers to a short polynucleotide that is used to detect a polynucleotide sequence, that is complementary to the probe, in a hybridization-based assay.

The abbreviation "SSR" stands for a "simple sequence repeat" and refers to any short sequence, for example, a mono-, di-, tri-, or tetra-nucleotide that is repeated at least once in a particular
10 nucleotide sequence. These sequences are also known in the art as "microsatellites." A SSR can be represented by the general formula $(N_1 N_2 \dots N_i)_n$, wherein N represents nucleotides A, T, C or G, i represents the number of the nucleotides in the base repeat, and n represents the number of times the base is repeated in a particular DNA sequence. The base repeat, i.e., $N_1 N_2 \dots N_i$, is also referred to herein as an "SSR motif." For example, (ATC)₄, refers to a tri-nucleotide ATC
15 motif that is repeated four times in a particular sequence. In other words, (ATC)₄ is a shorthand version of "ATCATCATCATC."

The term "complement of a SSR motif" refers to a complementary strand of the represented motif. For example, the complement of (ATG) motif is (TAC).

20 The term "SSR locus" refers to a location on a chromosome of a SSR motif; locus may be occupied by any one of the alleles of the repeated motif. "Allele" is one of several alternative forms of the SSR motif occupying a given locus on the chromosome. For example, the (ATC)₈ locus refers to the fragment of the chromosome containing this repeat, while (ATC)₄ and
25 (ATC)₇ repeats represent two different alleles of the (ATC)₈ locus. As used herein, the term locus refers to the repeated SSR motif and the flanking 5' and 3' non-repeated sequences. SSR loci of the invention are useful as genetic markers, such as for determination of polymorphism.

It will be appreciated by those skilled in the art that an SSR consists of repeats of a certain motif
30 (e.g. ATC), and that different alleles of the SSR locus may have different numbers of repeats [e.g. (ATC)₄ or (ATC)₇]. Furthermore, the same motif (ATC) may be present, and repeated at a different and unrelated SSR locus. Therefore an SSR locus is defined by the non-repeated sequences flanking the repeated motif. Primers complementary to the non-repeated flanking

sequences may be used to amplify the repeated region by polymerase chain reaction (PCR). The PCR products may be separated, by methods described herein, to identify individually possessing different alleles of the SSR locus, with different numbers of repeats. Thus the PCR primer sequences (excluding the italicised M13 and PIGtail sequences) in Table 2, and/or sequences complementary to those primer sequences (excluding the italicised M13 and PIGtail sequences), define the SSR markers specified in that table.

"Polymorphism" is a condition in DNA in which the most frequent variant (or allele) has a population frequency which does not exceed 99%.

The term "an SSR in linkage disequilibrium (LD) with CP34" means that the alleles of the SSR are in LD with the CP34 SSR marker.

The term "linkage disequilibrium" or LD as used herein, refers to a derived statistical measure of the strength of the association or co-occurrence of two independent genetic markers. Various statistical methods can be used to summarize linkage disequilibrium (LD) between two markers but in practice only two, termed D' and V^2 , are widely used.

"Altered" for any particular performance trait means altered relative to an animal of the same breed that does not possess the specified allele.

"Performance trait" means any trait of commercial significance in sheep breeding. Preferred performance traits include weaning weight (WWT), body weight at 8 months (LW8), body weight at 12 months (LW12), carcass weight (CW), adult ewe weight (EWT), eye muscle width (EMW), eye muscle depth (EMD), eye muscle area (EMA), fat depth (FD), carcass fat weight (FAT), carcass lean muscle weight (LEAN), number of lambs born (NLB), lamb fleece weight (LFW), hogget fleece weight (FW12), ewe (adult) fleece weight (EFW), hogget fibre diameter (FDIAM), and resistance to gastrointestinal parasitic nematode infection.

The applicants have identified several novel SSR markers that are in LD with the CP34 marker. The CP34 marker has previously been reported to be weakly associated with the resistance to parasitic nematode resistance. The applicants have now shown that, surprisingly, the CP34 marker, and several markers in LD with CP34, are strongly associated with several other

performance traits in ovine, and strongly associated with parasitic nematode resistance. That is the CP34 marker and the markers in LD with CP34, are themselves in LD with these performance traits.

- 5 The invention therefore provides a method for identifying an ovine with a genotype indicative of at least one, and preferably two altered performance traits, the method including the step of detecting, in a sample derived from the ovine, the presence of an allele of the CP34 simple sequence repeat (SSR) marker or an allele of a marker in linkage disequilibrium (LD) with CP34, wherein the presence of the allele is indicative of the altered performance traits in the
10 ovine.

Detecting specific polymorphic markers and/or haplotypes can be accomplished by methods known in the art for detecting sequences at polymorphic sites. For example, standard techniques for genotyping for the presence of single nucleotide polymorphisms (SNPs) and/or SSR markers
15 can be used, such as fluorescence-based techniques (Chen, X. et al., *Genome Res.* 9(5): 492-98 (1999)), utilizing PCR, LCR, Nested PCR and other techniques for nucleic acid amplification. Specific methodologies available for SNP genotyping include, but are not limited to, TaqMan genotyping assays and SNPLex platforms (Applied Biosystems), mass spectrometry (e.g., MassARRAY system from Sequenom), minisequencing methods, real-time PCR, Bio-Plex
20 system (BioRad), CEQ and SNPstream systems (Beckman), Molecular Inversion Probe array technology (e.g., Affymetrix GeneChip), BeadArray Technologies (e.g., Illumina GoldenGate and Infinium assays) and oligonucleotide ligation assay (OLA – Karim *et al.*, 2000, *Animal Genetics* 31: 396-399). By these or other methods available to the person skilled in the art, one or more alleles of polymorphic markers, including SSRs, SNPs or other types of polymorphic
25 markers, can be identified.

A number of methods are thus available for analysis of polymorphic markers. Assays for detection of markers fall into several categories, including, but not limited to direct sequencing assays, fragment polymorphism assays, hybridization assays, and computer based data analysis.
30 Protocols and commercially available kits or services for performing multiple variations of these assays are available. In some embodiments, assays are performed in combination or in hybrid (e.g., different reagents or technologies from several assays are combined to yield one assay). The following are non-limiting examples of assays are useful in the present invention.

Direct Sequencing Assays

In some embodiments of the present invention, markers are detected using a direct sequencing technique. In these assays, DNA samples, such as those derived from for example blood, saliva or mouth swab samples, are first isolated from an ovine using any suitable method. In some embodiments, the region of interest is cloned into a suitable vector and amplified by growth in a host cell (e.g., a bacteria). In other embodiments, DNA in the region of interest is amplified using PCR. DNA in the region of interest (e.g., the region containing the marker of interest) is sequenced using any suitable method, including but not limited to manual sequencing using radioactive marker nucleotides, or automated sequencing. The results of the sequencing are displayed using any suitable method. The sequence is examined and the presence or absence of a given polymorphic marker is determined.

PCR Assay

In some embodiments of the present invention, polymorphisms are detected using a PCR-based assay. In some embodiments, the PCR assay comprises the use of oligonucleotide primers to amplify a fragment containing the polymorphic marker of interest. Such methods are particularly suitable for detection of alleles of SSR markers. The presence of an additional repeats in such an SSR marker, results in the generation of a longer PCR product which can be detected by gel electrophoresis, and compared to the PCR products from individuals without that allele of the SSR marker.

In other embodiments, the PCR assay comprises the use of an oligonucleotide primer that distinguishes (by hybridisation or non-hybridisation) between an allele containing a specific marker, and alternative alleles. Thus in certain embodiments, if PCR results in a product, then the ovine has the marker, and if no PCR product is produced, the ovine does not have the marker.

Fragment Length Polymorphism Assays

In some embodiments of the present invention, presence of the marker is detected using a fragment length polymorphism assay. In a fragment length polymorphism assay, a unique DNA

banding pattern based on cleaving the DNA at a series of positions is generated using an enzyme (e.g., a restriction endonuclease). DNA fragments from a sample containing the marker of interest will have a different banding pattern samples that do not contain the marker.

5 *RFLP Assay*

In some embodiments of the present invention, presence of the marker is detected using a restriction fragment length polymorphism assay (RFLP). The region of interest is first isolated using PCR. The PCR products are then cleaved with restriction enzymes known to give a unique
10 length fragment for a given polymorphic marker. The restriction-enzyme digested PCR products may be separated by agarose gel electrophoresis and visualized by ethidium bromide staining. The length of the fragments is compared to molecular weight standards and fragments generated from test and control samples, to identify test samples containing the marker.

15 *CFLP Assay*

In other embodiments, presence of the polymorphic marker is detected using a CLEAVASE fragment length polymorphism assay (CFLP; Third Wave Technologies, Madison, WI; and U.S. Patent No.5,888,780).

20

Hybridization Assays

In preferred embodiments of the present invention, presence of a marker is detected by hybridization assay. In a hybridization assay, the presence or absence of a given marker
25 sequence is determined based on the ability of the DNA from the sample to hybridize to a complementary DNA molecule (e.g., a oligonucleotide probe). A variety of hybridization assays using a variety of technologies for hybridization and detection are available. A description of a selection of such assays is provided below.

Direct Detection of Hybridization

In some embodiments, hybridization of a probe to the marker sequence of interest is detected directly by visualizing a bound probe (e.g., a Northern or Southern assay; See e.g., Ausabel et al. (eds.), Current Protocols in Molecular Biology, John Wiley & Sons, NY, 1991). In these assays, genomic DNA (Southern) or RNA (Northern) is isolated from a subject. The DNA or RNA is then cleaved with a series of restriction enzymes that cleave infrequently in the genome and not near any of the markers being assayed. The DNA or RNA is then separated (e.g., agarose gel electrophoresis) and transferred to a membrane. A labeled (e.g., by incorporating a radionucleotide) probe or probes specific for the marker sequence being detected is allowed to contact the membrane under a condition of low, medium, or high stringency conditions. Unbound probe is removed and the presence of binding is detected by visualizing the labeled probe.

Detection of Hybridization Using "DNA Chip" Assays

In some embodiments of the present invention, the presence of the marker is detected using a DNA chip hybridization assay. In this assay, a series of oligonucleotide probes are affixed to a solid support. The oligonucleotide probes are designed to be unique to a given polymorphic maker sequence. The DNA sample of interest is contacted with the DNA "chip" and hybridization is detected.

In some embodiments, the DNA chip assay is a GeneChip (Affymetrix, Santa Clara, CA; See e.g., U.S. Patent No. 6,045,996) assay. In other embodiments, a DNA microchip containing electronically captured probes (Nanogen, San Diego, CA) is utilized (See for example U.S. Patent No. 6,068,818).

In still further embodiments, an array technology based upon the segregation of fluids on a flat surface (chip) by differences in surface tension (ProtoGene, Palo Alto, CA) is utilized (See for example U.S. Patent No. 6,001,311).

In yet other embodiments, a "bead array" is used for the detection of polymorphic marker (Illumina, San Diego, CA; See for example PCT Publications WO 99/67641 and WO 00/39587, each of which is herein incorporated by reference).

5 *Enzymatic Detection of Hybridization*

In some embodiments of the present invention, genomic profiles are generated using a assay that detects hybridization by enzymatic cleavage of specific structures (INVADER assay, Third Wave Technologies; See e.g., U.S. Patent No. 6,001,567). The INVADER assay detects specific
10 DNA and RNA sequences by using structure-specific enzymes to cleave a complex formed by the hybridization of overlapping oligonucleotide probes.

In some embodiments, hybridization of a bound probe is detected using a TaqMan assay (PE Biosystems, Foster City, CA; See e.g., U.S. Patent No. 5,962,233). The assay is performed
15 during a PCR reaction. The TaqMan assay exploits the 5'-3' exonuclease activity of the AMPLITAQ GOLD DNA polymerase. A probe, specific for a given allele or mutation, is included in the PCR reaction. The probe consists of an oligonucleotide with a 5'-reporter dye (e.g., a fluorescent dye) and a 3'-quencher dye. During PCR, if the probe is bound to its target, the 5'-3' nucleolytic activity of the AMPLITAQ GOLD polymerase cleaves the probe between
20 the reporter and the quencher dye. The separation of the reporter dye from the quencher dye results in an increase of fluorescence. The signal accumulates with each cycle of PCR and can be monitored with a fluorimeter.

In still further embodiments, presence of the marker sequence is detected using the SNP-IT
25 primer extension assay (Orchid Biosciences, Princeton, NJ; See e.g., U.S. Patent No. 5,952,174).

Mass Spectroscopy Assay

In some embodiments, a MassARRAY system (Sequenom, San Diego, CA.) is used to detect
30 presence of the polymorphic marker (See e.g., U.S. Patent No. 6,043,031).

Protein based marker detection

It will be appreciated that if the marker linked to CP34 is in a protein coding region, presence of the marker may result in an amino acid change in the encoded protein. In such cases, any suitable method for detecting the presence of the characteristic amino acid in a protein or polypeptide may be applied. Typical methods involve the use of antibodies for detection of the protein polymorphism. Methods for producing and using antibodies are well known to those skilled in the art and are described for example in *Antibodies, A Laboratory Manual*, Harlow A Lane, Eds, Cold Spring Harbour Laboratory, 1998.

The polynucleotides, markers, primers and probes of the invention can be used to derive estimates for the association of each allele of the markers, in a reference population measured, for the traits of interest using a variety of statistical methods such as mixed models. These estimates coupled with a derived economic value for each trait can be used to rank individuals based solely on their genotype at a young age, or a mixture of their genotype estimates and selected subsets of the traits of interest. This approach is useful to rank individuals for their breeding worth.

Alternatively, the genotype information that can be generated using the polynucleotides, markers, primers and probes of the invention, may be considered as a fixed or random effect in an animal model Best Linear Unbiased Prediction (BLUP) or via mixed models (Mrode, 1996) where animals have parentage and various combinations of traits recorded. This approach would be useful for young animals that have not been recorded for the traits of primary interest, to rank individuals on their likely future performance.

The above approaches are not limited to detecting only CP34, or markers in LD with CP34, but also to situations where CP34, or markers in LD with CP34, which are included as part of a larger marker set from several additional markers to many thousands of markers, and the combined estimates of all markers are used to estimate the genetic worth of an individual or its likely individual performance.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a linkage disequilibrium plot for 847 animals consisting of Coopworth, Perendale Romney, Texel and Composite sires used in the analysis. The upper diagonal lists the pairwise D' (D_p) LD measurement between markers and the lower diagonal lists the Cramer's V squared (V^2) LD measurement. The markers are listed in bovine genome order which is the inverse of the ovine genome order. In the current context markers with D' values with CP34 greater than 0.3 or V^2 greater than 0.1 are considered to define the boundaries of useful LD. This includes the region defined by BMS1887400 to BMS1081770.

Figure 2 shows a pairwise plot of the statistical significance of the linkage disequilibrium plot for the 847 animals consisting of Coopworth, Perendale Romney, Texel and Composite sires used in the analysis expressed on a $-\log_{10}(p)$ scale. All markers flanking CP34 and extending to BMS1887400 and BMS1081770 showed very highly significant association via linkage disequilibrium with CP34 with $-\log_{10}(p)$ values ranging from 3.6 to 338.8.

Figure 3 shows allele effect estimates by marker and the significance of the estimates expressed as probability (p) values.

EXAMPLES

The invention will now be illustrated with reference to the following non-limiting examples.

Example 1: Mapping performance traits in sheep in the ovine chromosome 3p region

Introduction

The only marker that had been previously described in the ovine chromosome 3p region in this work is CP34 (Ede et al. 1995). Beh *et al.*, (2002) reported a small QTL present in one sire for resistance to parasitic nematode infection as assessed by fecal egg count (FEC) in the autumn at the 5% chromosome wide significance threshold located near CP34. Crawford *et al.*, (2006) reported a similar result for 1 sire for FEC1, and another sire for abomasal adult *Ostertagia*

numbers, but in contrast Davies *et al.*, (2006) found no evidence of segregation in this region for FEC or antibody traits. To the applicant's knowledge no other trait associations have been reported in sheep in this region. In addition, work reported to date has been by linkage mapping which, at the marker density and animal numbers used, only defines a general region of perhaps 40cM (~40Mbp) in length in which the QTL may reside, and has little or no predictive value in industry because no marker allele associations have been determined that can be used on independent groups of animals. In order to create such associations typically marker density has to be higher than several markers per cM and numerous pedigrees need to be tested.

10 Methods

WormFEC sire resource

The WormFEC resource (McEwan et al 2006) consists of 987 primarily male progeny tested sheep sourced from New Zealand recorded flocks and consisting of individuals of Coopworth, Romney, Perendale, Texel, Composite and other minor breeds. A subset of 847 sires, derived from 111 flocks, were used for this analysis. There were 126,004 progeny weaned from these sires with a median progeny group size of 117 (range 1-2017).

They consisted of:

Coopworth. The breed sample consisted of 362 industry animals used between 2000 and 2006. All animals in this dataset are more than 50% Coopworth.

Perendale. The breed sample consisted of 148 industry animals used between 2000 and 2006. All animals in this resource are more than 50% Perendale.

Romney. The breed sample consisted of 279 animals used between 2000 and 2006. All animals in this dataset are more than 50% Romney.

Texel. The breed samples consist of 27 animals used between 2000 and 2006. All animals in this dataset are more than 50% Texel.

Composites. There were 31 Composites breed animals from the WormFec Sire resource used 2000-2006.

Parasite selection line resources

The Romney host resistance parasite selection line was initially created in 1979 and has been recently described by Morris et al (2000). Over the selection period these animals have diverged in fecal egg count (FEC) after a standard challenge by 40 fold. They currently consist of 3 FEC selection lines a low, a high and a control line. For the current work DNA samples were collected from 50 susceptible (high) line, 50 resistant (low) line and 53 control line animals in 1997 and were genotyped for the markers described below.

The Perendale host resistance parasite selection line was initially created in 1985 and has recently been described by Morris et al (2005). Over the selection period these animals have diverged in FEC after a grazing challenge by 4.9 fold. They currently consist of 2 selection lines a low and high FEC line respectively. For the current work DNA samples were collected from 107 susceptible line animals and 128 resistant line animals in 1998 and were genotyped for the markers described below.

SIL ACE EBVs

Performance recording and estimated breeding values (EBVs) are produced in New Zealand by Sheep Improvement Limited (SIL) a trading entity of Meat & Wool New Zealand. The underlying methodology and system used has been described in a number of papers (Geenty, 2000; Amer, 2000; Newman et al., 2000).

The traits recorded and described in this study and further background to the SIL system is at <http://www.sil.co.nz/Technical%20Bullentins/Technical%20Notes/> and trait descriptions from this site are attached to this document including: Young and Walker, (2007a) describing trait measurements and breeding values, Young and Walker (2007b) describing SIL indices and sub indices and economic weights, McEwan (2006) and Young (2006) describing recording for host resistance selection in sheep, and Young (2005) describing New Zealand wide across flock and breed genetic evaluations to produce SIL Advanced Central Evaluation (ACE) EBVs and indices. In turn the SIL ACE EBVs are underpinned by the nationwide central progeny test (CPT) project recently described by McLean et al. (2006).

In brief the genetic evaluations use an across flock and breed multi-trait animal model BLUP analysis for all traits, except for NLB and host resistance traits which used across flock and breed multi-trait repeated measures animal model BLUP. Typically these analyses are done in goal
5 trait group combinations. The outputs of these evaluations for individuals are breeding values corrected for flock, year and breed effects. These breeding values are “shrunk” based on the accuracy of the EBV, primarily in this case being affected by the number of measured progeny. This effect is particularly pronounced for situations where only low progeny numbers have been measured.

10 This analysis used the June 2007 across flock and breed SIL ACE evaluation EBVs for the sires. Values for the individual sires were downloaded from a direct database query as these estimates are not publicly available except to authorized personnel. Details of the overall evaluation description (Newman, 2007) are attached as an appendix. Only the subset of animals that were
15 genetically linked, as described by the SIL ACE criteria were included in this work.

