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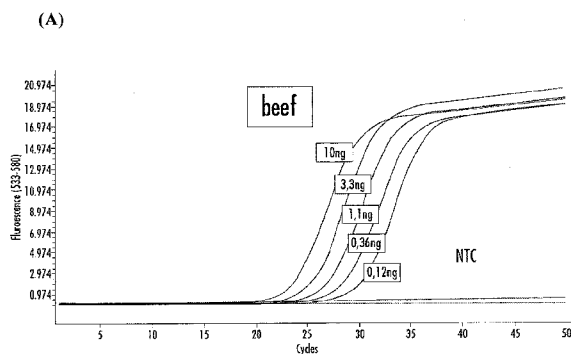
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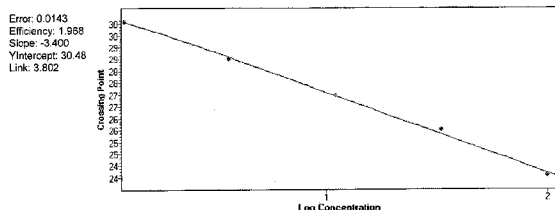
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(54) Title: DETECTION METHODS

FIGURE 3



(B)



(57) Abstract: A method for determining the species origin(s) of DNA in a sample comprising conducting meta-genomic sequence analysis of the sample to identify DNA from at least one species, followed by species specific quantitative polymerase chain reaction (qPCR) to amplify and quantify a species specific target from the identified species DNA.

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Detection methods

The invention relates to the characterization of the meat content of any food sample based on any high throughput sequencing technology used to sequence any identical gene fragment (genomic or mitochondrial) amplified from universal animal primers and identified based on the high information polymorphic content between those common primers.

The invention relates to analytical methods that have been developed to identify and quantify the more frequent animal species present in ground meat, meat preparations and meat products and to quantify the proportion of them.

Species identification is a major concern due to the increased awareness of consumers regarding the composition of foods, and the need to verify labelling statements. Ground meat, meat preparations and processed meat products are susceptible targets for fraudulent labelling due to the economic profit that results from selling cheaper meats as partial or total replacement for high-valued meats. Several analytical methods are used for authentication of meat and meat products. The analytical methods include polymerase chain reaction, chromatography, mass spectrometry, microscopy, spectroscopy, electronic spin resonance, and enzymatic assays. In species determination, analysis of DNA and protein are common practices.

Among DNA-based methods, Polymerase Chain Reaction (PCR) is an effective technique that is highly accurate and relatively fast. Conventional qualitative PCR methods have a satisfactory performance in the qualitative detection of meat species. However, the need for methods that give quantitative results has arisen following the introduction of labelling obligations. Moreover, quantification is also necessary for the detection of intentional adulteration of meat products or accidental contamination in the production line. There is therefore a need for improved methods for the quantitative determination of the species origin(s) of meat and meat products.

The invention provides a method for determining the species origin(s) of DNA in a sample comprising conducting metagenomic sequence analysis of the sample to identify DNA from the present species and the relative proportions of them. This may be followed by species specific quantitative polymerase chain reaction (qPCR) to amplify and quantify a species specific target from the identified species DNA.

Among new generation molecular technologies the metagenomic analysis has emerged as a powerful tool. Metagenomics applies a suite of genomic technologies and bioinformatics tools to

directly access the genetic content of entire communities of organisms. This technology is commonly used to describe microbial community profiles of various ecosystems like seas, soils, rumen, faeces, but also to study complex microbiota of foodstuff. The invention applies the technique of metagenomics in the first stage of a sequential identification, and proportion
5 estimation of animal species in a sample or quantitation of the origin of DNA in a sample.

In some embodiments, the metagenomic analysis comprises amplification and sequencing of a metagenomic target DNA sequence, said metagenomic target DNA sequence being selected to allow for: i) co-amplification of the metagenomic target DNA sequence from a plurality of species
10 using a set of conserved, common primers; and ii) the identification of species origin of any amplified metagenomic target DNA on the basis of its sequence. Preferably the metagenomic target DNA sequence is sequenced by a process for massively parallel sequencing. In some embodiments, the process for massively parallel sequencing is selected from emulsion sequencing, and solid phase sequencing.

15

The metagenomic DNA target sequence may be a **chromosomal** or **mitochondrial gene** conserved among all the animal species. The targeted gene has to be characterized both by conserved sequences usable for universal primers design and by a within primer sequence of lower conservation rich in polymorphisms within the various homologues of the species of interest, such
20 that the specific sequence of the amplified target, between the primer sequences, may be used to identify the species of origin. As the mammalian mitochondria exists in multiple copies per cell, any mitochondrial DNA region (mtDNA) could be used for **detection and identification of DNA traces** (ex: absence of pork meat in Halal market). The **chromosomal gene** present in one copy per cell is suitable for the identification and **estimation of relative proportion** of species in meat
25 products.

In the optional second stage of the method of the invention, real-time, or quantitative PCR (qPCR) is used to quantitate the amount of DNA of the species identified in the first stage as being present
30 in the sample. Real-time PCR has demonstrated the highest improvement among PCR-based quantitative methods in recent years. In real-time PCR, the exponential amplification of target-specific DNA is monitored by an increased fluorescence signal. If the species under study is present in the matrix, a specific signal can be observed. As well as meeting the need for quantitative determination in meat species, this technique also has other advantages like higher
35 sensitivity and specificity.

Quantitative PCR may be based on the use of intercalating dyes, or the use of a labelled reporter primer and/or probe. In some embodiments of the invention, therefore, the qPCR step is selected from qPCR using an intercalating dye and qPCR using a labelled reporter primer or probe. In
5 embodiments based on intercalating fluorescent dyes, the dye may be SYBRGreen or EvaGreen. Such methods require the greatest sequence specificity due to the fact that these types of dyes bind to all double-stranded DNA present, including any nonspecific PCR products and the primer-dimer complex.

10 In other, preferable embodiments, the real-time quantitative PCR procedure for species identification is generally based on the use of a labelled reporter primer or probe. Preferably, the labelled reporter primer or probe is part of a fluorescence/quencher reporter system or other fluorescence reporter system in which amplification of the species specific DNA target results in a reduction or elimination of fluorescence quenching, or other increase in fluorescence, to result in a
15 detectable fluorescent signal. For example a TaqMan fluorogenic probe (also referred to herein as a hydrolysis probe (the 5' to 3' exonuclease activity of the polymerase degrades the probe that has annealed to the template. Degradation of the probe releases the fluorophore from it and breaks the close proximity to the quencher, thus relieving the quenching effect and allowing fluorescence of the fluorophore)) may be used as the reporter system. This method uses an additional
20 oligonucleotide, which is also bound specifically to the target DNA sequence during the annealing step. This oligonucleotide has both a reporter fluorescent dye and a quencher dye attached. The accumulation of specific PCR products is detected by hybridization and cleavage of a double-labelled fluorogenic probe during the amplification reaction.

25 Other alternative reporter systems may be employed. For example, the reporter system may comprise a molecular beacon probe, a pair of dual hybridization probes, an amplifluor primer system, a scorpion primer system, a light-upon-extension system or a QZyme primer system. Other suitable systems will be known to the skilled person and may be used to provide quantitative real-time PCR reporting.

30

Any suitable target sequences may be used for either or both stages of the process of the invention. To be suitable for stage 1 of the process (metagenomic analysis) the target must allow for co-amplification from a plurality of species using a set of conserved, common primers. Preferably a single pair of primers (one forward primer and one reverse primer) is used to co-amplify the
35 metagenomic target DNA sequence from substantially all species of interest. However, the

invention is not limited to the use of just a single pair of primers. Metagenomic analysis may be improved, and expanded in scope by the addition of multiple forward and/or reverse primers which can allow for a broader range of species specific sequences that can be amplified. Multiple primers can also be used to ensure that amplification efficiency is broadly similar for all species of interest
5 in order to eliminate or reduce over-representation of one species, possibly at the expense of another, in the amplification process.

The metagenomic target sequence is preferably a sequence which has the same number of copies per genome in each of the species suspected as being present in the sample, so as to allow for a
10 determination of the relative proportions of the different identified DNAs by the metagenomic analysis.

The skilled person is able to determine appropriate primer pairs for the metagenomic analysis, based upon an examination of a line-up of sequences from a homologous gene shared by the
15 species of interest. Highly conserved regions of the gene of interest can be examined for the possibility of providing a relatively small number of primers capable of amplifying target from a large number of species. Preferably a small number of primers, for example 2 or 3 primers may be adequate to amplify a plurality of target sequences from e.g. at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or 13 or more species.

20 Primers may include one or more degenerate nucleotide bases in order to increase the range of species whose target DNA may be amplified in the metagenomic analysis. Primers may also be modified by the addition of adaptors or tags, or universal sequences for use in manipulation of amplicon products, including sequencing of the products.

25 In the metagenomic analysis, following amplification of target sequences, the amplicons so produced are sequenced to determine species origin. A further requirement, therefore, of the metagenomic target DNA sequence is that it allows for the identification of species origin of any amplified metagenomic target DNA on the basis of its sequence. This may be achieved by
30 providing PCR primers from highly conserved regions (as discussed above), which flank regions of lower conservation amongst the various homologues of the species of interest, such that the specific sequence of the amplified target, between the primer sequences, may be used to identify the species of origin.

35 ***Identification of animal species by NGS technology using chromosomal gene:***

The inventors have found that the myostatin (MSTN) gene is a suitable gene for use in the process of the invention, particularly in the identification and quantitation of species in meat products. The MSTN gene encodes the myostatin protein (also known as growth differentiation factor 8 or GDF-8). Myostatin is a secreted growth differentiation factor that is a member of the TGF beta protein family that inhibits muscle differentiation and growth in the process known as myogenesis. The gene is classified as a housekeeping gene, that is a group of genes coding mainly for essential proteins in the cellular basic function. These genes include conserved area useful for conserved primers design and variable area required for species identification and present in single copy in the genome, an important feature for the quantification method.

In some embodiments the myostatin gene is used in the invention to identify and quantitate DNA from at least one species from a genus selected from *Sus*, *Gallus*, *Bos*, *Ovis*, *Equus*, *Meleagris*, *Felis*, *Canis canis*, *capreolus capreolus*, *O.cuniculus*, *roe dear*, *Rabbit*, *Kangaro*, *Rattus rattus*, *mus musculus*, *Capra*, *Antilocapra*, *Cervus*, *Anas*, *Anser* and *Coturnix*, for example, *Sus scrofa*, *Gallus gallus*, *Bos Taurus*, *Ovis aries*, *Equus caballus*, *Meleagris gallopavo*, *Felis catus*, *Capra hircus*, *Antilocapra Americana*, *Cervus elaphus*, *Anas platyrhyncho*, *Anser anser* and *Coturnix chinensi*.

In some embodiments, the metagenomic target DNA sequence is therefore from the MSTN gene. Preferably, the metagenomic target DNA sequence is amplified by a set of conserved primers comprising at least a primer comprising the sequence of SEQ ID NO. 1 or SEQ ID NO. 2, and a primer comprising the sequence of SEQ ID NO. 3. In some embodiments the metagenomic target DNA sequence is amplified by a set of conserved primers comprising a primer comprising the sequence of SEQ ID NO. 1 and a primer comprising the sequence of SEQ ID NO. 2 and a primer comprising the sequence of SEQ ID NO. 3. In some embodiments, the primers consist of the sequences of SEQ ID NO. 1, SEQ ID NO. 2 and SEQ ID NO. 3. In some embodiments the primers having or comprising the sequences of SEQ ID No's 1, 2 or 3 are further modified by the addition of adaptors, tags or universal sequences depending of the NGS technology used.