SSR discovery and mapping process

Novel ovine SSR markers were identified and validated by the following process. The region of
20 interest from the orthologous section of the bovine genome was processed for suitable dinucleotide SSRs with more than 9 repeats using the program Sputnik and then primers designed using Primer 3 using an independent, but analogous approach to that described by Robinson et al. (2004). The bovine genome assembly used was version 3.1 and is available as <ftp://ftp.hgsc.bcm.tmc.edu/pub/data/Btaurus/fasta/> as the Btau20040927-freeze and distances are
25 reported on that basis. The primers had a M13 antisense and PIGtail sequence added to them and were then used to PCR amplify DNA samples in conjunction with a fluorescent M13 oligo as described by Boutin-Ganache et al. (2001) and Saito et al. (2005). The size of the resulting products were then measured using standard manufacturer procedures and protocols on a ABI 3730 sequencer. The primers were first screened over a panel of cattle, sheep and deer samples.
30 Markers that passed the initial screen (i.e. were polymorphic in sheep and of reasonable quality see tables 1 and 2 for a list of primers and markers finally selected) were subsequently genotyped across the International Mapping Flock (IMF; Maddox et al. 2001). This allowed the markers to be mapped confirming their location to the region of interest and their suitability for genotyping.

Distances and order reported here used markers available in the latest publicly available map v4.7 (<http://rubens.its.unimelb.edu.au/~jillm/jill.htm>) and the genotypes obtained from the present study. CRI-Map was used to do the linkage mapping using the process described by Maddox et al. (2001). Markers that mapped to the appropriate location were then genotyped by the same method for the WormFEC sires and Parasite Selection Line (PSL) resources. Results from all the genotyping from the 3730 were measured as raw allele lengths using ABI GeneMapper 4.0 and reported as fragment lengths in base pair units relative to internal standards. These results were binned into alleles on the basis of a cluster analysis based on Ward's distance using SAS (<http://www.sas.com/>) to define mean allele lengths and reporting variability. The allele names and bins for each marker are shown in Table 3.

Because of uncertainty of marker order and the quality of the bovine assembly a number of markers were mapped using an ovine 5000 RAD ovine Radiation hybrid panel (Eng et al. 2004). This can more accurately position closely spaced markers and acts as a check on the bovine genome assembly. Panel cell lines were genotyped in duplicate using the primers described above for the RH panel and visualised by running on 2% Agarose gels as described by Band et al. (2000). Presence or absence of markers in each cell line was scored and the resulting data mapped using RHmapper (Slonim et al. 1997).

20 **Estimation of linkage disequilibrium**

Linkage disequilibrium measures were calculated using the program **LDMAX** part of the **GOLD** package (Abecasis and Cookson, 2000) and the R statistical package (<http://www.r-project.org/>). The measures D' , the square of Cramer's V and the significance expressed as a probability of the association were calculated for all combinations of markers and plotted using a combination of the graphics facilities in SAS (<http://www.sas.com/>) and R. Each measure is useful for certain purposes and in this case we used a threshold of $D' > 0.3$ or $V^2 > 0.1$ and $p < 1 \times 10^{-10}$ with CP34 to delimit the boundaries of the region containing significant linkage disequilibrium. Because of the nature of linkage disequilibrium between individual markers, not all markers within this region may be in significant LD.

Analysis of selection line allele frequency differences

The genotype results for each marker, for the two Parasite selection lines were tested for differences in allele frequency using the computer program **Peddrift** (Dodds and McEwan, 1997). This program estimates the likely distribution of allele frequencies between selection lines caused by random founder effects and genetic drift by simulation using the actual recorded pedigree structure. Significant divergence from the expected distribution is evidence of selection on a variant, near the genotyped marker, affecting the trait under selection: in this case fecal egg counts after a field challenge of gastrointestinal internal nematode parasites.

Analysis of marker associations

Breeding values for the genotyped individuals were analyzed in the following manner. The EBVs for traits were adjusted for breed (even though EBVs had already been adjusted for this effect) with each marker allele fitted independently as a covariate (0=none, 1 = one allele, 2 = 2 alleles) in a least squares model after the method of Fan et al. (2006). Fitting breed reduces the bias of admixture i.e. when the marker is associated with breed and true differences exist between breeds.

Results

Markers and map positions

The markers and their map positions are tabulated in Table 1. The BTA version 3.1 bovine genome assembly position given is 300bp upstream of the actual dinucleotide repeat motif. The whole region is defined as including: the 300bp upstream fragment, the dinucleotide repeat motif itself, and 300bp downstream sequence. It was from this segment of DNA that the primers in Table 2 were designed. The markers are ordered in declining assembly order on bovine BTA11. The actual alleles observed and the length of their corresponding PCR products as measured by the ABI 3730 sequencer is tabulated in Table 3.

The IMF map positions are listed in centiMorgans (cM) defined from using a framework map starting from BMS1350 marker as 0 (not shown) and inserting the new BMS markers in their best location. Note some markers are unmapped and for some markers the order is not consistent with the bovine assembly order e.g. BMS1082722. The reasons for this are many. First the IMF resource can only reliably order markers greater than 5cM apart. There also exists the possibility the bovine assembly is incorrect or that a genotyping error has occurred. Although in the latter case all apparent double recombinants have had their genotypes checked and where necessary eliminated. In other cases linkage mapping ordered markers that are not positioned in the current bovine genome assembly but can be ordered by linkage mapping.

The radiation hybrid map orders the markers in centiRays (cR) starting from zero, for BMS1082956. In theory this mapping technique should be more sensitive for ordering markers than linkage mapping in the IMF and appears to be able to discriminate and order markers where linkage mapping could not. However there were some apparent differences in order between the ovine and bovine genomes and it is not clear whether these are real or minor assembly and mapping discrepancies.

Selection lines allele frequency differences

Table 4 lists the markers and the significance probability for an allele frequency difference between selection lines (resistant vs susceptible) after adjusting for founder effects and genetic drift. The assumption is that the allele frequencies have changed due to selection effects on a nearby locus in linkage disequilibrium with the measured marker. Four markers showed significant differences in allele frequency between selection lines in the Perendale flocks: BMS1784528, BMS1600436 BMS1081760 and BMS30480889. As shown later, all of these markers are located within the boundary defined by BMS1887400 to BMS1081770. In contrast no association was observed for any marker in the Romney selection lines.

WormFEC sire resource association with production and host resistance traits

Figure 3 lists for each marker tested for association in the WormFEC sire resource the various EBV allele estimates, their significance and the count of the alleles observed. All markers with the exception of BMS1080870 and BMS1082045 have allele significant associations ($P < 0.05$) for more than one trait and within the boundary defined by BMS1887400 to BMS1081770 it is typically many traits. For example for CP34 it is 24 of the 25 traits listed.

Marker linkage disequilibrium with CP34

In the current context, markers with D' values with CP34 greater than 0.3 or V^2 greater than 0.1 are considered to define the boundaries of useful LD, if they also have significant linkage disequilibrium with CP34. Based on the results presented in figure 1 and figure 2 this includes the region defined by BMS1887400 to BMS1081770. The linkage mapping distance between these 2 markers is 4.8cM. Its estimated ovine genomic length, based on direct comparison with the bovine assembly, it is slightly greater than 1 million base pairs.

Example of predictive ability of markers in industry animals

The utility of the predictive ability is provided in the following example, but is not restricted solely to this approach. Selected CP34 trait estimated breeding value allele associations and their economic values (Young and Walker, 2007b) have been combined into an economic index in Table 5. The individual allele estimates are additive so an animal that has a genotype of AA will have, in the absence of other information, a predicted value of $66+66 = 132$ cents versus an animal with a EE genotype of $-81+-81 = -162$ cents. Used in this way individual animals can be ranked for breeding purposes. When estimated breeding values and their accuracies derived from trait measurements have been calculated, these marker based estimates can be blended to create an overall index using selection index theory and the relative accuracies of the two predictions. A further alternative is to fit the CP34 allele as either a fixed or random effect within the standard animal model BLUP evaluation.

Table 1 below, shows the map positions of the SSR markers identified.

Table 1

Marker Name	Bovine BTA11 position (Mbp)	IMF position Chr3 (cM)	RH position Chr3 (cR)
BMS1084327	95234751	23.7	unmapped
BMS1082942	93758528	25.1	25.2
BMS1082956	93726770	25.1	0
BMS1082961	93712544	25.1	0
BMS1083945	93639984	25.1	25.2

Marker Name	Bovine BTA11 position (Mbp)	IMF position Chr3 (cM)	RH position Chr3 (cR)
BMS1083008	93473429	25.1	0
BMS1082252	89948180	unmapped	37.9
BMS1082669	88338219	30.4	65.5
BMS1082702	88245390	unmapped	unmapped
BMS1082722	88195495	29.4	65.5
BMS1082831	87126578	32.3	unmapped
BMS1887400	86996579	33	unmapped
BMS1887404	86985063	33	unmapped
BMS1784528	86739524	33	unmapped
BMS1600436	86671265	33.9	106.6
CP34	86655663	33.9	106.6
BMS1082043	86431911	35.2	98.5
BMS1082045	86438829	35.8	128.5
BMS1081952	86251004	35.8	101.2
BMS1081760	86017933	35.8	unmapped
BMS1081860	ChrUn.003.1357	35.8	128.5
BMS30480882	85850308	37.7	unmapped
BMS30480889	85863541	37.7	unmapped
BMS1081770	85981658	37.8	unmapped
BMS1081774	85964979	37.8	unmapped
RSAD2_1	85650772	38.9	135.7
BMS1081640	~85442209	41.1	89.9
BMS1080704	84881378	43.2	unmapped
BMS1080870	71477314	43.6	unmapped

* map positions refer to the relative start positions of the SSR

Table 2, below shows the primer sequences used to amplify the SSR markers identified.

Table 2

Marker name		Primer Sequences	SEQ ID NO:	(SSR Motif) ⁿ
BMS1084327	Fwd	<i>TGAAAACGACGGCCAGTTCCTTCCCCAGACAGTCAC</i>	1	AC
	Rev	<i>GTTTCTTTGTGTATTTGGGAGGGGTGT</i>	2	
BMS1082942	Fwd	<i>TGAAAACGACGGCCAGTCATGTGTGTCAACATCAATCCA</i>	3	AC
	Rev	<i>GTTTCTTTCCATCCAGACAATACAGCAA</i>	4	
BMS1082956	Fwd	<i>TGAAAACGACGGCCAGTACTGGTCAAGCAGACCATCT</i>	5	AC
	Rev	<i>GTTTCTTCCCATGTTTCAGGCGTTATCT</i>	6	
BMS1082961	Fwd	<i>TGAAAACGACGGCCAGTGGCAGGTGAAAATACTTGCTG</i>	7	AC
	Rev	<i>GTTTCTTTGATGAGGCAGCTCATTGAC</i>	8	
BMS1083945	Fwd	<i>TGAAAACGACGGCCAGTCAAGATGAATGATCCCATGC</i>	9	AG
	Rev	<i>GTTTCTTTCAGCCCAGGAGTTAAACATT</i>	10	
BMS1083008	Fwd	<i>TGAAAACGACGGCCAGTGCCTCTCAGATGGCAGAGC</i>	11	AC
	Rev	<i>GTTTCTTTGGAGACATTAGTGTGTGCTCAT</i>	12	
BMS1082252	Fwd	<i>TGAAAACGACGGCCAGTATGGTCACCACTGCACTGAC</i>	13	AC
	Rev	<i>GTTTCTTAAGGCAGGCAAGTATTTGGA</i>	14	
BMS1082669	Fwd	<i>TGAAAACGACGGCCAGTGGGGAGTATGCAATTCAGGA</i>	15	AC
	Rev	<i>GTTTCTTTACAGGCCAAAGGGAATTTG</i>	16	
BMS1082702	Fwd	<i>TGAAAACGACGGCCAGTGCGTGTGGATAGCGTGAGTA</i>	17	AC
	Rev	<i>GTTTCTTTTGAGACCCCAGTCCAGAAG</i>	18	
BMS1082722	Fwd	<i>TGAAAACGACGGCCAGTGGATATCAGGGAGTGGGATG</i>	19	AC
	Rev	<i>GTTTCTTTCCCCTGATGTTAGCAGCTT</i>	20	
BMS1082831	Fwd	<i>TGAAAACGACGGCCAGTCTGCTCCATATCACGACAGC</i>	21	AC
	Rev	<i>GTTTCTTTGGTCTTGGTGGTCTGTTG</i>	22	
BMS1887400	Fwd	<i>TGAAAACGACGGCCAGTGAAAGGTGGTGGTCTCCTTG</i>	23	AC
	Rev	<i>GTTTCTTTGAGAGAAGACCTGGGGAGA</i>	24	
BMS1887404	Fwd	<i>TGAAAACGACGGCCAGTGGGTCGTAGAGAGTTGAACACA</i>	25	AC
	Rev	<i>GTTTCTTGCTGTCTCTTTCACTCCAAAATC</i>	26	
BMS1784528	Fwd	<i>TGAAAACGACGGCCAGTCTCTGAGCCATATGGGAAGC</i>	27	AT
	Rev	<i>GTTTCTTTTCCACAGTGTTTCAGATGTATAGC</i>	28	
BMS1600436	Fwd	<i>TGAAAACGACGGCCAGTTCAGGAAGTGGTAGGCAGAGA</i>	29	AC
	Rev	<i>GTTTCTTTACCACTGAGCCACCAGAGA</i>	30	

Marker name		Primer Sequences	SEQ ID NO:	(SSR Motif) ⁿ
CP34	Fwd	<i>TGTAAAACGACGGCCAGT</i> GCTGAACAATGTGATATGTTTCAGG	31	AC
	Rev	<i>GTTTCTTGGGACAATACTGTCTTAGATGCTGC</i>	32	
BMS1082043	Fwd	<i>TGTAAAACGACGGCCAGT</i> GGGAAACCCACACAACAGAG	33	AC
	Rev	<i>GTTTCTTGGAGAATGGCATGGACAGAG</i>	34	
BMS1082045	Fwd	<i>TGTAAAACGACGGCCAGT</i> TCTTCAGCACTCAGCCTTCT	35	AC
	Rev	<i>GTTTCTTTCAGTCTGGATATGGTGGA</i>	36	
BMS1081952	Fwd	<i>TGTAAAACGACGGCCAGT</i> TGCAAGGTTAGACTTTGGTGA	37	AC
	Rev	<i>GTTTCTTTGTTCCAGACCAGTATTTTCAG</i>	38	
BMS1081760	Fwd	<i>TGTAAAACGACGGCCAGT</i> CTCAAAACGACAAAGCCACA	39	AT
	Rev	<i>GTTTCTTAGGACCGGCTGTATAGCACA</i>	40	
BMS1081860	Fwd	<i>TGTAAAACGACGGCCAGT</i> GCAGGCTGGTTCTTTACCAC	41	AC
	Rev	<i>GTTTCTTTTGTGGTAGGTTTCACCAAGG</i>	42	
BMS30480882	Fwd	<i>TGTAAAACGACGGCCAGT</i> GCAAATGGCCAAATGTCATC	43	AT
	Rev	<i>GTTTCTTCATGCACCCCAATGTTTCATA</i>	44	
BMS30480889	Fwd	<i>TGTAAAACGACGGCCAGT</i> CTTGATCACTGAGCCACCA	45	AC
	Rev	<i>GTTTCTTTCAGCAAAGAGGCTGGTACA</i>	46	
BMS1081770	Fwd	<i>TGTAAAACGACGGCCAGT</i> AAAGCGTTGCTATCTGTCACAA	47	AC
	Rev	<i>GTTTCTTGCTGTCCTGAGCACATAGGG</i>	48	
BMS1081774	Fwd	<i>TGTAAAACGACGGCCAGT</i> TGGAATCCCTTGGACAGAAC	49	AC
	Rev	<i>GTTTCTTCCCTGACTCCTAATGCCATC</i>	50	
RSAD2_1	Fwd	<i>TGTAAAACGACGGCCAGT</i> AGCAAACATGTGGGTGGTC	51	AC
	Rev	<i>GTTTCTTTTTGCAGAGCCGTATTTGTG</i>	52	
BMS1081640	Fwd	<i>TGTAAAACGACGGCCAGT</i> TTTATAGGTGTACAGCAGAGTGATG	53	AT
	Rev	<i>GTTTCTTGGAGGCTTGGTGTGCTACAG</i>	54	
BMS1080704	Fwd	<i>TGTAAAACGACGGCCAGT</i> ACTCACCTGAGTGCTCCAC	55	AC
	Rev	<i>GTTTCTTCTCCGGGGTTTCTCTTCTCT</i>	56	
BMS1080870	Fwd	<i>TGTAAAACGACGGCCAGT</i> AATGGGGCAGCAAAGAGTT	57	AC
	Rev	<i>GTTTCTTCTCCGGGGTTTCTCTTCTCT</i>	58	

*M13 sequence indicated in italic font (TGTAACGACGGCCAGT - SEQ ID NO:59)

Pigtail sequence indicated in italic font (GTTTCTT- SEQ ID NO:60)

Sequence not in italics, represents sequence of the ovine genome flanking the SSR marker and therefore is specific for the particular SSR locus

Table 3, below shows a summary of the allele information for the SSR markers identified.

Table 3

Marker name	No. of alleles	Bin name	Fragment sizes (bp)	Bin length (bp)	Number alleles CPRTC
BMS1084327	2	C	177.5 +/-0.7	2	
		D	179.5 +/-0.7		
BMS1082942	6	C	183.9 +/-0.7	2.2	
		D	186.1 +/-0.7		
		F	190.1 +/-0.7	2.1	
		G	192.2 +/-0.7		
		H	194.3 +/-0.7	2.1	
		I	196.4 +/-0.7	2.1	
BMS1082956	9	C	175.4 +/-0.7	2.2	1
		D	177.6 +/-0.7		74
		E	179.3 +/-0.7	1.7	664
		F	181.3 +/-0.7	2	263
		G	183.2 +/-0.7	1.9	287
		H	185.0 +/- 0.7	1.8	48
		I	186.9 +/-0.7	1.9	34
		J	188.7 +/-0.7	1.8	2
		K	190.5 +/-0.7	1.8	1
BMS1082961	2	C	176.1 +/-0.7	1.9	
		D	178.0 +/-0.7		
BMS1083945	3	C	154.6 +/-0.7	1.9	
		G	162.6 +/-0.7		
		H	164.5 +/-0.7		
BMS1083008	10	C	171.8 +/-0.45	2.1	1
		D	173.9 +/-0.45		
		E	175.7 +/-0.45	1.8	3
		F	187.4 +/-0.45		621

Marker name	No. of alleles	Bin name	Fragment sizes (bp)	Bin length (bp)	Number alleles CPRTC
		G	188.7 +/-0.45	1.3	243
		H	190.4 +/-0.45	1.7	496
		J	193.2 +/-0.45		2
		K	195.0 +/-0.45	1.8	
		L	196.9 +/-0.45	1.9	2
		M	204.4 +/-0.45		
BMS1082252	3	C	161.6 +/-0.7		
		D	163.5 +/-0.7	1.9	
		E	165.4 +/-0.7	1.9	
BMS1082669	10	C	183.7 +/-0.7		210
		D	185.6 +/-0.7	1.9	2
		F	189.6 +/-0.7		40
		J	197.1 +/-0.7		
		L	200.9 +/-0.7		16
		M	202.7 +/-0.7	1.8	738
		N	204.7 +/-0.7	2	223
		O	206.5 +/-0.7	1.8	129
BMS1082702	9	P	208.4 +/-0.7	1.9	8
		Q	210.3 +/-0.7	1.9	2
		C	199.5 +/-0.45		
		G	203.7 +/-0.45		
		I	205.6 +/-0.45		
		K	207.7 +/-0.45		
		L	213.8 +/-0.45		
		N	216.1 +/-0.41		