30

In some embodiments the set of primers for amplification of the metagenomic target DNA comprises a set of forward primers having the sequences of SEQ ID NO.s 4 and 5, and a set of reverse primers having the sequences of SEQ ID NO.s 6 to 13.

35

The MSTN gene is also suitable for use in the optional second stage of the process of the invention, that is the qPCR stage. Accordingly, in some embodiments, the species specific target DNA sequence is amplified by a set of primers and the resulting amplicon is detected by a labelled hybridisation probe, the primers and probes being selected from the following:

- a) primers comprising or consisting of the sequences of SEQ ID NOS. 17 and 18 and a probe comprising or consisting of the sequence of SEQ ID NO. 19 for the quantitation of DNA sequences from pork (*Sus scrofa*); or
- b) primers comprising or consisting of the sequences of SEQ ID NOS. 20 and 16 and a probe comprising or consisting of the sequence of SEQ ID NO. 21 for the quantitation of DNA sequences from chicken (*Gallus gallus*); or
- c) primers comprising or consisting of the sequences of SEQ ID NOS. 22 and 16 and a probe comprising or consisting of the sequence of SEQ ID NO. 23 for the quantitation of DNA sequences from beef (*Bos taurus*); or
- d) primers comprising or consisting of the sequences of SEQ ID NOS. 24 and 16 and a probe comprising or consisting of the sequence of SEQ ID NO. 25 for the quantitation of DNA sequences from sheep (*Ovis aries*); or
- e) primers comprising or consisting of the sequences of SEQ ID NOS. 26 and 27 and a probe comprising or consisting of the sequence of SEQ ID NO. 28 for the quantitation of DNA sequences from horse (*Equus caballus*); or
- f) primers comprising or consisting of the sequences of SEQ ID NOS. 29 and 16 and a probe comprising or consisting of the sequence of SEQ ID NO. 30 for the quantitation of DNA sequences from turkey (*Meleagris gallopavo*); or
- g) primers comprising or consisting of the sequences of SEQ ID NOS. 14 and/or 15 and 16 and a probe comprising or consisting of the sequence of SEQ ID NO. 31 or 32 for the quantitation of DNA from all species in the sample.

Preferably, the primers and probes consist of the sequences of SEQ ID NOS. 14 to 32 respectively.

In some embodiments, the forward primers selected for the various species may include primers with some degeneracy and/or may include a mixture of primers. Conveniently, for the quantitation of DNA sequences from chicken, beef, sheep or turkey, the forward primer noted above may be replaced by a mixture of primers having the sequences of SEQ ID NO.s 14 and 15.

In preferred embodiments, the quantitation of species specific target DNA sequences is compared to a control or reference target sequence. Preferably the control or reference target sequence is part of the same gene as the species specific target sequence. In some embodiments, therefore, a control

or reference target sequence is part of the MSTN gene sequence. In some embodiments the control or reference target sequence is co-amplified with the species specific target sequence, and is detected in real time (qPCR). In some embodiments a control or reference target sequence is amplified using a set of primers comprising or consisting of the sequences of SEQ ID NOs 14, 15 and 16, and detected using a probe comprising or consisting of the sequence of SEQ ID NO. 31 or SEQ ID NO. 32.

In another aspect, the invention provides the use of the primers as discussed above (comprising or consisting of the sequence of SEQ ID NOs 1, 2 and 3, or SEQ ID NOs 4 to 13) with the primers and probes also discussed herein (comprising or consisting of the sequences of SEQ ID NOs 14 to 32) for the sequential metagenomic identification and relative proportion determination and species specific quantitation of DNA in a sample, the selection of species specific primers and probes employed for quantitation being chosen on the basis of the metagenomic identification of species DNA present in the sample. Preferably the sample is a food sample such as a meat sample.

In a further aspect, the invention provides a kit for metagenomic identification of DNA present in a sample, comprising a set of primers for the metagenomic amplification of a metagenomic target sequence in the myostatin gene, said metagenomic target sequence being selected to allow for: i) co-amplification of the metagenomic target DNA sequence from a plurality of species using a set of conserved, common primers; ii) the identification of species origin of any amplified metagenomic target DNA on the basis of its sequence; and optionally iii) the relative proportions between the different identified DNA. In some embodiments the metagenomic target sequence is selected to allow for amplification of DNA from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or 13 different species using a set of conserved, common primers. In some embodiments the set of conserved, common primers includes no more than three primers, for example two or three primers.

Preferably, the set of primers of the kit comprises primers comprising the sequence of SEQ ID NO. 1 or SEQ ID NO. 2 and a primer comprising the sequence of SEQ ID NO. 3. In some embodiments, the set of primers consists of three primers comprising the sequences of SEQ ID NO. 1, SEQ ID NO. 2 and SEQ ID NO. 3 respectively. Preferably, the primers consist of the sequences of SEQ ID NO. 1, SEQ ID NO. 2 and SEQ ID NO. 3. Any one or more of the primers may be adapted by the addition of an adaptor, tag or universal sequence. In some embodiments of the kits, the primer of SEQ ID NO.1 may be replaced by a primer comprising or consisting of the sequence of SEQ ID NO. 4, the primer of SEQ ID NO. 2 may be replaced by a primer comprising or

consisting of the sequence of SEQ ID NO. 5 and/or the primer of SEQ ID NO. 3 may be replaced by one or more primers comprising or consisting of the sequences of SEQ ID NO.s 6 to 13.