Marker name	No. of alleles	Bin name	Fragment sizes (bp)	Bin length (bp)	Number alleles CPRTC
		O	217.0 +/-0.41	0.9	
		Q	219.1 +/-0.45		
		S	221.1 +/-0.45		
BMS1082722	7	C	172.6 +/-0.7		
		E	176.6 +/-0.7		
		G	181.0 +/-0.7		
		H	182.9 +/-0.7	1.9	
		I	185.1 +/-0.7	2.2	
		L	191.3 +/-0.7		
		P	199.7 +/-0.7		
BMS1082831	10	C	172.9 +/-0.7		
		D	174.8 +/-0.7	1.9	
		E	188.1 +/-0.7		
		F	190.0 +/-0.7	1.9	
		G	192.0 +/-0.7	2	
		H	193.9 +/-0.7	1.9	
		M	203.4 +/-0.7		
		N	205.2 +/-0.7	1.8	
		Q	211.0 +/-0.7		
		R	212.7 +/-0.7	1.7	
BMS1887400	10	C	196.1 +/-0.45		188
		J	209.4 +/-0.45		29
		L	211.2 +/-0.43		29
		M	212.1 +/-0.42	0.9	155

Marker name	No. of alleles	Bin name	Fragment sizes (bp)	Bin length (bp)	Number alleles CPRTC
		N	213.1 +/-0.42	1	216
		P	215.0 +/-0.45		42
		R	216.9 +/-0.45		215
		T	218.8 +/-0.45		638
		V	220.7 +/-0.45		142
		X	222.6 +/-0.45		
BMS1887404	5	C	217.2 +/-0.7		197
		D	218.9 +/-0.7	1.7	1452
		E	221.1 +/-0.7	2.2	
		F	222.8 +/-0.7	1.7	9
		H	226.6 +/-0.7		
BMS1784528	12	C	161.3 +/-0.45		348
		D	163.3 +/-0.45	2	315
		F	166.0 +/-1.46		466
		G	168.7 +/- 0.45	2.7	51
		L	178.7 +/-0.45		
		M	180.7 +/-0.45	2	129
		N	182.6 +/-0.45	1.9	24
		O	184.7 +/-0.45	2.1	15
		P	186.6 +/-0.45	1.9	6
		Q	188.7 +/-0.45	2.1	1
		R	190.3 +/-0.45	1.6	37
		S	192.2 +/-0.45	1.9	30
BMS1600436	15	C	178.6 +/-0.7		60
		G	187.2 +/-0.7		69

Marker name	No. of alleles	Bin name	Fragment sizes (bp)	Bin length (bp)	Number alleles CPRTC
		H	189.2 +/-0.7	2	196
		I	191.3 +/-0.7	2.1	292
		J	193.3 +/-0.7	2	513
		K	195.5 +/-0.7	2.2	174
		M	199.5 +/-0.7		16
		P	205.4 +/-0.7		
		Q	207.5 +/-0.7	2.1	128
		T	213.2 +/-0.7		
		U	215.3 +/-0.7	2.1	147
		V	217.3 +/-0.7	2	46
		W	219.8 +/-0.7	2.5	4
		X	221.6 +/-0.7	1.8	
		Y	223.4 +/-0.7	1.8	11
CP34	8	F	134.3 +/-0.7		443
		E	136.3 +/-0.7	2	373
		D	138.3 +/-0.7	2	308
		C	140.4 +/-0.7	2.1	4
		B	142.5 +/-0.7	2.1	297
		A	144.6 +/-0.7	2.1	181
		G	146.7 +/-0.7	2.1	13
		H	148.8 +/-0.7	2.1	5
BMS1082043	9	C	148.0 +/-0.7		4
		D	150.3 +/-0.7	2.3	194
		E	152.5 +/-0.7	2.2	950
		F	154.6 +/-0.7	2.1	30
		H	158.9 +/-0.7		149
		J	163.2 +/-0.7		80
		K	165.2 +/-0.7	2	
		M	169.2 +/-0.7		

Marker name	No. of alleles	Bin name	Fragment sizes (bp)	Bin length (bp)	Number alleles CPRTC
		O	173.9 +/-0.7		1
BMS1082045	2	C	160.1 +/-0.7		1209
		D	162.0 +/-0.7	1.9	155
BMS1081952	7	C	181.7 +/-0.7		10
		D	183.8 +/-0.7	2.1	1
		G	189.9 +/-0.7		158
		H	192.0 +/-0.7	21	525
		J	196.1 +/-0.7		71
		K	198.2 +/-0.7	2.1	610
		N	204.3 +/-0.7		31
BMS1081760	5	A	170.5 +/-0.7		31
		B	172.5 +/-0.7	2	
		C	174.5 +/-0.7	2	1258
		D	176.5 +/-0.7	2	1
		E	178.5 +/-0.7	2	158
BMS1081860	29	C	204.5 +/-0.7		1
		D	206.5 +/-0.7	2	1
		E	208.3 +/-0.7	1.8	96
		F	210.3 +/-0.7	2	28
		G	212.2 +/-0.7	1.9	29
		H	214.0 +/-0.7	1.8	327
		I	215.8 +/-0.7	1.8	60
		J	217.7 +/-0.7	1.9	30
		K	219.5 +/-0.7	1.8	96
		L	221.5 +/-0.7	2	5
		M	223.4 +/-0.7	1.9	28
		N	225.2 +/-0.7	1.8	28
		O	227.1 +/-0.7	1.9	20

Marker name	No. of alleles	Bin name	Fragment sizes (bp)	Bin length (bp)	Number alleles CPRTC
		P	229.0 +/-0.7	1.9	55
		Q	230.9 +/-0.7	1.9	130
		R	232.7 +/-0.7	1.8	93
		S	234.6 +/-0.7	1.9	6
		T	236.5 +/-0.7	1.9	26
		U	238.4 +/-0.7	1.9	20
		V	240.4 +/-0.7	2	3
		W	242.4 +/-0.7	2	2
		X	244.2 +/-0.7	1.8	44
		Y	246.2 +/-0.7	2	155
		Z	248.0 +/-0.7	1.8	9
		5	259.4 +/-0.7		13
		6	261.4 +/-0.7	2	5
		7	263.3 +/-0.7	1.9	
		a	269.0 +/-0.7		4
		b	271.0 +/-0.7	2	4
BMS30480882	3	C	198.4 +/-0.7		1389
		D	200.3 +/-0.7	1.9	172
		E	202.3 +/-0.7	2	17
BMS30480889	16	C	188.8 +/-0.7		18
		D	190.7 +/-0.7	1.9	39
		E	192.7 +/-0.7	2	
		F	194.6 +/-0.7	1.9	65
		G	196.7 +/-0.7	2.1	4
		H	198.6 +/-0.7	1.9	319
		I	200.5 +/-0.7	1.9	641
		J	202.3 +/-0.7	1.8	50
		K	204.2 +/-0.7	1.9	15
		L	206.1 +/-0.7	1.9	91
		M	208.3 +/-0.7	2.2	40
		N	210.4 +/-0.7	2.1	71
		O	212.4 +/-0.7	2	19
		P	214.5 +/-0.7	2.1	105

Marker name	No. of alleles	Bin name	Fragment sizes (bp)	Bin length (bp)	Number alleles CPRTC
		Q	216.5 +/-0.7	2	5
		R	224.1 +/-0.7		
BMS1081770	16	B	213.8 +/-0.45		1
		C	215.6 +/-0.45	1.8	56
		D	217.5 +/-0.45	1.9	145
		E	219.5 +/-0.45	2	254
		F	221.4 +/-0.45	1.9	2
		G	223.2 +/-0.45	1.8	19
		H	225.2 +/-0.45	2	5
		I	227.0 +/-0.45	1.8	13
		J	228.8 +/-0.45	1.8	108
		K	230.3 +/-0.45	1.5	334
		L	232.1 +/-0.45	1.8	1
		M	234.5 +/-0.45	2.4	2
		N	236.4 +/-0.45	1.9	138
		O	238.3 +/-0.45	1.9	311
		P	240.2 +/-0.45	1.9	74
		Q	242.2 +/-0.45	2	1
BMS1081774	6	C	184.4 +/-0.7		
		D	186.6 +/-0.7	2.2	
		E	188.6 +/-0.7	2	
		F	190.8 +/-0.7	2.2	
		H	194.8 +/-0.7		
		I	196.9 +/-0.7	2.1	
RSAD2_1	2	C	189.7 +/-0.7		
		D	191.7 +/-0.7	2	
BMS1081640	4	C	144.8 +/-0.7		479
		D	147.1 +/-0.7	2.3	300
		E	149.3 +/-0.7	2.2	533
		F	151.5 +/-0.7	2.2	110

Marker name	No. of alleles	Bin name	Fragment sizes (bp)	Bin length (bp)	Number alleles CPRTC
BMS1080704	8	C	182.1 +/-0.7		226
		D	184.2 +/-0.7	2.1	652
		E	186.3 +/-0.7	2.1	333
		F	188.4 +/-0.7	2.1	173
		G	190.5 +/-0.7	2.1	
		H	192.6 +/-0.7	2.1	
		I	194.6 +/-0.7	2	32
		J	196.7 +/-0.7	2.1	2
BMS1080870	7	C	156.0 +/-0.7		155
		D	158.0 +/-0.7	2	181
		E	160.1 +/-0.7	2.1	456
		F	161.9 +/-0.7	1.8	4
		K	171.6 +/-0.7		1
		L	173.5 +/-0.7	1.9	617
		M	175.6 +/-0.7	2.1	2

Table 4, below shows Peddrift results by selection line expressed as $-\log_{10}(\text{significance probability})$.

5 Table 4

Marker Name	RSL	PSL
BMS1084327		
BMS1082942		
BMS1082956	0.208	0.237
BMS1082961		
BMS1083945		
BMS1083008	0.456	0.325
BMS1082252		
BMS1082669	0.432	0.263
BMS1082702		
BMS1082722		

BMS1082831		
BMS1887400	0.340	0.753
BMS1887404	mono	0.785
BMS1784528	0.228	1.3224
BMS1600436	0.412	3.1549
CP34	0.842	0.799
BMS1082043	0.403	0.068
BMS1082045	0.080	0.112
BMS1081952	0.394	0.334
BMS1081760	0.347	1.3401
BMS1081860	0.236	0.412
BMS30480882	0.507	0.223
BMS30480889	0.011	1.367
BMS1081770	0.010	1.1238
BMS1081774		
RSAD2_1		
BMS1081640	0.215	0.636
BMS1080704	0.577	0.652
BMS1080870	0.282	1.161

* -log₁₀(p) values

RSL: Romney Selection Line

PSL: Perendale Selection Line

5 Allele effects by marker and significance are shown in Figure 3.

Table 5 below shows allele estimates for CP34 for the BV traits analyzed for the Romney, Coopworth, Perendale, Texel and Composite analysis in their standard SIL trait units coupled with combined standard SIL economic estimates in cents for: growth adjusted for meat value (Gm), Meat value adjusted for growth (Mg), wool, Number of lambs born/ewe wintered (NLB), and combined host resistance (FEC) plus their additive overall index sum. Significance values for each trait are listed at the bottom (* P<0.05, ** P<0.01, *** P<0.001)

Table 5.

allele	no.	WWTBV	EWTBV	CWBV	LFWBV	FW12BV	EFWBV	LEANBV	FATBV	NLBBV	FEC1BV	FEC2BV	AFECBV	Gm	Mg	wool	NLB	Fec	index
A	180	0.20	0.43	0.09	0.01	0.08	0.07	0.06	0.02	-0.01	-5.45	-6.15	-6.32	5	14	34	-36	49	66
B	297	0.06	-0.08	0.00	-0.01	-0.04	-0.03	0.00	0.00	0.02	3.58	3.64	4.26	13	0	-16	54	-32	19
C	4	-0.66	-0.52	-0.38	-0.03	-0.21	-0.19	-0.37	-0.04	-0.05	-3.03	-4.06	2.13	-92	-101	-91	-126	15	-394
D	307	-0.05	-0.01	-0.02	0.01	0.04	0.04	-0.01	0.00	0.00	0.26	0.55	-0.06	-7	-3	18	-11	-2	-5
E	373	-0.28	-0.61	-0.15	-0.01	-0.06	-0.05	-0.13	-0.04	0.00	-0.40	1.33	2.15	-10	-31	-24	-9	-8	-81
F	443	0.10	0.33	0.08	0.00	0.01	0.01	0.07	0.03	0.00	0.31	-1.09	-1.68	-1	15	5	0	6	25
G	13	1.41	1.90	0.69	0.00	0.04	0.03	0.76	0.05	-0.06	-6.55	-8.99	-11.67	123	214	14	-145	74	279
H	5	1.45	2.27	0.64	-0.02	-0.10	-0.08	0.53	0.05	-0.03	-11.09	-4.48	-5.35	94	146	-43	-72	59	184
sign		***	***	***	**	***	***	***	*	**	**	**	***						

The markers and associations described are useful for their predictive ability for a number of traits including host resistance. The industry utility of the invention is that young unmeasured progeny can be genotyped and their breeding worth predicted.

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The above Examples illustrate practice of the invention. It will be appreciated by those skilled in the art that numerous variations and modifications may be made without departing from the spirit and scope of the invention.

Appendix 1

1 of 6

From farm measurements to SIL indexes

SIL Technical Note

Relates to: Traits measured on farm and those in standard SIL economic indexes
Written by: Mark Young & Georgie Walker
Date: June 2007

Summary

- Many measurements can be made on farm – the SIL database can store almost anything
- Some measurements influence genetic merit in a number of traits
- Some traits are not measured directly – genetic merit for these is predicted from related measurements
- Not all estimates of genetic merit (breeding values) are used in SIL indexes
- SIL indexes have a balanced focus on farm profit

Background

SIL comprises a performance recording database and a genetic evaluation system. On-farm measurements and pedigree are used to derive best-bet estimates of genetic merit. Sheep breeders collect information on the pedigree and performance of their sheep, submit it to a SIL bureau that enters it onto the database and perform the genetic evaluations, returning results to the breeders.

This document describes standard measurement traits and how these are related to standard SIL estimates of genetic merit, both breeding values and indexes.

Another SIL Technical Note describes weightings used in the standard SIL indexes and provides a brief outline of the basis of economic selection indexes.

From farm measurement to genetic merit

Measurements of animal performance are not always a good indicator of genetic merit for a trait. In fact, often genetics have a relatively small influence compared to other factors.

SIL produces “best-bet” estimates of genetic merit by doing several things. Firstly, it corrects for known “environmental” effects. These are things that affect all animals subject to the same conditions and which are not genetic e.g. being born earlier, or having a younger mother (with less milk). SIL then uses pedigree information to look at how well relatives have performed and then it takes account of performance in other traits and the extent to which each trait is inherited. Modern computers allow a lot of calculations to be carried out for many animals simultaneously and very quickly. The result is the “best-bet” of genetic merit for each trait, often called a **breeding value**.

Breeding objectives

Breeding values are then grouped for related traits to focus on particular outputs or inputs of the farming system (e.g. Growth, Reproduction, Wool, Disease Resistance) that the breeding programme has as part of its goal for improvement. The common basis for this is in terms of profit, with units of cents per ewe lambing. Such groupings are sometimes called Goal Trait Groups and SIL produces sub-indexes of economic merit for these. Overall indexes of economic merit are produced simply by summing all the component sub-indexes.

Traits we cannot measure

Some traits of interest in the breeding objective can be measured easily, while others cannot. For example, we can determine whether all lambs have survived or not and measure a weaning weight on all surviving lambs. However, males cannot themselves produce lambs (litter size) and we don't want to sacrifice valuable breeding animals to obtain useful information on carcass merit. Similarly, we may want to select for a trait along time before it is manifest (e.g. adult size).

Consequently, we predict genetic merit from other information we have for related traits and/or from related animals. Often there are traits in the breeding objective that are predicted from other measurements. While many traits can be measured on farm, and SIL can record virtually anything, in practice only some are used in the genetic evaluations. Of these, some are very influential (e.g. weaning weight and autumn liveweight) as they are used in the prediction of genetic merit for a number of key traits.

Some of these traits are directly related to breeding values (SIL's estimate of genetic merit for a trait), while others predict breeding values for traits we do not measure directly. Of these breeding values, the key traits are used in SIL indexes to focus on farm profit.

The traits SIL uses in its evaluations, the breeding value traits it produces, and the breeding value traits used in indexes are detailed in tables at the end of this document.

Using SIL indexes in practice - Making sense of it all!

SIL indexes and sub-indexes are designed to aid selection. It is a top-down approach whereby the overall index balances merit across a range of traits on the basis of farm profit. Within this index are Goal Trait Group focused sub-indexes. SIL has sub-indexes for Growth, Meat (carcass merit), Wool, Reproduction (Adult Litter Size, Twinning Rate and Hogget Fertility & Hogget Litter Size), Survival (of lambs) and Resistance to disease (Internal Parasites, Dags, Facial Eczema). Splitting these further into their component breeding values can be useful at times but usually it leads to an overwhelming variety of information that makes it harder to focus on key attributes of a sheep.

SIL recommends ram buyers use indexes in most selection situations. Breeders may look at more detail when planning and fine-tuning the direction of their breeding programme.

Need more information?

Contact your SIL bureau, send an email to silhelp@sheepimprovement.co.nz or telephone 0800-745-435 (0800-SIL-HELP).

Appendix tables on following pages

Table 1 summarises the traits measured on farm that are used in SIL genetic evaluations (predictor traits) and the estimates of genetic merit that these evaluations produce (breeding values). Finally there is a list of the sub-set of these breeding values that are used in SIL indexes. NB: Trait abbreviations are listed in Table 3.

Table 2 shows which estimates of genetic merit (sub-indexes or goal trait groups) are influenced by each on-farm measurement.

Table 3 describes abbreviations used in Table 1.

3 of 6

Table 1. Traits measured on farm (predictor traits) used in SIL genetic evaluations. Abbreviations described in Table 2.

Growth	Meat	CtMeat	Reproduction	Twinning	Hogget Lambing	Survival	Dual Purpose Wool [§]	Mid-micron & Fine Wool [§]	Mid-micron & Fine Wool Quality [§]	Dags	Facial Eczema	Internal Parasites (FEC) [§]
Predictor Traits:												
WWT *LW6 *LW8 *LW10 LW12 LW18	WWT *LW6 *LW8 *LW10 LW12 EMD EMW FD	WWT *LW6 *LW8 *LW10 LW12 EMD EMW FD CTEMA CTFAT CTLEAN	(LW optional) *LW6 *LW8 *LW10 NLB (NLB1 optional) (PregSc optional)	TWIN	(LW optional) *LW6 *LW8 *LW10 HFER HNLB (PregSc optional)	SUR	WWT *LW6 *LW8 *LW10 LW12 FW12 CFW12 FDIAM FFINE CFY12 FDIAM FFINE	WWT FW12 CFW12 FDIAM FFINE CFY12	WWT FW12 CFW12 FDIAM FFINE CFY12 FDIACV FCURV STAPLN SSTR COLY COLYZ	DAG3 DAG8	GGT21	WWT *LW6 *LW8 *LW10 FW12 FEC1 FEC1B FEC2 FEC2B NEM1 NEM1B NEM2 NEM2B ELFC2
Breeding values provided for:												
WWT WWTm LW8 LW12 CW EWT	EMW EMD EMA FD FAT LEAN	EMW EMD EMA FD FAT LEAN	NLB	TWIN	HFER HNLB	SUR SURm	LFW FW12 EFW FDIAM	FW12 FDIAM EFW AFDIAM	FDIACV FCURV STAPLN SSTR COLY COLYZ	LDAG ADAG	GGT21	FEC1 FEC2 AFEC
SIL goal traits												
WWT WWTm CW EWT	FAT LEAN	FAT LEAN	NLB	TWIN	HFER HNLB	SUR SURm	LFW FW12 EFW	FW12 FDIAM EFW AFDIAM	FDIACV FCURV STAPLN COLY COLYZ	LDAG ADAG	GGT21	FEC1 FEC2 AFEC

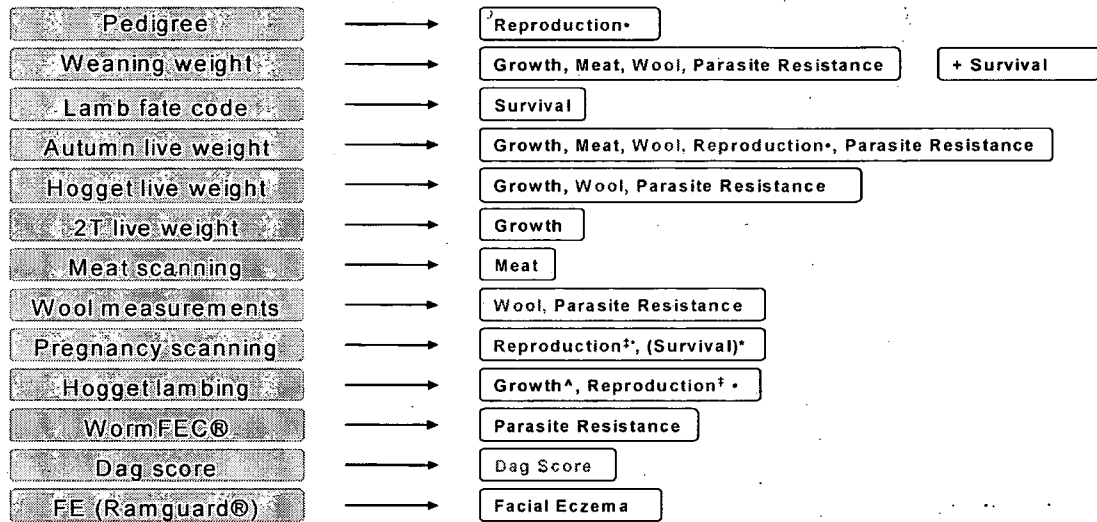
* SIL uses Autumn LW as a predictor trait. It selects either LW6, LW8 or LW10 for each contemporary group of animals – whichever has the most data collected

[§] SIL uses hogget fleece weight (FW12) as a predictor of wool production. Fleece weight measurements at other times, whether greasy or clean, may be used as proxies for this when it is not available.

Table 2. The influence of on-farm measurements on estimates of genetic merit (sub-indexes or goal trait groups).

Measurements on farm:

The sub indexes (goal trait groups)
these on-farm measurements go into:



*Pregnancy scanning & hogget lambing only used for Reproduction if asked for

*Pregnancy scanning results only used for Survival if asked for

^ Hogget Lambing information used for Growth to correct LW18 when predicting EWT BV

• Reproduction consists of Adult NLB and may also have Twinning Rate, Hogget Fertility &

Table 3. Trait name abbreviations used in Table 1.

Trait abbreviation	Type	Description
ADAG	Breeding value	Adult dag score
AFEC	Breeding value	Adult faecal egg count
AFDIAM	Breeding value	Adult fibre diameter
CFW12	On-farm measure	Clean fleece weight at 12 months
CFY12	On-farm measure	Clean fleece yield at 12 months
COLY	On-farm measure	Fleece colour - brightness
COLYZ	On-farm measure	Fleece colour - yellowness
CTEMA	On-farm measure	Eye muscle area from CT scan
CTFAT	On-farm measure	Fat weight in carcass from CT scan
CTLEAN	On-farm measure	Lean (muscle) weight in carcass from CT scan
CW	Breeding value	Carcass weight
DAG3	On-farm measure	Dag score at 3 months
DAG8	On-farm measure	Dag score at 8 months
EFW	Breeding value	Ewe (adult) fleece weight
ELFC2	On-farm measure	Blood test for resistance to internal parasites
EMA	Breeding value	Eye muscle area
EMD	On-farm measure	Eye muscle depth from ultrasound
EMD	Breeding value	Eye muscle depth
EMW	On-farm measure	Eye muscle width from ultrasound
EMW	Breeding value	Eye muscle width
EWT	Breeding value	Adult ewe weight
FAT	Breeding value	Carcass fat weight
FCURV	On-farm measure	Fibre curvature
FD	On-farm measure & breeding value	Fat depth
FDIACV	On-farm measure	Coefficient of variation in fibre diameter
FDIAM	On-farm measure & breeding value	Hogget fibre diameter
FEC1	On-farm measure & breeding value	Faecal egg count - summer challenge
FEC1B	On-farm measure	2nd FEC sample - summer challenge
FEC2	On-farm measure & breeding value	Faecal egg count - autumn challenge
FEC2B	On-farm measure	2nd FEC sample - autumn challenge
FFINE	On-farm measure	Fibre fineness (diameter) - assessed
FW12	On-farm measure	Hogget fleece weight
GGT21	On-farm measure & breeding value	GGT 21 day post-level (Facial Eczema)
HFERT	Breeding value	Hogget fertility (ability to produce a lamb)
HNLB	Breeding value	Hogget fecundity (number of lambs born)
LDAG	Breeding value	Lamb dag score
LEAN	Breeding value	Carcass lean (muscle) weight
LFW	Breeding value	Lamb fleece weight
LW6*	On-farm measure	Autumn weight (body weight) - 6 months
LW8*	On-farm measure	Autumn weight (body weight) - 8 months
LW8	Breeding value	Autumn body weight
LW10*	On-farm measure	Autumn weight (body weight) - 10 months
LW12	On-farm measure	Hogget weight (body weight) - 12 months
LW18	On-farm measure	2-tooth weight (body weight) - 18 months

NEM1	On-farm measure	Nematodirus faecal egg counts - summer-challenge
NEM1B	On-farm measure	Nematodirus faecal egg counts - summer challenge - 2nd sample
NEM2	On-farm measure	Nematodirus faecal egg counts - autumn challenge
NEM2B	On-farm measure	Nematodirus faecal egg counts - autumn challenge - 2nd sample
NLB	Breeding value	Number of lambs born (litter size)
NLB1 (optional)	On-farm measure	Number of lambs born at hogget lambing
PregSc (optional)	On-farm measure	Pregnancy scanning (litter size)
SSTR	On-farm measure	Wool staple strength
STAPLN	On-farm measure	Wool staple length - in fleece
STAPLN	Breeding value	Wool fibre length - after processing
SUR	On-farm measure	Survival to weaning
SUR	Breeding value	Survival to weaning - lamb effect
SURm	Breeding value	Survival to weaning - maternal (ewe) effect
TWIN	Breeding value	Twinning rate
WWT	On-farm measure	Weaning weight
WWT	Breeding value	Weaning weight - lamb effect
WWTm	Breeding value	Weaning weight - maternal (ewe) effect

* SIL uses Autumn LW as a predictor trait. It selects either LW6, LW8 or LW10 for each contemporary group of animals – whichever has the most data collected

Appendix 2

1 of 9

SIL standard index weightings – July 2007

SIL Technical Note

Relates to: Standard SIL indexes – breeding value traits and their economic weightings
 Written by: Mark Young & Georgie Walker
 Date: June 2007

Summary

- SIL has introduced some changes to standard SIL indexes
- There is now an economic value for the Facial Eczema resistance sub-index which is included in the Dual Purpose Overall index
- A Twinning Rate sub-index has been introduced for the Dual Purpose Overall indexes
- Breeding values can be produced for hogget fertility and hogget litter size. There are no economic weightings for these so they are not incorporated into SIL indexes
- Terminal Sire indexes have not changed. However breeding values for the new traits above can be produced and used on SIL reports for terminal sire sheep

Background

The amount of emphasis placed on key economic traits affecting prime lamb and wool production in New Zealand's national sheep flock was reviewed by SIL in 2004. New traits have now being added to the SIL Index system.

There are sub-indexes for Facial Eczema resistance and for Twinning Rate that are incorporated into SIL indexes where appropriate. A new analysis module for Hogget Lambing produces breeding values (BVs) for hogget fertility and for hogget litter size. Economic weightings are not available for these BVs so they are not included in SIL indexes.

SIL Overall indexes

These are used by many sheep breeders as an estimate of overall genetic merit for each animal, taking into consideration information from all recorded traits and from relatives. These indexes are important because a number of different traits are measured and selected for by sheep breeders. For example, a ram may be superior to other rams based on a single trait such as bodyweight, but his daughters may have below average performance for other traits, such as fleece weight and number of lambs born.

An overall index allows superiority in one trait to compensate for inferiority in other traits. Effectively **the index weights different traits depending on the income they generate, when you get this income and the proportion of animals that generate this sort of income.** This is why we call such indexes "economic indexes". Selection on these economic indexes leads to economically optimal genetic progress being made across the range of genetic traits assessed.

Estimates of income are based on projections of key product prices for lamb and wool by the Economic Service of Meat & Wool New Zealand. Many other economic and production parameters are incorporated into the index derivation. Predicted animal feed energy requirements, the current national lambing percentage, and typical commercial flock age structure are examples of these parameters.

SIL Terminal Sire Overall Index

There have been no changes made to the TSO by SIL. The terminal sire overall index has a focus on lamb production where the emphasis is on fast early growth for lambs. Lamb survival to weaning, fast early growth, carcass merit and some disease resistance traits (dag score & internal parasite resistance) for lambs are considered the key focus for selection with the SIL Terminal Sire index.

Facial eczema resistance is not included in the SIL Terminal Sire indexes since lambs are normally away before facing a natural challenge. However, facial eczema breeding values can be produced for use by Terminal Sire ram breeders and included on reports.

SIL Terminal Sire indexes do not contain any reproduction sub-indexes (Reproduction, Twinning Rate or Hogget Lambing). In a terminal sire system daughters of sires are not bred from so reproductive merit is not valued. Breeding values for twinning rate, hogget fertility and litter size (NLB or HNLB) can be produced and included in reports if required.

SIL Dual Purpose Overall Index

There are two changes to the SIL DPO index with the introduction of sub-indexes for Facial Eczema resistance and Twinning Rate. Hogget Lambing has been introduced as a new goal trait group but has no economic weightings so can not be included in the DPO index. Other sub-indexes remain unchanged.

Twinning rate is the propensity to have more twin litters per hundred ewes at the same average lambing percentage. High twinning rate will mean fewer ewes having triplets. Selection for twinning rate is recommended in situations where triplet lamb survival is low or variable, or when lower weaning weights incur a significant financial penalty. A sub-index for Twinning Rate (DPT) uses an economic weighting for TWIN BV.

Hogget Lambing is related to but not the same as adult reproduction. It is a function of both fertility (HFER) and fecundity (litter size, HNLB). Hogget Lambing BVs do not have economic weightings at this stage and so there is no sub-index for Hogget Lambing. However, the BVs can be included on SIL reports.

An economic weighting for facial eczema means there is a sub-index for Facial Eczema resistance, DPX, that is included in the DPO index. The weighting is based on the effects facial eczema has on survival and performance of breeding ewes and of young replacement ewe replacements over a 10 year period containing 2 severe and 3 moderate outbreaks.

Disease traits

Three disease traits are addressed in SIL indexes. Internal parasite resistance (WormFEC) and dag score sub-indexes remain unchanged. Facial eczema now has a sub-index (DPX) for Dual Purpose sheep.

SIL "Overall" and SIL "Production" indexes differ by the former including sub-indexes for disease traits in the evaluation while the Production indexes do not include these. Disease traits are not included in production indexes since the focus is on production traits. For example a DPO index might include Growth, Meat, Wool, Reproduction, Survival, Twinning Rate, Facial Eczema & WormFEC but the associated DPP would only contain Growth, Meat, Wool, Reproduction, Survival & Twinning Rate.

Other differences

Sub-indexes for apparently similar traits can differ between Dual Purpose indexes and Terminal Sire indexes. For example, while sub-indexes for Dual Purpose sheep include traits for older sheep, those for Terminal Sire sheep focus only on lambs.

In addition, the economic weights on the index traits can differ due to the relative importance of the trait when all lambs are for meat production compared to a situation where some are kept as replacements for the ewe flock.

SIL Wool Production System Overall Indexes

Wool Production System indexes introduced by SIL in 2004 make up the third category of standard SIL indexes, after Dual Purpose and Terminal Sire indexes. Four sets of wool indexes are available for ram breeders: Mid-micron Overall (MMO), "Medium-fine" Fine Wool (FWm), "Fine" Fine Wool (FWf) and the "Super-fine" Fine Wool (FWs) index.

There have been no changes made to the Wool Production System indexes. Facial Eczema resistance is generally not applicable to areas of New Zealand where fine wool production is typically carried out, hence there is not a Facial Eczema economic value for any of the Wool Production system overall indexes. Similarly, Twinning Rate and Hogget Lambing breeding values can also be produced but since there are not any economic weightings for this type of sheep they are not included in the wool indexes. Breeding values for Facial Eczema, Twinning Rate and Hogget Lambing can all be produced and used on reports alongside the wool production system index values if required.

SIL Standard Indexes

SIL standard indexes will give near optimal genetic gains for most farming conditions in New Zealand. They have been derived using technical and economic information relevant to the average flock in New Zealand. SIL recognises that breeders targeting specific, commercial farming conditions can be justified in pursuing objectives different to the industry average. However SIL standard indexes will suit a large number of breeding programmes. As well, use of standard indexes will lead to a more uniform understanding of evaluations for genetic merit by both ram buyers and ram breeders.

SIL bureaus have the means to generate custom indexes where this is relevant to do so.

Technical Notes

SIL has a number of different technical notes written specifically for SIL breeders. There are three that relate to the three changes SIL has just introduced:

- Genetic merit for twinning rate
- Selection to increase resistance to facial eczema
- Genetic merit for hogget lambing

SIL Technical Notes can be found on the SIL website www.sil.co.nz under Technical Notes.

Need more information?

Contact your SIL bureau, send an email to silhelp@sheepimprovement.co.nz or telephone 0800-745-435 (0800-SIL-HELP).

Appendix – SIL indexes. Tables on the following pages summarise the traits in SIL indexes and the economic weights used for each trait. These will be active from July 2007.

Tables are all in the same format. Where no economic weighting is given, that trait is not included in an index. This format has been used to highlight differences between indexes.

Table 1. Dual-Purpose Overall (DPO) index traits and weightings at July 2007

Sub-index	Sub-index short name	Goal trait breeding value full name	Breeding value short name	Economic weight (cents per ewe lambing)
Growth*	DPGm	Weaning weight – direct	WWT	116
		Weaning weight – maternal	WWTM	97
		Carcass weight	CW	140
		Ewe weight	EWT	-72
Meat	DPM	Lean weight	LEAN	293
		Fat weight	FAT	-183
Wool	DPW	Lamb fleece weight	LFW	416
		Hogget fleece weight	FW12	102
		Adult fleece weight	EFW	300
		Hogget fibre diameter	FDIAM	
		Adult fibre diameter	AFDIAM	
Wool Quality		CV of fibre diameter	FDIACV	
		Curvature	FCURV	
		Staple length	STAPLN	
		Brightness (Y)	COLY	
		Yellowness (Y-Z)	COLYZ	
Reproduction	DPR	Number of lambs born (litter size)	NLB	2430
Twinning Rate	DPT	Twinning rate adjusted for NLB	TWIN	3000
Hogget Lambing	DPH	Hogget fertility	HFER	<i>Not available</i>
		Hogget litter size	HNLB	<i>Not available</i>
Survival	DPS	Survival to weaning – direct	SUR	6329
		Survival to weaning – maternal	SURM	6371
WormFEC	DPF	FEC1%	FEC1	-2.9
		FEC2%	FEC2	-2.9
		Adult FEC%	AFEC	-2.5
Dag Score	DPD	Lamb Dag Score	LDAG	-254
		Adult Dag Score	ADAG	-687
Facial Eczema	DPX	GGT21	GGT21	-903
*Growth if Meat <u>NOT</u> selected	DPG	Weaning weight – direct	WWT	134
		Weaning weight – maternal	WWTM	112
		Carcass weight	CW	199
		Ewe weight	EWT	-72

Table 2. Terminal Sire Overall (TSO) index traits and weightings at July 2007

Sub-index	Sub-index short name	Goal trait breeding value full name	Breeding value short name	Economic weight (cents per ewe lambing)
Growth*	TSGm	Weaning weight – direct	WWT	66
		Weaning weight – maternal	WWTM	
		Carcass weight	CW	70
		Ewe weight	EWT	
Meat	TSM	Lean weight	LEAN	320
		Fat weight	FAT	-200
Wool		Lamb fleece weight	LFW	
		Hogget fleece weight	FW12	
		Adult fleece weight	EFW	
		Hogget fibre diameter	FDIAM	
		Adult fibre diameter	AEDIAM	
Wool Quality		CV of fibre diameter	FDIACV	
		Curvature	FCURV	
		Staple length	STAPLN	
		Brightness (Y)	COLY	
		Yellowness (Y-Z)	COLYZ	
Reproduction		Number of lambs born (litter size)	NLB	
Twinning Rate		Twinning rate adjusted for NLB	TWIN	
Hogget Lambing		Hogget fertility	HFER	
		Hogget litter size	HNLB	
Survival	TSS	Survival to weaning – direct	SUR	4110
		Survival to weaning – maternal	SURM	
WormFEC	TSF	FEC1%	FEC1	-1.56
		FEC2%	FEC2	-1.56
		Adult FEC%	AFEC	
Dag Score	TSD	Lamb Dag Score	LDAG	-254
		Adult Dag Score	ADAG	
Facial Eczema		GGT21	GGT21	
*Growth if Meat <u>NOT</u> selected	TSG	Weaning weight – direct	WWT	66
		Weaning weight – maternal	WWTM	
		Carcass weight	CW	158
		Ewe weight	EWT	

Table 3. Mid-Micron Overall (MMO) index traits and weightings at July 2007

Sub-index	Sub-index short name	Goal trait breeding value full name	Breeding value short name	Economic weight (cents per ewe lambing)
Growth*	MMGm (=DPCm)	Weaning weight – direct	WWT	116
		Weaning weight – maternal	WWTM	97
		Carcass weight	CW	140
		Ewe weight	EWT	-72
Meat	MMM (=DPM)	Lean weight	LEAN	293
		Fat weight	FAT	-183
Wool	MMW	Lamb fleece weight	LFW	
		Hogget fleece weight	FW12	96
		Adult fleece weight	EFW	271
		Hogget fibre diameter	FDIAM	-21
		Adult fibre diameter	AFDIAM	-28
Wool Quality	MMQ	CV of fibre diameter	FDIACV	-8
		Curvature	FCURV	0
		Staple length	STAPLN	3
		Brightness (Y)	COLY	9
		Yellowness (Y-Z)	COLYZ	-6
Reproduction	MMR (=DPR)	Number of lambs born (litter size)	NLB	2430
Twinning Rate		Twinning rate adjusted for NLB	TWIN	
Hogget Lambing	MMH	Hogget fertility	HFER	Not available
		Hogget litter size	HNLB	Not available
Survival	MMS (=DPS)	Survival to weaning – direct	SUR	6329
		Survival to weaning – maternal	SURM	6371
WormFEC	MMF (=DPF)	FEC1%	FEC1	-2.9
		FEC2%	FEC2	-2.9
		Adult FEC%	AFEC	-2.5
Dag Score	MMD (=DPD)	Lamb Dag Score	LDAG	-254
		Adult Dag Score	ADAG	-687
Facial Eczema		GGT21	GGT21	
*Growth if Meat NOT selected	MMG (=DPG)	Weaning weight – direct	WWT	134
		Weaning weight – maternal	WWTM	112
		Carcass weight	CW	199
		Ewe weight	EWT	-72

Table 4. "Medium-fine" Fine Wool (FWm) index traits and weightings at July 2007

Sub-index	Sub-index short name	Goal trait breeding value full name	Breeding value short name	Economic weight (cents per ewe lambing)
Growth*		Weaning weight – direct	WWT	
		Weaning weight – maternal	WWTM	
		Carcass weight	CW	
		Ewe weight	EWT	
Meat		Lean weight	LEAN	
		Fat weight	FAT	
Wool	FWmW	Lamb fleece weight	LFW	
		Hogget fleece weight	FW12	1219
		Adult fleece weight	EFW	931
		Hogget fibre diameter	FDIAM	-1378
		Adult fibre diameter	AFDIAM	-664
Wool Quality	FWmQ	CV of fibre diameter	FDIACV	-231
		Curvature	FCURV	-9
		Staple length	STAPLN	22
		Brightness (Y)	COLY	59
		Yellowness (Y-Z)	COLYZ	-59
Reproduction	FWR	Number of lambs born (litter size)	NLB	2618
Twinning Rate		Twinning rate adjusted for NLB	TWIN	
Hogget Lambing	FWH	Hogget fertility	HFER	<i>Not available</i>
		Hogget litter size	HNLB	<i>Not available</i>
Survival	FWS	Survival to weaning – direct	SUR	6412
		Survival to weaning – maternal	SURM	2630
WormFEC	FWmF	FEC1%	FEC1	-2.3
		FEC2%	FEC2	-2.3
		Adult FEC%	AFEC	-3.1
Dag Score		Lamb Dag Score	LDAG	
		Adult Dag Score	ADAG	
Facial Eczema		GGT21	GGT21	
*Growth if Meat <u>NOT</u> selected	FWG	Weaning weight – direct	WWT	111
		Weaning weight – maternal	WWTM	93
		Carcass weight	CW	58
		Ewe weight	EWT	-188