5 The invention further provides a kit for quantitative PCR analysis of a species specific target sequence in a sample, said kit comprising a set of primers and probes for the amplification and real-time detection of a sequence from the myostatin gene, said sequence being selected to allow for species specific amplification and/or detection. In some embodiments, the species specific amplification and/or detection can distinguish between species from a genus selected from *Sus*, *Gallus*, *Bos*, *Ovis*, *Equus*, *Meleagris*, *Felis*, *Capra*, *Antilocapra*, *Cervus*, *Anas*, *Anser* and *Coturnix*,
10 for example, *Sus scrofa*, *Gallus gallus*, *Bos Taurus*, *Ovis aries*, *Equus caballus*, *Meleagris gallopavo*, *Felis catus*, *Capra hircus*, *Antilocapra Americana*, *Cervus elaphus*, *Anas platyrhyncho*, *Anser anser* and *Coturnix chinensis*.

In preferred embodiments, the set of primers and probes is selected from at least one of:

- 15 a) primers comprising or consisting of the sequences of SEQ ID NOS. 17 and 18 and a probe comprising or consisting of the sequence of SEQ ID NO. 19 for the quantitation of DNA sequences from pork (*Sus scrofa*); or
- b) primers comprising or consisting of the sequences of SEQ ID NOS. 20 and 16 and a probe comprising or consisting of the sequence of SEQ ID NO. 21 for the
20 quantitation of DNA sequences from chicken (*Gallus gallus*); or
- c) primers comprising or consisting of the sequences of SEQ ID NOS. 22 and 16 and a probe comprising or consisting of the sequence of SEQ ID NO. 23 for the quantitation of DNA sequences from beef (*Bos taurus*); or
- d) primers comprising or consisting of the sequences of SEQ ID NOS. 24 and 16 and
25 a probe comprising or consisting of the sequence of SEQ ID NO. 25 for the quantitation of DNA sequences from sheep (*Ovis aries*); or
- e) primers comprising or consisting of the sequences of SEQ ID NOS. 26 and 27 and a probe comprising or consisting of the sequence of SEQ ID NO. 28 for the quantitation of DNA sequences from horse (*Equus caballus*); or
- f) primers comprising or consisting of the sequences of SEQ ID NOS. 29 and 16 and
30 a probe comprising or consisting of the sequence of SEQ ID NO. 30 for the quantitation of DNA sequences from turkey (*Meleagris gallopavo*); or
- g) primers comprising or consisting of the sequences of SEQ ID NOS. 14 and/or 15 and 16 and a probe comprising or consisting of the sequence of SEQ ID NO. 31 or
35 32 for the quantitation of DNA from all species in the sample.

In some embodiments of the kit primers having the sequences of SEQ ID NOs 20, 22, 24 and/or 29 may be replaced by primers comprising or consisting of the sequences of SEQ ID NOs 14 and 15.

- 5 In some embodiments the kits further contain a probe having a sequence of SEQ ID NO. 31 or SEQ ID NO. 32, which acts as a probe for a control or reference sequence in the MSTN gene.

The invention further provides a kit having some or all of the features recited above for metagenomic analysis and further having some or all of the features recited above for qPCR
10 analysis. Optionally the kit may further comprise any reagent suitable for use in the metagenomic or qPCR steps of the process of the invention.

The invention will now be described in further detail with reference to the following examples and figures, in which:

15

Figure 1 shows an alignment of myostatin Exon1 from 12 mammalian and bird species (frequently found in meat and meat products).

20

Figure 2 shows the binding site of primers and probes designed on myostatin exon 1 for pork, beef, horse, sheep, chicken and turkey. (1) represents Forward primer; (3) : reverse primer; (2):Taqman probe

25

Figure 4 shows metagenomic analysis of meat samples

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Figure 5 shows relative proportion of mammals and poultry composition in 20 DNA mixes using myostatin as target gene. The table below include all the sequences analysed and identified as belonging to one of the 8 animal species (all the numbers <100 are not representative). Those results are not corrected for the genome size explaining the difference to the expected 50-50 % or 25-25-25-25 % of different species.

Figure 6 shows relative proportion of 14 mammals and poultry identified by Next generation sequencing.

Identification of animal species by NGS technologie using mitochondrial gene.

35

The mitochondrial gene coding for the ribosomal 12S ribosomal RNA is known for his impact in the higher eukaryotes taxonomy. These genes include conserved area useful for conserved primers design and variable area required for species identification. Inside the higher eukaryotic cell the mitochondria number vary between 10 and 1000 units. This target gene could be chosen to detect and identify tiny DNA traces of animal species.

Material and methods

DNA isolation

10

Twenty-five gram sample of meat or meat product was homogenized for 1 minute in 225 ml in a tempo bag (bioMérieux Basingstoke, England, ref 80015) with sterile physiologic water using a stomacher apparatus. 1.5 ml of the suspension was then used for total genomic DNA extraction using DNeasy Blood & Tissue Kit (QIAGEN, Crawley, UK). The DNA concentrations were evaluated by fluorometric ds DNA quantification using PicoGreen.

Metagenomic analysis using MSTN gene

Conserved primers design for pyrosequencing

20

The myostatin exon 1 sequence from 12 frequent species present in meat products (*Sus scrofa*, *Bos taurus*, *Gallus gallus*, *Equus caballus*, *Ovis aries*, *Capra hircus*, *Anas platyrhynchos*, *Anser anser* and *Coturnix chinensis*, *Cervus elaphus*, *Antilocapra Americana*), were aligned to compare conserved area used for the conserved primers design (fig. 1). 3 primers are designed to amplified a PCR fragment of 313 bases (MSTN-E1-UP1 :AGTCTATGTTTATATTTACCT (SEQ ID NO. 1), MSTN-E1-UP2 :AATCTYTGTTTATATTTACCT (SEQ ID NO. 2), MSTN-E1-DN :TCATCRTCTTCCAARGAGCC (SEQ ID NO. 3)). The amplified fragment shows a sequence diversity sufficient to identify species by sequencing. The oligonucleotide design included 454 Life Sciences A or B sequencing titanium adapters (Roche Diagnostics, Vilvoorde, Belgium) and multiplex identifiers (MIDs) fused to the 5' end of reverse primer.