Table 5. "Fine" Fine Wool (FWF) index traits and weightings at July 2007

Sub-index	Sub-index short name	Goal trait breeding value full name	Breeding value short name	Economic weight (cents per ewe lambing)
Growth*		Weaning weight – direct	WWT	
		Weaning weight – maternal	WWTM	
		Carcass weight	CW	
		Ewe weight	EWT	
Meat		Lean weight	LEAN	
		Fat weight	FAT	
Wool	FWFW	Lamb fleece weight	LFW	
		Hogget fleece weight	FW12	2483
		Adult fleece weight	EFW	1883
		Hogget fibre diameter	FDIAM	-3095
		Adult fibre diameter	AFDIAM	-1255
Wool Quality	FWFQ	CV of fibre diameter	FDIACV	-437
		Curvature	FCURV	-40
		Staple length	STAPLN	71
		Brightness (Y)	COLY	45
		Yellowness (Y-Z)	COLYZ	-200
Reproduction	FWR	Number of lambs born (litter size)	NLB	2618
Twinning Rate		Twinning rate adjusted for NLB	TWIN	
Hogget Lambing	FWH	Hogget fertility	HFER	<i>Not available</i>
		Hogget litter size	HNLB	<i>Not available</i>
Survival	FWS	Survival to weaning – direct	SUR	6412
		Survival to weaning – maternal	SURM	2630
WormFEC	FWWF	FEC1%	FEC1	-4.8
		FEC2%	FEC2	-4.8
		Adult FEC%	AFEC	-6.3
Dag Score		Lamb Dag Score	LDAG	
		Adult Dag Score	ADAG	
Facial Eczema		GGT21	GGT21	
*Growth if Meat <u>NOT</u> selected	FWG	Weaning weight – direct	WWT	111
		Weaning weight – maternal	WWTM	93
		Carcass weight	CW	58
		Ewe weight	EWT	-188

Table 6. "Super-fine" Fine Wool (FWs) index traits and weightings at July 2007

Sub-index	Sub-index short name	Goal trait breeding value full name	Breeding value short name	Economic weight (cents per ewe lambing)
Growth*		Weaning weight – direct	WWT	
		Weaning weight – maternal	WWTM	
		Carcass weight	CW	
		Ewe weight	EWT	
Meat		Lean weight	LEAN	
		Fat weight	FAT	
Wool	FWsW	Lamb fleece weight	LFW	
		Hogget fleece weight	FW12	7171
		Adult fleece weight	EFW	3999
		Hogget fibre diameter	FDIAM	-10829
		Adult fibre diameter	AFDIAM	-7136
Wool Quality	FWsQ	CV of fibre diameter	FDIACV	-2484
		Curvature	FCURV	-40
		Staple length	STAPLN	71
		Brightness (Y)	COLY	45
		Yellowness (Y-Z)	COLYZ	-200
Reproduction	FWR	Number of lambs born (litter size)	NLB	2618
Twinning Rate		Twinning rate adjusted for NLB	TWIN	
Hogget Lambing	FWH	Hogget fertility	HFER	<i>Not available</i>
		Hogget litter size	HNLB	<i>Not available</i>
Survival	FWS	Survival to weaning – direct	SUR	6412
		Survival to weaning – maternal	SURM	2630
WormFEC	FWsF	FEC1%	FEC1	-14.0
		FEC2%	FEC2	-14.0
		Adult FEC%	AFEC	-18.5
Dag Score		Lamb Dag Score	LDAG	
		Adult Dag Score	ADAG	
Facial Eczema		GGT21	GGT21	
*Growth if	FWG	Weaning weight – direct	WWT	111
Meat <u>NOT</u>		Weaning weight – maternal	WWTM	93
selected		Carcass weight	CW	58
		Ewe weight	EWT	-188

Appendix 3



Breeding Sheep Resistant to Internal Parasites

John McEwan

WormFEC Service Coordinator, AgResearch, Invermay

It is estimated that approximately 30% of New Zealand's sheep meat and wool production is dependent on the use of anthelmintics. In economic terms \$1200 million worth of sheep exports are supported by the use approximately \$80 million of anthelmintic. Alternative methods of controlling internal parasites are needed, because of the widespread anthelmintic resistance by the parasites concerned (greater than 65% of farms have a species resistant to at least one chemical action family) and the costs of the chemical control.

One method is to breed sheep resistant to the internal parasites themselves. Based on research work undertaken by AgResearch over the past 2 decades, sheep breeders can now include this trait in their selection criteria.

Using the results from experimental work and a demand by sheep breeders, the WormFEC Service commenced in late 1994. WormFEC provides sheep breeders with the tools and advice required so they can select sheep resistant to internal parasites in their own breeding flocks. The service is provided in association with Sheep Improvement Limited or SIL as it is commonly known.

Commercial farmers wishing to obtain rams showing enhanced resistance to internal parasites only need ask for WormFEC tested rams from their breeders. The latest across flock and breed WormFEC ram rankings are also available via www.silace.co.nz. The WormFEC symbol is shown in figure 1.

The selection objective recommended by the WormFEC Service is "high producing animals which are also resistant to internal parasite establishment".

The aim of breeding sheep resistant to internal parasites is to reduce susceptibility to infection and thereby reduce pasture contamination. Available information suggests that both susceptible and resistant stock benefit from a reduced intake of internal parasite larvae. Pasture contamination and subsequent larval challenge

levels can be reduced by grazing more resistant animals. Hence, production benefits from breeding sheep resistant to internal parasites are indirect and benefit the whole flock rather than the individual.



Figure 1. The WormFEC symbol that sheep breeders evaluating rams for their resistance to internal parasites display on advertising

Research has shown that young lambs are initially very susceptible to infection with internal parasites, but by about 12 months of age they have developed a degree of immunity. In the adult ewe resistance levels are high, but immunity is depressed during the late pregnancy and early lactation period, causing a peri-parturient rise in faecal egg count (FEC).

The rate of development of resistance and the level achieved in the adult are under genetic control and it is therefore possible to breed for more resistant animals. This variation in the development of immunity is shown graphically in figure 2. Animals more resistant as lambs are also more resistant at older ages and females have a smaller peri-parturient rise.

Resistance to internal parasites can be measured in a variety of ways, but faecal egg counts, after a known challenge of infective larvae is the most

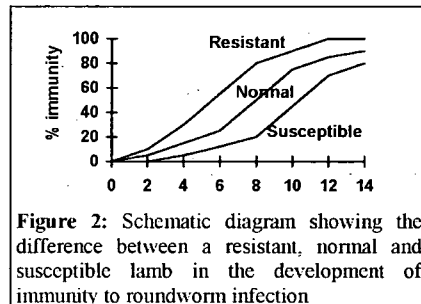


Figure 2: Schematic diagram showing the difference between a resistant, normal and susceptible lamb in the development of immunity to roundworm infection

commonly used method (figure 3). The lambs are drenched at weaning, exposed to a pasture larval challenge for 6 to 8 weeks, and then faecal sampled (FEC1). This is followed by another drench with another sample taken after a further 6 to 8 weeks (FEC2). Two samples are taken to provide a more accurate estimate of an individual's genetic level of resistance. However, any combination is possible, and collecting 2 samples several days apart at the end of the summer challenge is currently the most popular option (FEC1a, FEC1b).

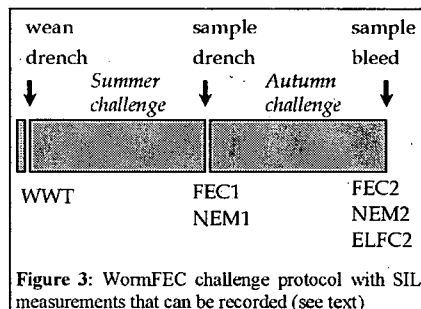


Figure 3: WormFEC challenge protocol with SIL measurements that can be recorded (see text)

Animals with lower faecal egg counts are considered more resistant and those with higher egg counts are less resistant.

Alternatively, animal resistance can be determined by measuring its parasite antibody level (ELFC2) at 7 to 9 months of age. Blood samples are collected and sent for laboratory analysis. This method reduces the work and cost to the breeder, but the genetic progress in reducing FEC will be slower.

WormFEC resistance breeding values are calculated using the latest breeding methods via SIL. No matter what resistance measurements have been collected, they are combined together and expressed as a breeding value for lamb FEC. For example a FEC1 BV% of minus 20 means that an animal has a breeding value for FEC as a lamb 20% below the average of the flock during the summer. Notice that **negative breeding**

values indicate more resistant animals as they will have lower faecal egg counts.

Currently, commercial breeders using WormFEC select on the basis of an economically based SIL Dual Purpose WormFEC index which combines the economic benefits of parasite resistance and the other production traits. In the selection lists breeding values for the relevant traits are tabulated for each animal. These are then combined into a variety of sub-indices, several detailing their economic breeding merit for various production traits and one **DPF** (dual purpose FEC) the expected economic breeding merit for host resistance to internal parasites. The sum of these is the overall economic merit. The use of sub-indices allows the breeder to quickly identify which components are contributing to the total merit of an individual.

Calculations using this Dual Purpose WormFEC index selecting for highly productive and resistant animals, suggests that 10 years of selection will reduce lamb FEC by 40% relative to unselected animals given a similar parasite challenge and adult ewe FEC will also be reduced by a similar amount. In a flock the reduction will be greater because the reduced number of parasite eggs shed by the resistant animals will also lower the number of infective parasite larvae available on the pasture. The reduction in pasture larval challenge will result in better lamb and wool production, alternatively drenching frequency could be reduced resulting in savings of chemical and labour. More than 50 stud flocks spread throughout New Zealand have used the WormFEC service, a large proportion continuously since 1994.

For further information about the WormFEC Service contact:

North Island

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Private Bag 3123, Hamilton
PH (07) 838 5421
A/H (07) 855 9479
FAX (07) 838 5013
E-Mail neville.amyes@agresearch.co.nz

South Island

Gordon Greer,
Invermay Agricultural Centre,
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FAX (03) 489 9038
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Appendix 4

1 of 4

ACE evaluations

SIL Technical Note

Relates to: Comparing genetic merit across flock and across breed

Written by: Mark Young

Date: 18 November 2005

Summary

- ACE evaluations consider genetic merit for key production traits in sheep
- Listings are posted on the internet for the top performing sheep across a variety of traits and indexes
- ACE indexes are based on standard SIL indexes but are not the same in all cases
- SIL is working to enhance ACE evaluations – to add traits, to increase the pool of animals evaluated and to fine tune analyses
- Check out www.silace.co.nz

Background

Gains through genetic improvement require a means to validly compare genetic merit of animals. Within flock, this requires correction for known, non-genetic effects and the use of information about the performance of relatives. This can be extended to across flock comparisons provided there is the means to make meaningful estimates of non-genetic, flock effects. In practice this means “benchmarking” lamb performance through use of common sires.

Until recently this was very demanding on technical resources – computer hardware and software specifically. As the power of these technologies has increased we can now extend this further and begin to make comparisons across breed as well as across-flock.

It is well-known that in most situations there is more genetic variation within breed than between breeds. Such across-flock, across-breed comparisons can be used to find the best animals for specific production characteristics, irrespective of the breed or the flock they are from.

Who set up ACE?

ACE stands for Advanced Central Evaluation. It is an initiative of SIL and it's collaborators. ACE evaluations would not be possible without access to the data from the Alliance initiated Central Progeny Test trials, which have evolved, and now include data from three progeny test sites – Woodlands (Southland), Lincoln (Canterbury) and Poukawa (Hawkes Bay). A variety of groups have made significant contributions to this work and facilitated the ACE evaluations. The assistance of Alliance, AgResearch, Lincoln University, On-Farm Research and Abacus Biotech are gratefully acknowledged. Meat & Wool New Zealand, as well as funding SIL, is also contributing funds for ongoing support of these progeny test sites.

What ACE is

ACE ranks animals for genetic merit according to specific criteria. A variety of lists are produced, to characterise animals from different perspectives.

In order to participate in ACE evaluations breeders must be recording pedigree and performance on farm, and using the SIL system.

Many breeders in New Zealand give permission for their flock data to be used in the ACE evaluation. However, ACE will only rank animals where good genetic links between flocks allow valid comparisons to be made. Some good animals may not appear on ACE lists if they have not given permission for their data to be used, or if they are not well linked for the traits in question. Without such links their merit cannot be validly compared to others in the evaluation. A later section looks at linkage briefly.

ACE only lists animals of high genetic merit. The aim is to make widespread use of these in the industry. For this large-scale evaluation, there is no value in identifying and publishing lists containing information on animals of lower genetic merit.

ACE uses the SIL system to estimate genetic merit. Reports are formatted in the same way as those used by SIL breeders.

ACE will update the evaluations regularly. Keep an eye on the website for this.

What ACE is not!

ACE does not provide the definitive description of genetic merit. For several reasons.

Firstly, not all sheep are farmed in the same way, for the same purpose. ACE focuses on the two dominant types – **dual-purpose** sheep, where some lambs are destined for meat production while others are kept as replacements for the ewe flock, and **terminal sire** sheep, where, commercially, all lambs born to a sire are destined for meat production. Clearly, maternal production traits are important in the former case but not the latter.

Not all breeders will face the same challenges to their breeding programme and some will be aiming for a different sector of the market. ACE recognizes this and produces a variety of listings that will be of interest to most breeders.

So ACE does not identify the top, single sheep in New Zealand!

While ACE ranks animals on key production traits, it does not do so for ALL traits important to sheep production. SIL focuses on traits amenable to measurement on farm and genetic analysis. Other traits, such as structural soundness, are not part of the SIL system at this time. As with SIL, the ACE system is another powerful tool that breeders can usefully apply to their breeding programme.

In addition, two features of the SIL system are NOT part of ACE – the trait of Survival and maternal breeding values are routinely part of many SIL evaluations but are not part of ACE.

Survival is a “new trait” not considered directly before the SIL system was developed. Recording methods for Survival data vary considerably between flocks which may cause problems in such a large analysis. For this reason it is currently excluded from the ACE rankings.

Maternal breeding values cannot be estimated because of the scale of the genetic ACE analysis and limits imposed by the hardware and software we are currently using.

Both these limitations are being addressed.

ACE lists

Currently, the following listings are available on the ACE website.

These lists are based on “ACE indexes” which are similar but not necessarily the same as SIL standard indexes. If you are familiar with SIL indexes, check out the equivalence of ACE indexes with those you are using. Do this by looking at what breeding values are included, and the weightings on these, for the indexes that you are interested in.

List	Composition
<u>Composite indexes</u>	<i>Made up of these single trait sub-indexes</i>
ACE Terminal Sire	TS Growth + TS Meat
ACE Dual Purpose	DP Reproduction + DP Growth* + DP Wool
ACE High Performance Dual Purpose	HP Reproduction** + DP Growth* + DP Wool
ACE Maternal	DP Reproduction + DP Growth*
ACE Dual Purpose WormFEC	DP Reproduction + DP Growth* + DP Wool + DP Meat + DP WormFEC
<u>Single Trait Indexes</u>	<i>Traits in index as breeding values</i>
DP Reproduction	NLB
Dual Purpose Growth	WWT, CW, EWT
Terminal Sire Growth	WWT, CW
TS Meat	LEAN, FAT
DP Wool	LFW, FW12, EFW
DP WormFEC	FEC1, FEC2, AFEC

* DP Growth does NOT contain the maternal weaning weight BV (WWT_M)

** HP Reproduction has a lower weighting in the index than DP Reproduction – so NLB BV will have less impact on the overall index

A work in progress

ACE is an ambitious undertaking. It is a good start but there are some issues requiring more attention. The following list of issues are currently being addressed. Others will be added to the list as we become aware of them and their importance to the industry.

- ACE will increase in value as we are able to rate animals in more flocks. This requires more flocks to agree to participate and for these flocks to become linked, directly or indirectly, with the main ACE evaluation group of flocks.
- Maternal breeding values cannot be estimated since the ACE evaluation is so large. SIL is working to expand the capability of the software and hardware to overcome this limitation.

- Some ACE indexes have fewer traits in them than commonly used SIL indexes. As linkage between flocks and breeds improves for all traits, and as we address issues limiting the current analysis (maternal BVs), ACE will be able to offer more comprehensive indexes for ranking animals. However, single-trait focused lists will always be important while we have breeders pursuing slightly different breeding objectives.
- Current ACE evaluations do not account for hybrid vigour. Experts believe this will have little effect on Growth, Meat and Wool traits. While it is more likely to affect Reproduction, much of the breed crossing of interest occurs with similar breeds (Romney, Coopworth, Perendale) and more significant crosses are already present in the composite breeding flocks. Preliminary indications are that attempts to address hybrid vigour will yield only small gains as the effects are likely to be small and are hard to quantify from field data. SIL is working to implement a robust method that will address hybrid vigour without introducing biases to the analysis. It is reassuring that much genetic progress has been made in the past, in the presence of hybrid vigour (e.g. in the development of new breeds) and experts believe the effect of hybrid vigour, while present, does not invalidate the ACE evaluation.

ACE has value to the industry and this value will increase as these issues are addressed.

Flock linkage

Across-breed links are obtained from the information collected at the three progeny test sites. Here, rams of different breeds are mated to ewes and the performance of their progeny measured. In some cases daughters are kept for evaluation of maternal traits.

Within-breed links are obtained largely from existing collaborative breeding groups in the industry. These are usually based on sire referencing whereby common rams are used so that reference sires have progeny in more than one flock.

Some flocks may be well-linked with other flocks in a collaborative breeding group. However, if this group is not linked to one of the progeny test sites that ACE uses then the whole group will be excluded from the rankings that ACE publishes.

ACE publishes, on the website, visual depictions of a linkage analysis for key traits. These help show which flocks are well linked and which are not.

A brief point about linkage must be made. Good linkage is obtained when a sire has progeny in two, or more, flocks. Buying a young ram from another breeder which then has all its progeny in your own flock does not give adequate linkage for across-flock comparisons. SIL can provide more detailed information on linkage if you require it.

Using ACE lists

Listings available on the website (www.silace.co.nz) are formatted in the same way as those used by breeders using the SIL system. From this website you can download descriptions on how to interpret ACE information.

Need more information?

Contact your SIL bureau or call 0800-745-435 (0800-SIL-HELP).

Appendix 5

1 of 3

Selection to increase resistance of sheep to internal parasites

SIL Technical Note

Relates to: Selection for low worm faecal egg counts

Written by: Mark Young

Date: 17 May 2006

Summary

- Resistance to internal parasites is moderately heritable (c.30%)
- Resistance incurs a small cost on metabolism, so resistant sheep may be slightly less productive and can be slightly more daggy.
- SIL offers selection indexes that work against these weak associations so that animals can be selected for that are more resistant while being more productive and less daggy.
- Genetic improvement through selection offers one of the best long-term solutions to the increasing problem of drench resistance in the internal parasites of sheep.

Background

Control measures for internal parasites, or worms, have a very significant effect on farm profit and on farm management. Susceptibility to worms leads to loss of production and to the maintenance of a large population of worm larvae on pasture that can reinfect stock later.

Many industry experts believe that the building resistance of worms to the drenches used to control them will soon lead to a very significant problem for farmers. Breeding sheep to be less susceptible to worms is one way to address this problem. Selection may be for "resistance" or "resilience" when faced with a challenge by worms.

Resistant animals mount an immune response to reduce or eliminate the population of worms in their gut. **Resilient** animals do not appear to mount any significant response and appear not to show reductions in productivity. By comparison, "**susceptible**" animals show marked decreases in productivity.

Some studies have shown that the resistance of sheep to worms has side effects. These need to be considered. Resistant animals may show slightly lower productivity and may be slightly more daggy when faced with a worm challenge. However, when not challenged we wouldn't expect to see these effects.

These associations with resistance are not strong and so it is possible to select for resistance without compromising production, and without increasing dagginess. In order to achieve this we need to consider all these traits when making selection decisions.

Resistance *versus* resilience

Some people advocate selection to increase resistance while others argue for resilience. The two traits are not so different under a selection system designed to improve productivity while reducing parasite loads and reducing traits such as dagginess. Other SIL Technical Notes discuss these issues in more detail.

SIL considers that in the context of sheep breeding, there are more similarities than differences between resistance and resilience.

Definition of resistance

In practice, resistance to internal parasites is measured as low faecal egg counts (FEC). Lower FEC is associated with animals mounting a challenge to the worm population in their gut and this challenge can reduce both the number of worms and the amount of eggs they produce.

As part of resistance, sheep mount an immunological response to the worm infection. This can be measured by assessing levels of an antibody in the blood of sheep that have been challenged. However, it is less well related to resistance than FEC.

FEC is the on-farm measure most commonly used by SIL breeders to predict genetic merit for resistance to worms.

Genetics of resistance

Resistance (FEC) is moderately heritable (25-30%). It is more heritable if two measurements are made at different times. This is because taking an extra measurement helps when it is not always possible to collect representative faecal samples from each sheep.

There are unfavourable, but weak, associations between resistance and production traits, and between resistance and dag score. Under a worm challenge, more resistance sheep can produce slightly less and be slightly more daggy. Fortunately there is a favourable correlation between dag score and production traits – more productive sheep have lower dag scores.

Unfavourable associations do not mean resistance is an unrealistic selection objective. Far from it. Since these associations are not strong it is quite reasonable to expect that we can simultaneously improve these traits through selection. The unfavourable associations just mean progress will be a little slower.

Measuring resistance as FEC

SIL uses the WormFEC protocol for assessing FEC as part of a breeding programme. Developed by AgResearch, information collected on farm following this protocol is used by SIL to produce estimates of genetic merit for resistance, the breeding values for FEC.

The genetic evaluation module used by SIL assumes FEC information has been collected under particular conditions. Details of this can be obtained from AgResearch (see contacts below). Briefly, this involves –

- Drenching lambs at weaning
- Collecting a faecal sample after a summer challenge of 6-8 weeks (FEC1 measurement), followed by a second drench
- Collecting a faecal sample after an autumn of 6-8 weeks challenge (FEC2 measurement).
- Sometimes a 2nd sample is collected a few days after FEC1 instead of a FEC2 collection. This is known as FEC1B. It is desirable to have a second sample measured later, but a compromise can be made to ensure a second sample is collected. Bear in mind that it is important to have repeat measurements on each animal.
- There is the option of taking a blood sample at 7-9 months of age and measuring the level of worm antibody. This method can reduce work and cost but genetic progress will be slower because it is less well related to resistance than two FEC measurements.

Animals need to be challenged. In some situations (e.g. dry seasons) the challenge period may need to be extended, to obtain higher average egg counts from which we can see variation

between animals. The period of challenge can be extended until the average FEC reaches around 800 eggs per gram (it is not recommended to collect faecal samples if the mob average is below 500 eggs per gram). Call SIL or AgResearch for advice relevant to your situation.

Faecal samples are sent to a laboratory accredited to produce WormFEC results. It is important that results are obtained following a standard method, and expressed in a standard way, so that the information derived is compatible with the SIL genetic evaluation module.

Worm eggs are counted as *Nematodirus* (NEM) or "other" (FEC). This is because only *Nematodirus* eggs are easily distinguishable from other worm species.

Contemporary groups – Animals may have had different drenching histories, or exposure to a parasite challenge. Where this can be identified as a mob effect, FEC samples or data should be recorded as being from such different management groups. This is to ensure that variation between mobs due to management does not bias or estimates of genetic merit for resistance.

The SIL genetic evaluation of resistance

SIL uses FEC and NEM data as well as information on body weight (WWT and autumn LW) and fleece weight (FW12) to predict resistance.

SIL evaluations will be most accurate if two samples are collected per animal, and if there are good numbers of animals tested. It is best to have 25-30 animals measured per sire family.

Breeding values are produced for FEC1, FEC2 and adult FEC (AFEC). The units of the breeding value are in percentage terms relative to the average FEC for that flock. For example, a figure of -20% says the animal has a FEC BV 20% below the flock average in the base year. Conversely, +45% shows an animal has a FEC BV that is 45% above the flock average in the base year. SIL uses a base year, when the average animal is 0%, to allow progress to be assessed. As gains in resistance accumulate, fewer animals will have positive breeding values or negative FEC sub-indexes.

Reporting on Resistance

SIL recommends using overall indexes (e.g. DPO or TSO), incorporating estimates of genetic merit for resistance. The overall indexes can be broken down into sub-indexes, one of which is for worm resistance or FEC. In the dual purpose index this sub-index is DPF. Previously this was named DPD (disease) but the abbreviation DPD is now used for Dag Score.

Breeding values can be placed on a report. Note that with the sub-indexes, positive is better for resistance, while with FEC breeding values, negative is better.

In dual purpose sheep the sub-index for FEC (DPF) incorporates breeding values for FEC1, FEC2 and AFEC. These are estimated from the information available for that genetic analysis run. For terminal sire sheep, the sub-index for FEC (TSF) is based only on breed for their value relative to other traits in the overall index.

For animals evaluated using the WormFEC system, SIL reports show a WormFEC logo.

Need more information?

- Contact your SIL bureau, local SIL adviser or call 0800-745-435 (0800-SIL-HELP).
- Details on the WormFEC service offered by AgResearch can be obtained from Gordon Greer (03-489-3809) or Neville Amyes (07-838-5421).

Appendix 6

ACE technical history

- 5 The objectives of the Advanced Central Evaluation (ACE) analysis were to:
- Identify the **best** rams used in participating flocks, across all breeds, for specific traits and a variety of useful industry endpoints,
 - Make these results available to both breeders and commercial farmers,
 - Over time introduce analyses for additional traits and flocks as genetic links
- 10 improve and flocks involved increase.

NOTE WELL: It is not a breed evaluation and the wide mixture of breeds and breed crosses in the top echelons of the sire lists makes this obvious.

- 15 This document is written for interested researchers and breeders using performance recording systems. It is not intended for commercial farmers. However, it should be readily understandable to those interested in performance recording.

The Advanced Central Evaluation (ACE) analysis was undertaken in the following way:

20

Flock selection and data validation

- All SIL breeders were posted letters in November 2003 and December 2004 asking if they wished to take part under the conditions outlined.
 - Initially 154 breeders from a wide variety of breeds agreed to take part. Currently
- 25 208 breeders (301 flocks) are included.
- A preliminary analysis was undertaken in July 2004 and genetic linkages examined to identify those flocks that were well enough linked to be included in the analysis.
 - Some ram parentage and anomalous results were followed up with individual
- 30 breeders.

- A revised and updated analysis was undertaken in late June 2004 and the individual breeders involved were sent their draft within flock results and asked to check parentage identification and breed composition of listed animals.
- During that period a number of independent checks of the results were undertaken by SIL, AgResearch and Abacus Biotech staff including:
 - consistency of results with the existing within breed analyses,
 - contacting breeders and checking of results and stock management for key across breed linkages external to the Alliance CPT,
 - summary of breeding value means, and ranges, for individual traits by breed and subsequent following up of any unusual results.
- Since that time ACE reports have been released and further checks on links and anomalous results are undertaken.

Listing criteria and economic indices used

- SIL and Alliance CPT management committee met and resolved the criteria for listing rams within the constraints of the breeder agreements in August 2004 including:
 - Rams had to have both parents listed.
 - Rams bred outside the ACE linked flocks had to have 100 measured progeny in ACE flocks. This typically meant that they had been evaluated in two or more flock/years and provided sufficient progeny for accurate evaluation given the lack of parental and half sib data.
 - Rams had to have been used in the last 3 birth years, and be less than 10 years old.
 - Rams born in ACE flocks required 20 measured progeny to be listed, but they also have extensive information from parents and relatives.
 - The exact format of the lists was determined including what indices to be used and their format. The intention was to provide a minimum of information, while conveying all that is essential.
 - Breed composition is listed for the two most predominant breeds in a ram's pedigree
 - Revised SIL economic values released in September 2004 were accepted for use in indexes of genetic merit. Index lists were for the Terminal Sire

index, Dual Purpose index and a High Performance Dual Purpose index developed as part of the ACE project. The latter list is suitable for ram clients weaning over 155% lambs weaned/ewes mated. In addition, "trait leader lists" are listed for key objectives.

- One new SIL innovation used was the calculation and listing of number of lambing records available from daughters and from half sibs.
- Because of concerns about variability between farms in recording lamb survival, this trait was not included in the current indexes.
- Initially wool records were not included due to lack of information in some breeds in the dual purpose listings. It was felt more valuable to include additional flocks which had reproductive records. However the increased number of analysis flocks has meant that there are sufficient flocks linked for wool as well as growth and reproduction (86 flocks in May 2005 versus 43 in October 2004) for the dual purpose and high performance dual purpose indexes to be based on all 3 goal trait groups, rather than just growth and reproduction.
- New lists have been developed for flocks linked for growth and reproduction with dual purpose maternal and high performance dual purpose maternal indexes.
- A small number of flocks had extensive records including parasite resistance as well as growth, wool, ultrasound measurements and reproduction. These were used in the ACE Dual Purpose WormFEC listing.

25 **June 2007 Analysis**

- An updated data file was created from the SIL database on 3 June 2007.
- The data was analysed using the existing SIL genetic engine for all traits and based on genetic linkages certain flocks were listed. The exact description of the method used is a multi-trait, repeated trait, animal model BLUP.
- Because of the number of animals involved maternal breeding values for weaning weight were not calculated.
- There was no correction for hybrid vigour for further details see notes.

- All animals born between 1990 and 2006 and their parentage information were used in the analysis. The total number of animals was 2,640,000 born in 302 flocks.
- The SIL base year is set to 1995: i.e. the year where the average animal born has a breeding value of zero for all traits.
- There were 185 report flocks for the ACE terminal sire flock lists and 2854 sires satisfied the criteria for listing. Of these, the top 200 were listed.
- Corresponding numbers for the dual purpose and high performance dual purpose index lists were 100 report flocks and 22087 rams, with 200 listed.
- Numbers for the dual purpose maternal (growth and reproduction) index list were 168 flocks and 3304 rams, with 200 listed.
- For the Dual Purpose WormFEC list there were 35 flocks and 933 rams, with 100 listed. Inclusion of additional flocks has identified flocks with lamb survival recording problems and survival has been dropped from the Dual Purpose WormFEC list at this stage.
- For Trait leader lists the flock numbers (and eligible sires for listing) involved were 244 (4280) for growth, 185 (2854) for meat, 173 (3342) for reproduction, 107 (2283) for wool and 38 (973) for host resistance to parasites.
- Lists of the top 15% of all sires used are available at <http://www.sil.co.nz/>
- The breeding values will be stored within the SIL database and breeders can obtain lists for all animals including rising two-tooth sires for their flock via their SIL bureau.
- Genetic linkages between linked flocks for key traits are available on the website at <http://www.sil.co.nz/>.
- Genetic trends for the national evaluation are also available off the website at <http://www.sil.co.nz/> . These trends are very useful as they clearly show genetic progress is occurring for a large fraction of the sheep industry.

Future Intentions

These lists will be updated 2 monthly, with overall summary lists posted on the website only. Breeding values will be available in the SIL database for all animals involved and individual breeders can list the results for their flocks as required.

However, once further genetic linkages are available and additional flocks participating there is the possibility of shifting to a monthly evaluation.

Queries

- 5 People interested in further reading about performance recording and genetic improvement in sheep using SIL are referred to "Introduction to SIL & Performance Recording" 2006. 35pp, Mark Young, ISBN 0-473-10810-0 and "**A guide to genetic improvement in sheep**" 2000. 80pp, Ed KG Geenty, Sheep Improvement Limited. ISBN 0-908-768-97-4. These are available from Mark Young e-mail:
- 10 mark.young@sheepimprovement.co.nz or phone 027-220-6780.

CLAIMS:

1. A method for identifying an ovine with a genotype indicative of at least two altered performance traits, the method including the step of detecting, in a sample derived from the ovine, the presence of at least one allele of the CP34 simple sequence repeat (SSR) marker, or at least one allele of a marker in linkage disequilibrium (LD) with CP34, wherein the presence of the allele is indicative of the altered performance traits in the ovine.
2. The method of claim 1 in which the performance trait is selected from the group consisting of: weaning weight (WWT), body weight at 8 months (LW8), body weight at 12 months (LW12), carcass weight (CW), adult ewe weight (EWT), eye muscle width (EMW), eye muscle depth (EMD), eye muscle area (EMA), fat depth (FD), carcass fat weight (FAT), carcass lean muscle weight (LEAN), number of lambs born (NLB), lamb fleece weight (LFW), hogget fleece weight (FW12), ewe (adult) fleece weight (EFW), hogget fibre diameter (FDIAM), and resistance to gastrointestinal parasitic nematode infection.
3. A method for identifying an ovine with a genotype indicative of at least one altered performance traits selected from the group consisting of: weaning weight (WWT), body weight at 8 months (LW8), body weight at 12 months (LW12), carcass weight (CW), adult ewe weight (EWT), eye muscle width (EMW), eye muscle depth (EMD), eye muscle area (EMA), fat depth (FD), carcass fat weight (FAT), carcass lean muscle weight (LEAN), number of lambs born (NLB), lamb fleece weight (LFW), hogget fleece weight (FW12), ewe (adult) fleece weight (EFW), hogget fibre diameter (FDIAM), and resistance to gastrointestinal parasitic nematode infection, the method including the step of detecting, in a sample derived from the ovine, the presence of at least one allele of the CP34 simple sequence repeat (SSR) marker, or at least one allele of a marker in linkage disequilibrium (LD) with CP34, wherein the presence of the allele is indicative of the altered performance traits in the ovine.
4. A method for identifying an ovine with a genotype indicative of at least one altered performance traits selected from the group consisting of: weaning weight (WWT), body weight at 8 months (LW8), body weight at 12 months (LW12), carcass weight (CW), adult ewe weight (EWT), eye muscle width (EMW), eye muscle depth (EMD), eye muscle area (EMA), fat depth

(FD), carcass fat weight (FAT), carcass lean muscle weight (LEAN), number of lambs born (NLB), lamb fleece weight (LFW), hogget fleece weight (FW12), ewe (adult) fleece weight (EFW), and hogget fibre diameter (FDIAM), the method including the step of detecting, in a sample derived from the ovine, the presence of at least one allele of the CP34 simple sequence repeat (SSR) marker, or at least one allele of a marker in linkage disequilibrium (LD) with CP34, wherein the presence of the allele is indicative of the altered performance traits in the ovine.

5 5. The method of any one of claims 1 to 4 in which the marker in LD with CP34 is an SSR marker.

10 6. The method of claim 5 in which the SSR marker in LD with CP34 is selected from the group consisting of BMS1084327, BMS1082942, BMS1082956, BMS1082961, BMS1083945, BMS1083008, BMS1082252, BMS1082669, BMS1082702, BMS1082722, BMS1082831, BMS1887400, BMS1887404, BMS1784528, BMS1600436, BMS1082043, BMS1082045,
15 BMS1081952, BMS1081760, BMS1081860, BMS30480882, BMS30480889, BMS1081770, BMS1081774, RSAD2_1, BMS1081640, BMS1080704, and BMS1080870 as herein defined.

20 7. The method of claim of any one of claims 1 to 6 in which the allele of CP34 is selected from the group consisting of: allele A, allele B, allele C, allele D, allele E, allele F, allele G and allele H, as herein defined.

8. The method of claim 7 in which the allele of CP34 is allele A, G or H.

9. The method of claim 7 in which the allele of CP34 is allele A.

25 10. The method of claim 7 in which the allele of CP34 is allele C or E.

11. The method of claim 10 in which the allele of CP34 is allele E.

30 12. The method of any one of claims 1 to 11 in which the allele is detected using a polymerase chain reaction (PCR) step.

13. The method of claim 12 in which the allele is detected by amplifying the marker with primers comprising sequence complimentary to sequence of the ovine genome flanking the marker.

5 14. The method of claim 12 in which the marker is amplified using at least one primer selected from those set forth in Table 2.

15. The method of any one of claims 1 to 11 in which the allele is detected by a probe-based methods.

10

16. The method of claim 15 in which the allele is detected by a probe comprising the sequence of or complementary to the marker.

15

17. The method of any one of claims 1 to 16 in which the presence of a combination of more than one allele of the CP34 SSR marker, or more than one allele of a marker in linkage disequilibrium (LD) with CP34, is detected to identify the ovine.

18. The method of claim 17 in which a combination of at least one allele of the CP34 SSR and at least one allele of a marker in LD with CP34, is detected to identify the ovine.

20

19. A method for selecting an ovine with at least two altered performance traits, the method comprising selecting an ovine identified by a method of any one of claims 1 and 4 to 17.

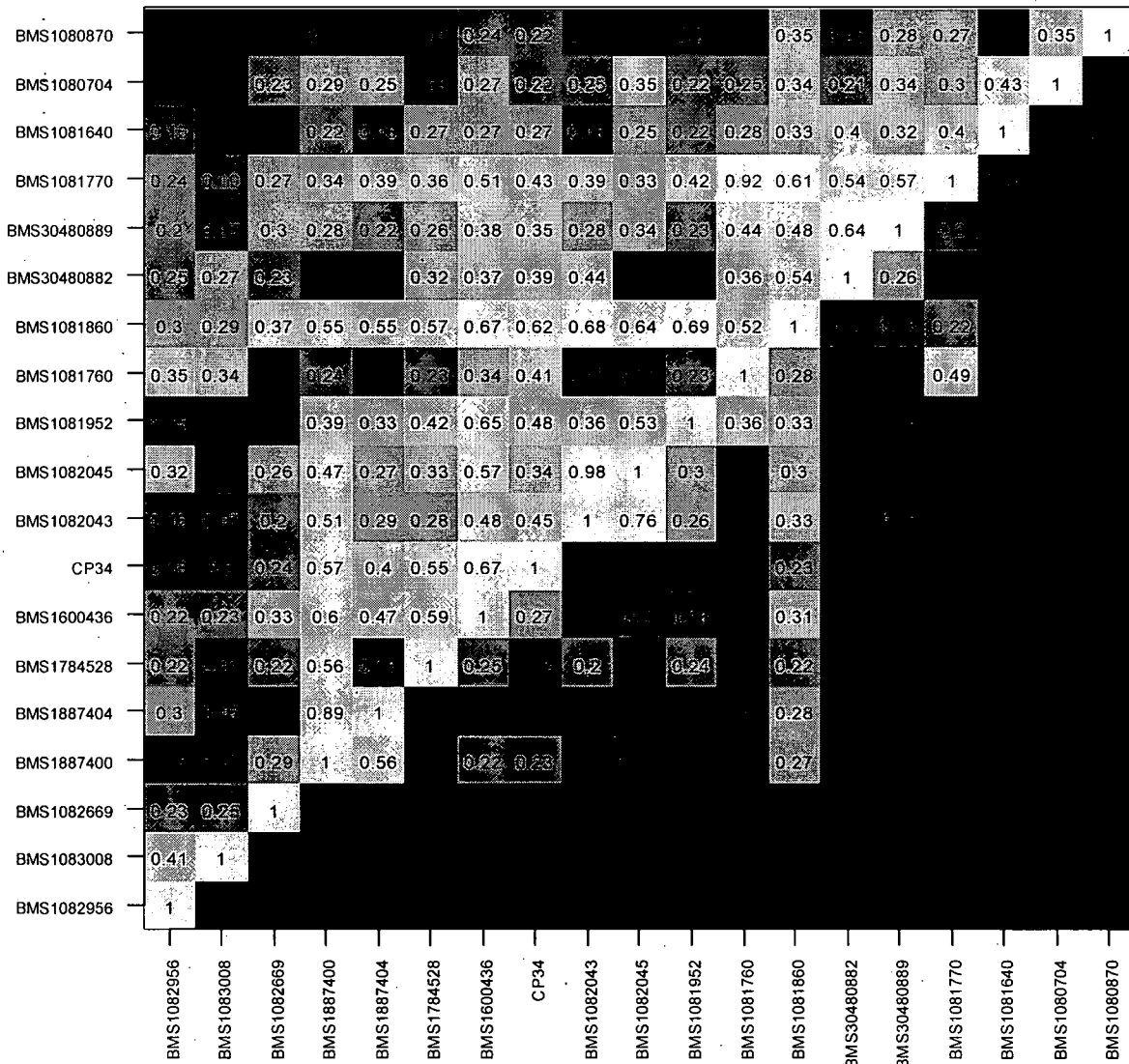
25

20. A method of selecting an ovine with a genotype indicative of at least one altered performance traits selected from the group consisting of: weaning weight (WWT), body weight at 8 months (LW8), body weight at 12 months (LW12), carcass weight (CW), adult ewe weight (EWT), eye muscle width (EMW), eye muscle depth (EMD), eye muscle area (EMA), fat depth (FD), carcass fat weight (FAT), carcass lean muscle weight (LEAN), number of lambs born (NLB), lamb fleece weight (LFW), hogget fleece weight (FW12), ewe (adult) fleece weight (EFW), hogget fibre diameter (FDIAM), and resistance to gastrointestinal parasitic nematode infection, the method selecting an ovine identified by a method of any one of claims 2 and 4 to 17.