ribosomal 12S RNA:

The ribosomal 12S RNA sequences from 13 frequent species present in meat products were aligned to design conserved primers (fig 2). 3 primers are designed to amplified a PCR fragment of 514 bases (NGS12S-FW1: 5'-AYACCGCCCGTCACCCTC-3'; NGS12S-REV15'-TWGGCTTTTACCTCTAC - 3'; NGS12S-REV2: 5'- TWGGCATGTCACCCTAC - 3')

	FORWARD PRIMERS	REVERSE PRIMERS
5		
	EquusCaballus ACACCGCCCGTCACCCTC-----	GTACCGTAAGGGAACGATGA
	FelisCatus ACACCGCCCGTCACCCTC-----	GTACCGTAAGGGAACGATGA
	BT1 ACACCGCCCGTCACCCTC-----	GTACCGCAAGGGAACGATGA
	BT2 ACACCGCCCGTCACCCTC-----	GTACCGCAAGGGAACGATGA
10	CapraHircus ACACCGCCCGTCACCCTC-----	GTACCGTAAGGGAATGATGA
	CanisLupusfamiliaris ACACCGCCCGTCACCCTC-----	GTACCGTAAGGGAATGATGA
	SS-Pietrain ACACCGCCCGTCACCCTC-----	GTACCGTAAGGGAAGATGA
	SS-LW ACACCGCCCGTCACCCTC-----	GTACCGTAAGGGAAGATGA
15	GallusGallus1 ATACCGCCCGTCACCCTC-----	GTACCGCAAGGGAAGATGA
	GallusGallus2 ATACCGCCCGTCACCCTC-----	GTACCGCAAGGGAAGATGA
	Meleagris Gallopavo ATACCGCCCGTCACCCTC-----	GTACCGTAAGGGAAGATGA
	AnserAnser ATACCGCCCGTCACCCTC-----	GTACCGTAAGGGAAGATGA
	AnasPlatyrynchos ATACCGCCCGTCACCCTC-----	GTACCGTAAGGGAAGATGA
20	* * * * * * * * * * * * * * * * *	***** * * * * * * * * * *

Conserved sequences observed and used for common primers design after ribosomal 12S RNA sequences alignment of 13 frequent mammalian and bird species.

The 2 amplified fragments show a sequence diversity sufficient to identify species by sequencing. The oligonucleotide design included 454 Life Sciences A or B sequencing titanium adapters (Roche Diagnostics, Vilvoorde, Belgium) and multiplex identifiers (MIDs) fused to the 5' end of reverse primer. These amplicons may be used with or without NGS technology.

A full set of primers designed for 454 Life Sciences sequencing is as follows:

Fusion FW : (B adaptor)-(MSTN-E1-UP)

- MSTNE1-UP1:5'-CCTATCCCCTGTGTGCCTTGGCAGTCTCAGAGTCTATGTTTATATTTACCT-3' (SEQ ID NO. 4)
- MSTNE1-UP2:5'-CCTATCCCCTGTGTGCCTTGGCAGTCTCAGAATCTYTGTTTATATTTACCT-3' (SEQ ID NO. 5)

Fusion Rev : (A adaptor)-Key-MID- (MSTN-E1-DN)

- MSTNE1-DN-MID100 :5'-CCATCTCATCCCTGCGTGTCTCCGACTCAGAGACTGCACCTCATCRTCTTTCCAARGAGCC-3 (SEQ ID NO. 6)
- MSTNE1-DN-MID101 :5'-CCATCTCATCCCTGCGTGTCTCCGACTCAGATCGCAGGCTCATCRTCTTTCCAARGAGCC-3 (SEQ ID NO. 7)
- MSTNE1-DN-UM102 :5'-CCATCTCATCCCTGCGTGTCTCCGACTCAGACGCTCGACATCATCRTCTTTCCAARGAGCC-3 (SEQ ID NO. 8)
- 45 MSTNE1-DN-UM103 :5'-CCATCTCATCCCTGCGTGTCTCCGACTCAGAGACGACTCTCATCRTCTTTCCAARGAGCC-3 (SEQ ID NO. 9)
- MSTNE1-DN-UM104 :5'-CCATCTCATCCCTGCGTGTCTCCGACTCAGAGCACTGTAGTCATCRTCTTTCCAARGAGCC-3 (SEQ ID NO. 10)
- 50 MSTNE1-DN-UM105 :5'-CCATCTCATCCCTGCGTGTCTCCGACTCAGATCAGACACGTCATCRTCTTTCCAARGAGCC-3 (SEQ ID NO. 11)
- MSTNE1-DN-UM106 :5'-CCATCTCATCCCTGCGTGTCTCCGACTCAGATATCGGAGTCATCRTCTTTCCAARGAGCC-3 (SEQ ID NO. 12)
- MSTNE1-DN-UM107 :5'-CCATCTCATCCCTGCGTGTCTCCGACTCAGCGTGTCTATCATCRTCTTTCCAARGAGCC-3 (SEQ ID NO. 13)

These amplicons may be used with or without NGS technology.

For ribosomal 12S RNA gene.

5

Fusion FW : (B adaptator)-key-MID-(NGS12S-FW1)

NGS12S-FW MID100: 5'-
CCATCTCATCCCTGCGTGTCTCCGACTCAGAGACTGCACAYACCGCCCGTCACCCTC -3'

10

NGS12S-FW MID101: 5'-
CCATCTCATCCCTGCGTGTCTCCGACTCAGAGCGCGCAYACCGCCCGTCACCCTC -3'
NGS12S-FW MID102: 5'-
CCATCTCATCCCTGCGTGTCTCCGACTCAGAGCTCTATCAYACCGCCCGTCACCCTC -3'

15

Fusion Rev : (A adaptator)-key-(NGS12S-REV1)

NGS12S-REV1.1 : 5'- CCTATCCCCTGTGTGCCTTGGCAGTCTCAGTWGGCTTTTCACCTCTAC -3'
NGS12S-REV1.2 : 5'- CCTATCCCCTGTGTGCCTTGGCAGTCTCAGTWGGCATGTCACCTCTAC -3'
NGS12S-REV1.3 : 5'- CCTATCCCCTGTGTGCCTTGGCAGTCTCAG TWGGCWTKTCACCTCTA -3'

20

These amplicons may be used with or without NGS technology.