30

21. A method of selecting an ovine with a genotype indicative of at least one altered performance traits selected from the group consisting of: weaning weight (WWT), body weight at 8 months (LW8), body weight at 12 months (LW12), carcass weight (CW), adult ewe weight (EWT), eye muscle width (EMW), eye muscle depth (EMD), eye muscle area (EMA), fat depth (FD), carcass fat weight (FAT), carcass lean muscle weight (LEAN), number of lambs born (NLB), lamb fleece weight (LFW), hogget fleece weight (FW12), ewe (adult) fleece weight (EFW), and hogget fibre diameter (FDIAM), the method selecting an ovine identified by a method of any one of claims 3 to 17.
22. An isolated polynucleotide comprising an SSR marker selected from the group consisting of BMS1084327, BMS1082942, BMS1082956, BMS1082961, BMS1083945, BMS1083008, BMS1082252, BMS1082669, BMS1082702, BMS1082722, BMS1082831, BMS1887400, BMS1887404, BMS1784528, BMS1600436, BMS1082043, BMS1082045, BMS1081952, BMS1081760, BMS1081860, BMS30480882, BMS30480889, BMS1081770, BMS1081774, RSAD2_1, BMS1081640, BMS1080704, and BMS1080870 as herein defined.
23. A primer suitable for amplifying a polynucleotide of claim 22, the primer comprising a sequence complimentary to sequence of the ovine genome flanking the marker.
24. A primer of claim 23, selected from the primers set forth in Table 2.

of animals = 847 , breed = CPRTC



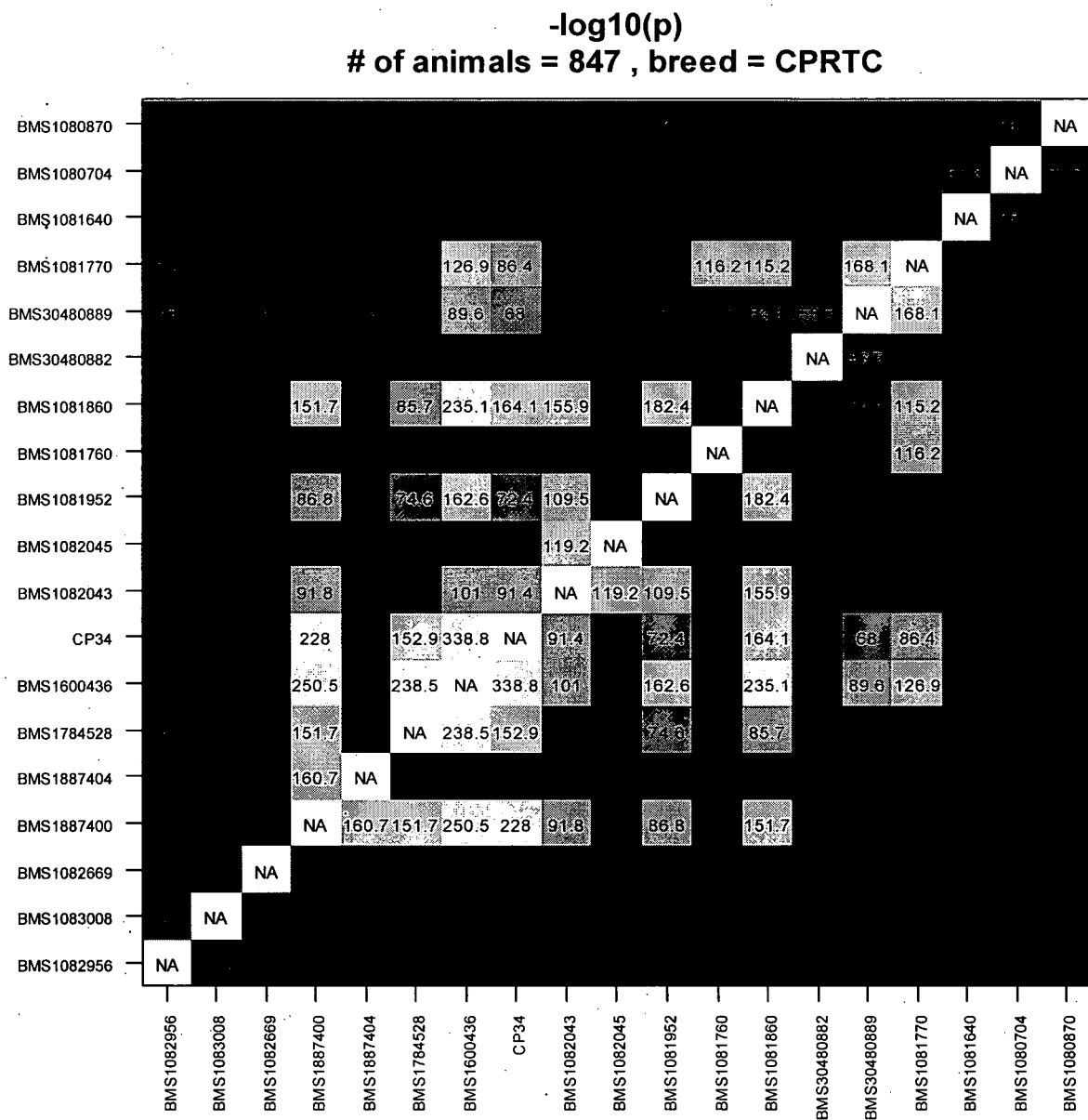


Figure 3

BMS1082956																			
Allele	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	LB	Count
C	-8.904	-9.113	-8.491	0.823	0.389	-0.409	-0.767	-0.020	2.071	0.124	-0.077	1.280	-7.002	-8.352	-7.205	-8.586	-10.885	-6.149	1
D	0.979	0.918	-0.486	0.023	0.038	0.121	0.242	0.062	0.092	0.039	0.098	0.131	0.533	-0.048	-1.276	-0.123	-0.648	0.273	74
E	-0.819	-0.849	-0.899	-0.038	-0.024	-0.008	-0.010	-0.022	-0.219	-0.013	-0.013	-0.076	-0.967	-0.899	-0.877	-1.080	-0.978	-0.923	684
F	1.038	0.751	-0.482	-0.080	-0.012	-0.098	-0.128	-0.141	-0.208	-0.013	-0.013	0.012	-1.979	-0.827	-1.149	0.518	1.216	0.350	263
G	1.167	1.442	2.850	0.144	0.063	0.071	0.077	0.160	0.598	0.028	0.000	0.161	4.272	3.378	3.825	2.215	1.544	0.126	287
H	-1.709	-1.362	0.788	-0.041	-0.089	0.072	0.077	0.028	-0.026	0.002	-0.017	-0.334	4.414	-1.421	-0.353	1.455	1.127	1.975	48
I	0.039	0.240	-1.186	0.114	0.053	-0.034	-0.080	0.002	0.570	0.027	-0.003	0.141	-0.711	-0.583	-1.140	-2.045	-1.973	-1.342	34
J	-23.789	-24.559	-26.210	0.340	0.018	-0.791	-0.851	-1.577	1.530	0.177	0.131	0.133	-26.471	-26.185	-27.456	-23.773	-23.719	-25.338	2
K	0.840	-0.117	3.501	-0.112	0.195	1.500	1.879	2.172	1.507	-0.009	0.329	0.695	0.740	-2.805	-1.144	0.188	5.958	8.735	1
Pvalue	0.863	0.821	0.324	0.012	0.002	0.060	0.154	0.061	0.024	0.484	0.473	0.013	0.058	0.200	0.077	0.671	0.733	0.721	0.004

BMS1083008																			
Allele	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	LB	Count
D	1.684	9.649	-7.486	0.309	-0.171	0.691	0.650	1.320	3.550	0.215	0.370	0.006	-2.163	-9.216	-19.161	13.026	10.635	5.560	1
E	16.597	19.944	8.635	0.460	-0.163	0.713	1.052	1.161	2.314	0.091	0.150	-0.830	20.109	15.602	11.180	11.780	8.912	5.909	3
F	0.119	0.265	0.671	0.049	0.024	0.042	0.061	0.062	0.166	0.007	0.001	0.051	0.792	0.907	0.600	0.973	0.773	0.750	621
G	2.592	2.660	2.030	0.011	-0.011	-0.083	-0.057	0.074	0.124	0.009	0.010	-0.015	2.957	2.621	2.365	1.721	1.456	1.846	243
H	-1.557	-1.762	-1.965	-0.072	-0.027	-0.068	-0.114	-0.125	-0.285	-0.014	-0.008	-0.059	-2.611	-2.069	-2.056	-2.187	-1.787	-1.860	496
J	-4.143	-1.025	6.132	0.564	0.287	0.432	0.470	0.735	1.824	0.283	0.325	0.707	5.527	2.457	4.519	3.864	1.363	7.908	2
M	12.684	2.734	17.019	-0.216	0.538	-0.144	0.168	-0.224	-3.007	-0.311	-0.274	1.215	7.590	16.120	24.388	2.884	6.137	9.014	1,039
Pvalue	0.356	0.237	0.155	0.029	0.091	0.146	0.168	0.155	0.160	0.527	0.795	0.175	0.053	0.128	0.132	0.356	0.537	0.474	0.250

BMS1082669																			
Allele	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	LB	Count
C	-2.381	-2.818	-1.779	-0.056	-0.039	-0.128	-0.153	-0.258	-0.288	-0.003	-0.002	-0.136	-2.514	-1.676	-1.102	-3.161	-2.864	-2.596	210
D	-8.503	-8.974	3.601	0.522	0.111	0.031	0.291	-0.298	1.515	0.177	0.226	0.395	-6.303	-3.679	0.282	-2.323	-1.408	7.734	2
F	-2.264	-2.367	-0.870	-0.122	-0.080	-0.050	-0.059	-0.219	-0.448	0.037	0.067	-0.349	0.106	-0.349	-0.670	-1.907	-2.024	-1.187	40
L	0.544	0.889	-1.455	0.147	-0.030	0.488	0.694	0.856	1.032	-0.040	-0.010	-0.223	2.457	1.138	-1.059	-0.705	-1.297	-1.967	16
M	1.358	1.514	1.425	-0.011	-0.006	-0.011	-0.031	-0.006	0.023	0.002	-0.005	-0.014	1.509	1.389	1.368	1.579	1.533	1.535	738
N	-0.251	0.062	-0.012	0.145	0.062	0.073	0.126	0.123	0.505	0.020	0.006	0.171	0.408	-0.264	-0.278	0.597	0.138	0.243	223
O	-2.530	-3.050	-4.377	-0.082	0.014	0.080	0.109	0.179	-0.546	-0.043	-0.006	0.115	-0.030	-4.321	-4.775	-3.764	-3.984	-3.984	129
P	-7.266	-8.859	-8.945	-0.134	0.024	0.081	0.101	0.285	-0.214	-0.067	-0.009	0.027	-8.178	-8.414	-7.747	-8.918	-9.835	-10.323	8
Q	16.582	11.671	5.949	0.272	0.358	0.813	1.551	0.961	0.698	0.013	0.404	1.280	3.239	6.680	3.351	10.544	11.792	8.913	2
Pvalue	0.450	0.253	0.173	0.058	0.022	0.022	0.028	0.005	0.054	0.573	0.736	0.009	0.122	0.229	0.212	0.203	0.234	0.173	0.014

BMS1887400																			
Allele	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	LB	Count
C	-5.226	-5.316	-4.254	0.027	0.084	-0.075	-0.115	-0.090	0.081	0.006	-0.003	0.237	-5.463	-4.810	-4.187	-5.842	-5.340	-4.474	188
J	-6.951	-7.600	-5.226	-0.065	0.011	-0.058	-0.144	0.137	-0.438	-0.088	-0.142	0.076	-7.927	-6.161	-4.490	-8.390	-7.306	-6.227	29
L	-5.772	-6.846	-4.836	0.365	0.009	0.301	0.510	0.529	1.405	0.053	0.140	-0.111	-3.419	-4.380	-3.327	-5.032	-6.317	-6.266	29
M	1.085	0.850	1.851	-0.208	-0.140	-0.152	-0.217	-0.330	-0.804	-0.022	-0.033	-0.468	0.427	1.299	1.849	0.937	1.697	1.977	155
N	1.409	1.617	0.304	-0.032	0.004	-0.038	-0.068	-0.055	-0.079	0.013	0.021	0.022	0.885	0.817	0.277	1.076	1.083	0.937	216
P	-2.523	-2.751	-4.014	-0.007	-0.059	0.043	0.096	0.096	-0.012	-0.050	-0.065	-0.232	-4.120	-3.847	-4.284	-3.802	-3.520	-3.798	42
R	3.745	3.119	3.305	0.065	0.017	0.020	0.045	0.045	-0.068	0.007	0.022	0.077	3.759	3.558	3.552	3.873	3.472	3.043	215
T	0.942	1.067	0.759	0.017	0.003	0.052	0.076	0.075	0.163	0.000	0.002	0.004	1.162	0.747	0.568	1.167	0.886	0.962	638
V	-2.968	-2.103	-2.025	0.005	0.037	-0.001	-0.020	-0.008	0.066	0.008	-0.013	0.106	-1.955	-1.747	-1.964	-2.167	-1.842	-2.094	142
Pvalue	0.008	0.001	0.004	0.838	0.066	0.039	0.039	0.025	0.010	0.562	0.068	0.005	0.005	0.007	0.016	0.003	0.004	0.016	0.004

BMS1887404																			
Allele	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	FW12BV	WWTBV Count
C	1.820	1.480	2.284	-0.175	-0.116	-0.152	-0.223	-0.287	-0.713	-0.022	-0.031	-0.378	0.708	1.630	1.845	2.322	2.322	2.322	197
D	-0.159	-0.104	-0.231	0.025	0.015	0.022	0.031	0.042	0.101	0.004	0.006	0.050	-0.011	-0.152	-0.099	-0.203	-0.203	-0.203	1452
F	-14.218	-15.613	-12.809	-0.155	0.033	-0.228	-0.188	-0.481	-0.133	-0.123	-0.133	-11.192	-13.733	-11.192	-9.433	-20.104	-18.022	-16.766	9
Pvalue	0.131	0.103	0.067	0.002	0.002	0.012	0.018	0.004	0.002	0.204	0.088	0.050	0.203	0.187	0.165	0.036	0.031	0.030	4.8E-04

BMS1784528																			
Allele	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	FW12BV	WWTBV Count
C	1.551	1.008	0.738	-0.090	-0.021	-0.081	-0.134	-0.113	-0.355	-0.022	-0.031	-0.020	0.970	1.395	1.213	0.424	0.424	0.424	348
D	1.140	1.806	1.557	0.054	0.022	0.096	0.162	0.081	0.166	0.012	0.010	0.049	2.408	1.603	1.455	1.572	1.572	1.572	315
F	-0.705	-0.831	-0.028	0.010	0.023	-0.029	-0.057	0.000	-0.008	0.008	0.009	0.083	-0.073	-0.676	-0.224	-0.030	0.141	0.208	486
G	3.060	2.844	0.919	0.089	0.019	-0.014	-0.022	0.041	0.723	-0.002	-0.030	0.017	2.001	1.433	1.049	1.926	1.277	0.692	51
M	-3.571	-4.019	-3.527	-0.131	-0.087	-0.140	-0.168	-0.255	-0.387	-0.045	-0.056	-0.315	-4.759	-3.948	-3.736	-4.432	-3.961	-3.555	129
N	1.473	1.757	2.098	0.150	-0.031	0.292	0.412	0.483	0.877	0.075	0.163	-0.161	3.831	1.269	0.865	5.015	2.552	3.356	24
O	-8.360	-5.965	-3.021	0.437	0.122	0.660	0.895	1.184	2.296	0.085	0.129	-0.223	-0.949	-2.899	-3.272	-5.118	-5.988	-2.811	15
P	-6.812	-5.300	-2.388	0.041	-0.050	0.106	0.139	0.082	-0.008	0.031	0.012	-0.210	-3.979	-3.781	-1.994	-6.605	-6.022	-2.948	6
Q	18.582	17.687	6.053	0.711	-0.158	0.123	0.503	0.143	2.130	0.037	0.089	-0.898	6.384	5.649	-1.787	0.637	-0.808	-1.180	1
R	-3.773	-2.574	-3.943	0.246	-0.051	0.423	0.866	0.656	0.367	0.058	0.158	-0.181	-2.546	-3.090	-4.175	-2.438	-3.398	-3.816	37
S	-0.453	0.264	-5.070	0.067	0.050	-0.102	-0.062	-0.307	0.322	0.028	0.004	0.070	-3.195	-3.262	-5.027	-2.245	-2.384	-5.208	30
Pvalue	0.536	0.520	0.496	0.013	0.018	0.3E-05	0.3E-05	0.001	0.018	0.398	0.020	0.024	0.311	0.522	0.490	0.514	0.617	0.555	0.003

BMS1600436																			
Allele	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	FW12BV	WWTBV Count
C	0.733	0.319	0.613	0.136	0.020	-0.043	-0.087	-0.001	0.170	0.043	0.034	0.110	1.546	1.227	1.395	0.979	0.048	-0.306	60
G	-1.132	-2.949	-4.092	-0.322	-0.071	-0.111	-0.099	-0.211	-1.212	-0.122	-0.073	-0.132	-6.526	-4.336	-4.942	-4.410	-3.019	-3.101	89
H	1.132	-0.632	-0.331	-0.043	-0.050	0.058	-0.080	0.041	-0.198	0.003	0.005	-0.184	-0.237	-0.129	-0.145	-0.273	-0.045	0.372	196
I	2.736	2.205	2.688	-0.020	-0.021	-0.087	-0.120	-0.135	-0.166	-0.011	-0.029	-0.071	2.605	2.817	3.061	2.331	2.423	2.309	292
J	-0.367	0.137	-0.237	0.068	0.032	0.068	0.103	0.093	0.238	0.022	0.023	0.087	0.718	-0.007	-0.134	0.251	-0.162	-0.372	513
K	-0.313	-0.069	-1.152	0.042	0.002	0.003	-0.034	0.072	0.320	0.002	-0.019	-0.022	-0.223	-0.396	-0.890	-1.141	-1.394	-1.479	174
M	2.741	3.761	3.616	0.166	0.001	0.434	0.566	0.735	1.096	0.133	0.268	-0.081	6.433	3.034	2.118	7.640	4.372	5.158	16
Q	2.928	1.783	0.554	-0.295	-0.076	-0.233	-0.324	-0.392	-1.034	-0.061	-0.038	-0.290	-0.675	1.314	2.565	2.039	-0.089	-0.264	128
U	-4.360	-4.219	-2.883	0.072	0.071	0.027	0.040	0.056	0.239	0.015	0.018	0.280	-3.878	-3.514	-2.898	-4.270	-3.827	-2.864	46
V	-0.172	-0.373	0.664	0.048	0.040	-0.036	-0.095	0.021	0.610	-0.016	-0.058	-0.197	-0.815	1.514	1.624	0.905	0.047	0.905	4
W	3.377	8.200	17.219	1.367	0.010	1.219	1.806	2.026	6.339	0.402	0.516	-0.790	27.906	18.746	21.680	15.460	8.468	12.508	4
Y	-6.498	-7.063	-7.853	0.224	0.030	0.432	0.737	0.828	0.838	-0.033	-0.027	-0.022	-4.218	-5.425	-6.406	-9.662	-10.139	-9.560	11
Pvalue	0.311	0.396	0.143	0.4E-03	1.9E-04	6.4E-05	1.4E-04	3.0E-04	6.1E-04	1.0E-04	0.3E-04	4.4E-04	0.218	0.124	0.056	0.158	0.225	0.305	5.7E-08

CP34																			
Allele	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	FW12BV	WWTBV Count
A	-6.314	-6.127	-4.672	0.093	0.070	0.024	0.030	0.075	0.432	0.017	0.020	0.247	-5.452	-4.988	-4.309	-6.150	-5.755	-5.156	181
B	4.266	3.402	3.260	0.001	-0.031	-0.004	-0.016	0.052	-0.081	0.001	0.013	-0.101	3.587	3.584	3.400	3.847	3.310	3.133	297
C	2.129	-0.158	-2.455	-0.381	-0.186	-0.192	-0.016	-0.755	-0.522	-0.037	0.109	-0.685	-0.328	-0.582	-1.618	-4.058	-2.290	-3.422	4
D	-0.052	0.317	0.221	-0.018	0.038	-0.028	-0.060	-0.024	-0.014	-0.002	-0.020	0.117	0.288	0.247	0.148	0.550	0.693	0.329	308
E	2.154	1.508	0.998	-0.154	-0.048	-0.095	-0.134	-0.163	-0.611	-0.041	-0.030	-0.099	-0.399	0.541	0.350	1.329	1.948	1.795	373
F	-1.675	-0.896	-0.823	0.079	0.009	0.059	0.102	0.032	0.328	0.027	0.015	-0.021	0.316	-0.579	-0.472	-1.083	-1.553	-1.275	443
G	-11.668	-10.604	-11.766	0.685	0.030	1.010	1.543	1.716	1.897	0.053	0.156	0.033	-6.545	-10.928	-11.661	-8.990	-12.498	-12.229	13
H	-5.346	-5.248	-6.939	0.636	-0.080	0.505	0.736	1.195	2.266	0.047	0.150	-0.437	-1.083	-7.736	-7.788	-4.474	-4.268	-6.126	5
Pvalue	0.000	0.002	0.003	1.7E-07	9.0E-05	5.6E-05	2.8E-05	3.8E-05	2.0E-05	0.001	0.008	0.003	0.007	0.003	0.003	0.003	0.003	0.003	1.2E-07

BMS1082043																			
Allele	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	AFCB	FW12BV	WWTBV Count
C	2.452	4.320	8.634	0.377	0.124	0.526	0.576	0.986	1.482	0.196	0.204	0.317	9.990	7.031	5.978	12.309	10.448	11.813	4
D	-2.586	-2.339	-1.274	0.057	-0.016	0.065	0.103	0.090	0.183	0.005	0.008	-0.095	-1.984	-1.721	-1.151	-1.555	-1.477	-1.367	194
E	0.315	0.181	0.345	-0.011	-0.002	-0.016	-0.022	-0.021	-0.067	-0.001	0.002	0.004	0.213	0.249	0.318	0.138	0.180	0.372	950
F	-3.859	-2.018	-6.164	0.173	0.022	0.066	0.140	0.045	0.919	0.041	0.021	-0.074	-5.251	-5.513	-6.554	-2.924	-3.414	-5.618	30
H	-2.855	-2.289	-2.005	-0.005	0.025	-0.005	-0.007	-0.043	0.063	0.005	-0.013	0.068	-2.009	-2.296	-1.806	-1.719	-2.374	-2.374	149
J	9.023	8.133	5.084	-0.106	0.005	-0.025	-0.106	-0.025	-0.258	-0.038	-0.045	0.063	7.171	7.069	5.320	5.332	4.797	4.797	80
O	12.490	14.570	4.121	1.615	0.024	1.217	1.639	1.950	5.936	0.458	0.456	0.140	27.752	10.825	4.601	21.489	7.113	3.174	1
Pvalue	0.017	0.043	0.164	0.128	0.888	0.425	0.437	0.463	0.225	0.458	0.607	0.758	0.047	0.048	0.163	0.317	0.342	0.254	0.057

BMS108160		AFCcNbV	AFCcNbV	CWB	EFWB	EMABV	EMdBV	EMWbV	EVTBv	FATBV	FDBV	FDAMBv	FEC1BV	FEC1mBV	FEC1xNB	FEC2BV	FEC2mBV	FEC2nBV	PW12BV	LEANBV	LFWBV	LW12BV	LW8BV	NLBVB	WWTBV	Count
A	-40.568	-40.640	-38.947	-1.032	-0.321	-0.083	0.366	-0.647	-4.494	-0.332	-0.116	-0.741	-49.170	-43.234	-43.665	-39.924	-34.807	-33.760	-0.366	-0.578	-0.056	-4.312	-3.068	0.035	-1.595	1
B	-6.189	-10.053	1.155	0.402	-0.235	0.393	0.445	0.550	1.698	0.187	0.164	-0.853	1.109	-3.474	2.668	-5.142	-10.229	-0.952	-0.256	0.292	-0.042	1.521	1.236	-0.041	0.184	1
C	-1.679	-2.982	-4.284	-0.176	-0.053	-0.050	0.021	-0.171	-0.869	-0.076	-0.044	-0.172	-0.363	8.935	-4.757	-3.976	-2.968	-0.063	-0.114	-0.010	-0.585	-0.515	0.007	-0.199	98	
D	13.386	14.692	9.777	0.254	0.171	0.279	0.304	0.541	1.171	0.092	0.101	0.630	15.805	13.918	10.855	10.046	9.026	8.701	0.197	0.208	0.030	1.212	0.789	0.056	0.344	28
E	6.992	5.698	4.924	-0.102	-0.031	0.132	0.262	0.079	-0.665	-0.023	0.032	-0.010	4.127	4.323	2.887	6.796	6.653	5.840	-0.035	-0.018	-0.004	-0.681	-0.316	-0.032	-0.158	29
F	-3.297	-3.009	-1.805	0.041	-0.004	0.042	0.056	0.057	0.125	0.023	0.032	-0.026	-1.954	-1.901	-1.429	-2.935	-2.921	-2.261	-0.004	0.033	-0.001	0.179	0.136	-0.003	0.069	327
G	-2.056	-1.863	-1.366	0.063	-0.015	-0.052	-0.119	-0.043	0.330	0.012	-0.031	-0.092	-0.078	-1.540	-1.246	-0.418	-1.680	-1.607	-0.017	0.018	-0.002	0.202	0.166	0.018	0.038	60
H	7.155	3.716	-0.048	-0.017	-0.204	0.337	0.266	0.331	-0.015	0.081	0.081	-0.126	4.778	4.553	3.616	4.816	4.572	3.811	-0.019	0.008	-0.004	0.252	-0.149	0.017	-0.121	30
I	-0.121	0.513	-0.081	0.037	-0.014	-0.028	-0.081	-0.058	0.110	0.039	0.025	-0.085	0.410	0.182	-0.092	0.868	0.875	-0.024	-0.015	-0.010	-0.140	0.087	-0.031	-0.077	96	
J	15.762	18.557	9.830	0.404	0.057	0.625	0.949	0.810	1.435	0.153	0.225	-0.033	21.304	14.340	9.356	15.101	11.043	10.387	0.066	0.426	0.010	1.576	1.281	0.151	0.563	5
K	-0.332	-0.432	-2.263	0.209	-0.015	0.151	0.282	0.291	0.743	0.019	0.025	-0.111	-0.867	-2.136	-2.897	-2.256	-3.103	-1.787	-0.018	0.196	-0.004	0.927	0.637	-0.012	0.517	28
L	-3.018	-1.539	-1.349	0.003	-0.058	0.141	0.115	0.285	-0.110	0.042	0.042	-0.081	-0.336	-2.335	-2.261	1.646	0.555	-0.212	-0.066	0.035	-0.010	-0.133	0.031	0.004	-0.148	28
M	-0.090	-5.941	0.543	-0.063	0.058	-0.080	-0.176	-0.052	0.027	-0.057	-0.127	0.157	-3.698	-3.817	-3.633	-7.082	-6.470	-5.719	0.068	-0.039	0.011	-0.186	-0.021	0.027	-0.232	20
N	0.571	0.594	2.839	0.026	0.046	-0.046	-0.072	0.001	0.030	-0.046	-0.108	0.120	0.929	3.004	4.185	-0.127	0.552	1.469	0.053	0.042	0.009	0.083	0.079	-0.013	0.111	55
O	1.183	-0.538	-0.768	-0.383	-0.079	-0.298	-0.393	-0.516	-1.403	-0.097	-0.055	-0.104	-3.629	-1.546	-1.578	-1.280	0.271	-0.101	-0.093	-0.014	-1.486	-1.171	-0.004	-0.614	130	
P	10.032	8.310	10.315	0.093	0.007	-0.118	-0.155	-0.075	0.063	-0.029	-0.074	0.068	10.007	10.051	10.866	9.433	9.235	9.784	0.006	0.066	0.001	0.145	0.266	0.034	0.321	93
Q	-2.550	-3.976	-0.051	0.279	0.007	-0.201	-0.265	-0.230	0.369	0.058	-0.015	0.008	0.541	1.168	2.899	-4.885	-4.721	-3.023	0.006	0.159	0.000	0.870	0.912	-0.018	0.749	6
R	-5.465	-4.967	-3.199	-0.009	-0.133	-0.014	-0.040	-0.002	-0.165	0.018	0.033	-0.435	-6.807	-6.136	-5.297	-1.715	-1.555	-0.879	-0.152	-0.022	-0.024	-0.193	-0.032	0.008	-0.020	26
S	-4.970	-6.069	-5.095	0.234	-0.037	0.481	0.543	0.835	1.600	0.132	0.181	-0.261	1.341	-2.930	-4.844	-1.112	-3.770	-3.320	-0.041	0.247	-0.009	1.419	0.699	0.045	0.195	20
T	-17.993	-21.780	-19.517	-0.750	-0.140	-0.064	0.039	0.011	-2.956	-0.332	-0.208	-0.378	-22.310	-19.153	-18.026	-28.010	-25.819	-23.641	-0.167	-0.439	-0.022	-3.013	-2.294	-0.078	-1.056	3
U	43.272	41.193	50.144	0.736	0.153	0.387	0.375	1.157	-0.805	-0.023	0.119	0.462	35.814	37.001	41.921	47.475	49.334	60.387	0.179	0.105	0.028	-0.520	-0.114	-0.086	0.314	2
V	-0.141	3.332	1.881	0.422	0.274	0.399	0.528	0.647	1.353	0.089	0.022	0.834	6.336	2.498	1.854	3.598	1.502	1.985	0.320	0.424	0.049	1.770	1.375	-0.009	0.682	44
W	-0.806	-0.446	-1.567	-0.016	-0.023	-0.052	-0.071	-0.125	0.051	0.019	0.018	0.068	-1.252	-1.410	-2.036	-0.093	-0.161	-1.093	0.027	-0.038	0.004	-0.028	-0.057	-0.009	-0.080	155
X	-12.350	-12.303	-6.063	0.383	0.123	-0.133	-0.280	0.031	2.659	0.060	0.013	0.046	-6.806	-6.527	-1.876	-11.318	-11.201	-10.275	0.143	0.019	2.288	1.039	-0.079	0.745	19	
Y	2.213	2.307	2.821	0.058	0.038	0.146	0.156	0.346	0.107	-0.062	-0.129	0.098	3.601	3.275	3.446	3.065	2.963	1.629	0.042	0.125	0.007	0.172	0.203	0.006	0.030	13
Z	11.398	8.759	2.251	0.131	0.098	-0.097	-0.242	0.287	1.103	-0.042	-0.037	0.346	5.646	7.155	5.804	3.508	2.568	-1.746	0.111	0.027	0.015	1.122	0.352	0.054	0.469	5
a	-1.530	-2.699	6.426	0.400	0.040	-0.142	-0.181	-0.356	1.597	0.173	0.119	-0.091	6.760	5.403	9.315	3.547	2.111	3.150	0.048	0.190	0.005	1.738	1.212	0.043	0.798	4
b	7.724	13.844	8.459	0.141	0.008	0.828	1.424	1.043	-0.092	-0.031	0.147	-0.808	2.303	5.496	4.816	13.775	16.088	12.940	0.013	0.404	-0.001	0.386	0.520	-0.078	0.346	4
c	0.004	0.002	-4.0E-07	1.5E-05	0.002	1.4E-04	3.2E-05	0.003	0.001	0.001	0.001	8.6E-05	1.5E-05	0.001	0.001	0.015	0.016	0.006	1.4E-05	0.1E-06	3.0E-06	3.5E-07	4.4E-04	4.1E-05	0.001	0.001

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BMS1081770	A	-8.998	-5.789	-26.071	-0.066	-0.176	0.414	0.640	0.683	0.440	-0.154	-0.159	-0.739	-22.283	-21.680	-27.215	-9.277	-9.930	-25.286	-0.205	0.154	-0.029	-0.001	-0.312	-0.124	-0.140	1	
Ala	B	8.513	5.432	0.130	0.025	0.077	0.149	0.174	0.456	0.000	0.025	0.050	0.050	5.159	5.981	4.264	8.140	8.524	6.935	0.029	0.103	0.003	0.606	0.398	0.002	0.369	58	
C	D	0.206	0.314	-0.236	-0.178	-0.040	-0.045	-0.104	-0.055	-0.781	-0.044	-0.054	-0.039	-0.666	-0.121	-0.094	-0.659	-0.008	-0.045	-0.046	-0.128	-0.008	-0.947	-0.555	0.005	-0.148	145	
E	F	-2.026	-1.932	-1.742	-0.038	0.037	-0.062	-0.104	-0.059	-0.020	-0.006	0.002	0.171	-2.945	-1.174	-2.316	-1.839	-1.224	-1.119	0.041	-0.494	0.008	-0.020	-0.120	0.010	-0.020	254	
F	G	30.297	23.074	10.312	-0.588	-0.085	-0.449	-0.488	-0.817	-2.397	-0.005	0.184	0.132	11.096	13.046	8.774	19.994	20.827	12.288	-0.080	-0.046	-0.012	-2.546	-1.862	-0.025	-0.695	2	
G	H	3.945	5.543	3.136	0.396	0.178	0.088	0.160	0.105	1.729	0.103	0.084	0.524	5.741	4.894	2.837	4.142	3.109	3.644	0.204	0.282	0.031	1.868	1.210	-0.022	0.745	19	
H	I	11.066	9.371	8.389	0.854	0.073	0.443	0.418	0.884	2.750	0.184	0.058	0.009	20.940	10.078	9.322	15.973	7.719	7.278	0.088	0.508	0.012	2.420	1.928	-0.012	0.726	5	
I	J	-12.107	-10.430	-7.866	0.040	-0.108	0.200	0.369	0.288	0.547	-0.073	-0.091	-0.420	-12.124	-8.803	-7.781	-9.728	-8.415	-8.147	-0.124	-0.140	-0.020	0.286	0.052	-0.058	0.064	13	
J	K	2.770	2.230	1.215	0.084	-0.025	-0.045	-0.084	-0.080	0.187	0.022	-0.008	-0.116	1.976	2.011	1.908	2.413	1.917	0.459	-0.028	0.023	-0.004	0.145	0.183	0.004	0.094	108	
K	L	0.128	-0.229	0.735	0.056	0.024	0.022	0.041	0.058	0.045	0.000	-0.006	0.084	0.683	0.306	0.733	0.293	-0.050	0.713	0.028	0.055	0.004	0.190	0.191	0.010	0.161	334	
L	M	2.117	4.322	27.739	1.087	0.561	1.023	1.476	1.541	3.890	0.115	-0.030	1.745	32.921	27.233	38.301	14.011	10.424	16.703	0.651	1.083	0.068	3.620	3.141	-0.075	1.622	1	
M	N	-1.356	-1.792	-0.570	-0.029	-0.012	-0.003	-0.015	0.003	0.241	0.012	0.009	-0.029	0.231	-0.467	-0.101	-0.721	-1.302	-1.105	0.013	0.003	-0.032	-0.174	-0.385	-0.012	-1.081	2	
N	O	-1.593	-1.792	-0.570	-0.029	-0.012	-0.003	-0.015	0.003	0.241	0.012	0.009	-0.029	0.231	-0.467	-0.101	-0.721	-1.302	-1.105	0.013	0.003	-0.032	-0.174	-0.385	-0.012	-1.081	2	
O	P	-1.255	-1.912	-0.504	-0.026	-0.008	0.053	0.086	0.015	0.087	0.014	0.022	-0.125	0.921	0.500	0.376	-0.646	-0.709	-0.927	-0.029	0.002	-0.004	-0.307	-0.011	-0.021	-0.079	311	
P	Q	-1.604	-1.335	-1.359	-0.081	-0.085	-0.081	-0.093	-0.166	-0.898	-0.029	-0.011	-0.260	-0.438	-0.373	-3.037	-0.707	-0.135	-0.524	-0.099	-0.110	-0.015	-0.702	-0.419	-0.018	-0.019	74	
Q	Value	12.260	12.558	9.307	0.650	0.216	0.766	0.957	1.440	2.530	0.293	0.473	0.696	21.991	11.797	7.694	16.856	9.088	11.022	0.250	0.577	0.037	3.570	2.145	0.175	1.546	1	
		0.664	0.006	0.006	0.004	0.016	0.436	0.736	0.008	0.008	0.485	0.687	0.002	0.120	0.097	0.449	0.853	0.646	0.762	0.005	0.014	0.012	0.003	0.008	0.096	0.096	0.096	1
		0.348	0.422																									

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ2008/000173

A. CLASSIFICATION OF SUBJECT MATTER		
Int. Cl.		
C12Q 1/68 (2006.01)		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED		
Minimum documentation searched (classification system followed by classification symbols)		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)		
MEDLINE, CAPLUS, BIOSIS, AGRICOLA, WPI, EPODOC, TXTEN full text databases, GENOMEQUEST: sheep, ovine, ovis, aries, cp34, oarcp34, QTL, quantitative trait loci, performance trait, linkage disequilibrium, linkage analysis, marker, MAS, EBV, estimated breeding value, microsatellite, partial sequence identities corresponding to Bovine SSR markers represented by SEQ ID: 1, 9, 5, 17, 23, 27, 33, 37, 41, 45, 49, 51, 57		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Genbank accession no DU461994, 1098421135022 CHORI-243 <i>Ovis aries</i> genomic clone CH243-223K10, genomic survey sequence, DALRYMPLE B.P. et al, 6 October 2005	22-24
X	Genbank accession no CZ419102, SONSTEGARD T.S. et al, 1014805 RP42 <i>Bos taurus</i> genomic clone RP42-45J24, genomic survey sequence, 6 April 2005	22-24
A	ARRANZ, J. et al, "Genetic variation at microsatellite loci in Spanish sheep", Small Ruminant Research", 2001, Vol. 39, No. 1, pages 3-10	
A	EDE A.J. et al, "Ovine microsatellites at the OarCP34, OarCP38, OarCP43, OarCP49, OarCP73, OarCP79 and OarCP99 loci", Animal Genetics, 1995, Vol. 26, No. 2, pages 130-131.	
☐ Further documents are listed in the continuation of Box C ☐ See patent family annex		
* "A"	Special categories of cited documents: document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E"	earlier application or patent but published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O"	document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family
"P"	document published prior to the international filing date but later than the priority date claimed	
Date of the actual completion of the international search 15 October 2008		Date of mailing of the international search report 29-10-08
Name and mailing address of the ISA/AU AUSTRALIAN PATENT OFFICE PO BOX 200, WODEN ACT 2606, AUSTRALIA E-mail address: pct@ipaustralia.gov.au Facsimile No. +61 2 6283 7999		Authorized officer SUSAN MACKENZIE AUSTRALIAN PATENT OFFICE (ISO 9001 Quality Certified Service) Telephone No : +61 2 6283 2690