25 MSTN gene library construction and pyrosequencing

The amplification mix contained 5 U of FastStart high fidelity polymerase (Roche Diagnostics, Vilvoorde, Belgium), 1x enzyme reaction buffer, 200 μM dNTPs (Eurogentec, Liège, Belgium), 0.2 μM of each primer and 100 ng of genomic DNA in a volume of 25 μl. Thermocycling conditions consisted of a denaturation at 94°C for 10 min followed by 25 cycles of 94°C for 30 s, 50°C for 30 s, 72°C for 1 min and a final elongation step of 7 min at 72°C. These amplifications were performed on an Ep Master system gradient apparatus (Eppendorf, Hamburg, Germany). The PCR products of approximately 313 bp were checked by gel electrophoresis and purified using the AMPure kit (Agencourt Bioscience Corporation, Beverly, USA) to remove amplicons shorter than 100 bp. Equal amounts of each of the PCR products were pooled and subsequently amplified by emulsion PCR before sequencing. Pyrosequencing was performed with the Roche 454 GS Junior Sequencer (Roche, Basel, Switzerland).

30

35

Bioinformatic analysis

40

Image and data processing for amplicon sequencing was performed using the Genome Sequencer FLX System Software Package 2.3 (Roche, Basel, Switzerland). The Mothur program was used for

the first part of the sequences analysis (SCHLOSS et al., 2009). The shorter sequences were discarded. The sequences with ambiguous bases or homopolymers longer than ten nucleotides and with an average quality score lower than 25 were removed along with tag and primer sequences. Sequences from multiplexed samples were assigned based on the presence of the unique barcodes assigned to each sample. A distance matrix was prepared, (distance= 0.01) and the sequences were clustered to operational taxonomic units (OTUs). The representative sequences of each OTU were compared to the NCBI database using the Basic Local Alignment Search Tool (BLASTN) a private database of in-house sequences.

10 Genbank myostatin gene sequences were:

- 5178958|ref|NM_21445.2| *Sus scrofa* myostatin (MSTN), mRNA
- 241897522|gb|GQ184147.1| *Bos taurus* myostatin mRNA, complete cds
- 4782570|ref|NM_001001461.1| *Gallus gallus* myostatin (MSTN), mRNA
- 12652492|ref|NM_001081817.1| *Equus caballus* myostatin (MSTN), mRNA
- 57164246|ref|NM_001009428.1| *Ovis aries* myostatin (MSTN), mRNA
- 289600017|gb|GQ246166.1| *Capra hircus* myostatin precursor, mRNA
- 17064128|gb|AF440861.1| *Anas platyrhynchos* myostatin (MSTN) mRNA,
- 1706410|gb|AF440862.1| *Anser anser* myostatin (MSTN) mRNA
- 14984905|gb|EF62955.1| *Cervus elaphus xanthopygus* myostatin mRNA
- 482746|gb|AY62909.1| *Antilocapra americana* myostatin mRNA
- 1706414|gb|AF440864.1| *Coturnix chinensis* myostatin (MSTN) mRNA
- 512867089:168-1181|*Xenopus (Silurana) tropicalis* myostatin (mstn), mRNA
- 410969071|ref|XM_00990972.1|*Felis catus* myostatin (MSTN), mRNA

Sequences shown in the sequence listing numbered 80 to 93 inclusive are myostatin sequences from various animals from genbank.

30 Sequences shown in the sequence listing numbered 94 to 103 inclusive are mitochondrial 12S sequences from various animals from genbank.

Quantification by qPCR using MSTN gene

35 Oligonucleotides primers and probes

A TaqMan-based real-time Polymerase Chain Reaction (qPCR) assay was developed for quantify 6 frequent species present in meat products (*Sus scrofa*, *Bos taurus*, *Gallus gallus*, *Equus caballus*, *Ovis aries* and *Meleagris gallopavo*). By aligning the myostatin Exon 1 DNA sequence of these species according to the NCBI database forward and reverse primers and Taqman probes were

designed for each meat-specific region (fig.2). The list of these primers and probes is shown in Table 1.

		sequence
pork	forward primer	5'-CTGATTGTTGCTGGTCCC-3'
	reverse primer	5'-GTTCCGTCGTAGCGTGA-3'
	Taqman probe	5'-(FAM)-TGTAATGCATGTATGTGGAGACAAA-(BHQ)-3'
chicken	forward primer	5'-GCTAGCAGTCTATGTTTATATTACCT-3'
	reverse primer	5'-TCATCRTCCTCCAARGAGCC-3'
	Taqman probe	5'-(FAM)-TTCATGCAGATCGCRGTTGATCC-(BHQ)-3'
beef	forward primer	5'-ACTGCAAATCTCTGTTTATATTACCT-3'
	reverse primer	5'-TCATCRTCCTCCAARGAGCC-3'
	Taqman probe	5'-(FAM)-TGTTTGTGGAGGGAAAACACTACATCCTC-(BHQ)-3'
sheep	forward primer	5'-ACTGCAAATCTTTGTTTATATTACCT-3'
	reverse primer	5'-TCATCRTCCTCCAARGAGCC-3'
	Taqman probe	5'-(FAM)-CATGCTTGTGGAGACAAAACAATAAATCCT-(BHQ)-3'
horse	forward primer	5'-GCAAATCTCTGTTTATATTACCTGTTTG-3'
	reverse primer	5'-GGTAATGATTGTTTCCGTCGTC-3'
	Taqman probe	5'-(FAM)-TTCTTGCTGGTCCAGTGGATCTAA-(BHQ)-3'
turkey	forward primer	5'-GCTAGCAGTCTATGTTTATATTACCT-3'
	reverse primer	5'-TCATCRTCCTCCAARGAGCC-3'
	Taqman probe	5'-(FAM)-TGCAGATTTAGTTCATCCGGT-(BHQ)-3'
normalizer control	forward primer	5'-GCTAGCAGTCTATGTTTATATTACCT-3'
	reverse primer	5'-TCATCRTCCTCCAARGAGCC-3'
5	Taqman probe	5'-(FAM)-GGAAGTATTGATCA-(BHQ)-LNA-3'

Table 1 : Sequences of primers and probes used in this study.

10 The sequences in Table 1 have the following SEQ ID NOs:

Pork forward primer: SEQ ID NO. 17. Pork reverse primer: SEQ ID NO.18. Pork Taqman probe: SEQ ID NO. 19.

15 Chicken forward primer: SEQ ID NO. 20. Chicken reverse primer: SEQ ID NO.16. Chicken Taqman probe: SEQ ID NO. 21.

Beef forward primer: SEQ ID NO. 22. Beef reverse primer: SEQ ID NO.16. Beef Taqman probe: SEQ ID NO. 23.

Sheep forward primer: SEQ ID NO. 24. Sheep reverse primer: SEQ ID NO. 16. Sheep Taqman probe: SEQ ID NO. 25.

20 Horse forward primer: SEQ ID NO. 26. Horse reverse primer: SEQ ID NO.27. Horse Taqman probe: SEQ ID NO. 28.

Turkey forward primer: SEQ ID NO. 29. Turkey reverse primer: SEQ ID NO.30. Turkey Taqman probe: SEQ ID NO. 31.

Normalizer forward primer: SEQ ID NO. 14. Normalizer reverse primer: SEQ ID NO. 16.
Normalizer Taqman probe: SEQ ID NO. 31. A further normalizer Taqman probe that may be use is:

FAM-AGTGGAGGAGCYTTGGGYAAAAG-BHQ (SEQ ID NO. 32)

5

The forward primers for chicken, beef, sheep and turkey noted above may be replaced by a mixture of the following two primers:

GCTAGCAGTCTATGTTTATATTTACCT (SEQ ID NO. 14)

10

ACTGCAAATCTYTGTTTATATTTACCT (SEQ ID NO. 15) .

Conventional PCR protocol

15 Real-time PCR was performed using the LightCycler 480 system (Roche, Basel, Switzerland). The PCR reaction mixtures were placed in a 12 μ l final volume containing 6 μ l of LC480 probe master mix (Roche, Basel, Switzerland), 2 μ l of template DNA (at 5ng/ μ l), 0,25 μ l of primer pair (10 μ M each), 0,125 μ l of Taqman probe (10 μ M). The reaction conditions included the initiation step for 10 min at 95°C, followed by 40 cycles of 15s at 95°C and 1 min at 60°C. The real-time system is
20 supplied with the Lightcycler 480 Software version 1.5 using unique Roche algorithms for highly accurate and robust automated data analysis

Specificity and sensitivity test.

25 The specificity of each species test was confirmed by the amplification of 100ng of chicken, turkey, horse, donkey, pork, bovine and ovine genomic DNA and a negative control without DNA (NTC). Each assay was tested against DNA from all six species, against its target species and the 5 remaining species to confirm specificity. In sensitivity test of the specific primers and probes, PCR amplifications were examined between specific primers and 3-fold serial dilutions of DNAs
30 isolated from the meat of each target species ranging from 10ng to 0,4 ng. The standard curves for all the 6 detection systems were constructed by using the Cp value obtained from the corresponding DNA concentration (fig 3).

Results

35

In this study, metagenomic and real-time PCR assays based on the amplification of same fragment of genomic myostatin gene were developed and evaluated for detection and quantification of 6 frequent species present in meat and meat products (pork, beef, horse, sheep, chicken and turkey).

5 *Metagenomic analysis using MSTN gene*

The metagenomic assay was applied to two commercial meat preparations, the first composed of 50% of beef and 50% of pork meat, the second composed of 50% of beef and 50% of horse meat. The treated sequences were compared to the NCBI database using the Basic Local Alignment
10 Search Tool (fig. 4). The metagenomic analysis allowed identification of all the meat components but the proportions are not fully representative. The proportion of beef are more important in the two samples tested to the detriment of the 2 others species. To obtain more quantitative analysis its important to avoid competition between meat components thus to analyse in the early part of the exponential phase because of all reagents are still in excess and the species which is present in a
15 low amount will not compete with the others.

Quantification by qPCR using MSTN gene

Species specific primers and Taqman probes were designed and amplification conditions were
20 optimized by using these primers and probes.

Specificity of the Taqman probe systems.

The specificity of the 6 systems were tested for 8 common and commercial meat 100% pure
25 species (pork, beef, horse, sheep, chicken, turkey, rabbit, duck). No cross-reaction was obtained with any of the non target species DNA (table 2).

species	DNA concentration (ng)	Average Cp value \pm SD					
		pork	beef	sheep	horse	turkey	chicken
target species	10	23,57 \pm 0,11	23,99 \pm 0,39	23,5 \pm 0,05	24,14 \pm 0,43	22,69 \pm 0,15	23,34 \pm 0,48
	3,3	25,16 \pm 0,06	25,66 \pm 0,19	25,06 \pm 0,08	24,59 \pm 0,62	24,29 \pm 0,22	24,49 \pm 0,51
	1,1	26,86 \pm 0,02	27,28 \pm 0,4	26,78 \pm 0,05	26,99 \pm 0,15	25,96 \pm 0,15	26,08 \pm 0,47
	0,36	28,47 \pm 0,12	28,8 \pm 0,25	28,45 \pm 0,23	28,99 \pm 0,64	28,07 \pm 0,74	27,98 \pm 0,19
	0,12	30,08 \pm 0,03	30,44 \pm 0,32	29,93 \pm 0,11	30,0 \pm 0,31	29,29 \pm 0,11	29,73 \pm 0,06
	0,04	\pm	31,8 \pm 0,14	31,4 \pm 0,58	32,12 \pm 0,61	30,94 \pm 0,16	31,14 \pm 0,2
qPCR efficiency		1,937	1,968	1,886	1,991	1,963	1,99
chicken	10	ND	ND	ND	ND	ND	23,231 \pm 0,4
turkey	10	ND	ND	ND	ND	22,72 \pm 0,13	ND
horse	10	ND	ND	ND	24,04 \pm 0,37	ND	ND
donkey	10	ND	ND	ND	ND	ND	ND
pork	10	23,39 \pm 0,41	ND	ND	ND	ND	ND
beef	10	ND	24,01 \pm 0,32	ND	ND	ND	ND
sheep	10	ND	ND	23,46 \pm 0,082	ND	ND	ND
rabbit	10	ND	ND	ND	ND	ND	ND
duck	10	ND	ND	ND	ND	ND	ND

Table 2 : Specificity and sensitivity test results obtained with the species specific primers-probe sets. ND = not detected.

5

Sensitivity and linearity of Taqman probe systems.

The sensitivity and linearity of the 6 Taqman systems were tested by using a 3-fold dilutions series of the genomic DNA obtained from each target species starting with 10ng target DNA. The standard curve was generated by plotting the resulting Cp value compared with the logarithm of the target DNA concentration to test linearity. These linear regression were made by the LC480 software using the own Roche algorithms. The efficiency values (provided by the Roche algorithms) for the pork ; beef ; sheep ; horse ; turkey and chicken systems were respectively 1,937 ; 1,968 ; 1,886 ; 1,991 ; 1,963 and 1,99. As is well known, an acceptable range to determine the efficiency of a qPCR reaction and thus the linear relationship between the Cp value and the DNA concentration is between 1,8 and 2,2 (Efficiency= $-1+10^{(-1/slope)}$; a perfect efficiency= 2).

Normalization methods

Sources of variability could be diversified (the nature and amount of starting sample, the DNA isolation process or lastly real-time PCR amplification). Normalization is essentially the act of neutralizing the effects of variability which could prevent the ability to compare data and lead to erroneous conclusions. The use of a normalizer gene is the most thorough method of addressing almost every source of variability in real-time PCR. In this study we have decided to use as normalizer a highly conserved region from myostatin fragment amplified (fig.2). This normalizer should have a similar amplification efficiency because we use the similar primers to amplify it.

To quantify data we could use comparative quantification and the $\Delta\Delta C_t$ method. With this method C_{ts} for the gene of interest in both the test sample and calibrator sample (here we use a 100% pure target species) are adjusted in relation to the normalizer gene C_t from the same 2 samples (ΔC_t sample - ΔC_t calibrator = $\Delta\Delta C_t$). The resulting $\Delta\Delta C_t$ value is incorporated to determine the fold difference in expression (fold difference = $2^{-\Delta\Delta C_t}$).

The invention is not limited by the Examples and the skilled person will appreciate alternatives and modifications that might be made to any step or component as herein described. The invention is therefore limited only by the scope of the claims.

10

Results

Metagenomic analysis using MSTN gene

15 The metagenomic assay was applied to 20 different DNA mixes including 8 different mammals and poultry DNA (beef, pork, horse, sheep, rabbit, goat, turkey and chicken), 13 mixes composed of 2 species at 50% of each DNA and 7 mixes composed of 4 species DNA at 25% of DNA.

The DNA of each species were prepared and eluted to the same concentration before mixing them. Because of differences in genome size, 100 ng of DNA will contain different amount of the common myostatin target gene from one species to an other one explaining why in a 50-50 % mixture, small genome species (poultry, rabbit,..) will be overestimated compared with bigger genome species like mammals.

25 For example, because the genome size of poultry are twice as small as mammals genome, 100 ng of DNA will correspond to $3,5 \cdot 10^3$ copy numbers of beef genomes compared to $9 \cdot 10^3$ copy numbers of the chicken genomes). Thus at same concentration, chicken proportion are twice as much as mammals proportion.

30 The treated sequences were compared to a private database using the Basic Local Alignment Search Tool. All the 8 species are correctly identified in the 20 samples tested. The proportions of each are almost representative taking into account the genome size (fig 5)

Metagenomic analysis using ribosomal 12S rRNA.

35 The metagenomic assay was applied to a mix of 14 mammal and poultry DNA all added at the same concentration (*Sus scrofa*, *Anser anser*, *Gallus gallus*, *Bos Taurus*, *Ovis aries*, *Equus caballus*,

Meleagris gallopavos, *Capra hircus*, *Antilocapra Americana*, *Cervus elaphus*, *Anas platyrhyncho* and *Coturnix japonica* (fig 6). The treated sequences were compared to the NCBI database using the Basic Local Alignment Search Tool. The metagenomic analysis allowed the identification of all the 14 components but the proportions are not representative (depend on the meat tissues used and the 5 mitochondria content of each).

Claims

- 5 1. A method for determining the species origin(s) of DNA in a sample comprising
conducting metagenomic sequence analysis of the sample to identify DNA from at
least one species, wherein the metagenomic analysis comprises amplification and
sequencing of a metagenomic target DNA sequence, said metagenomic target DNA
10 DNA sequence being selected to allow for: i) co-amplification of the metagenomic target
DNA sequence from a plurality of species using a set of conserved, common primers;
and ii) the identification of species origin of any amplified metagenomic target DNA
on the basis of its sequence.
2. The method of claim 1 further comprising species specific quantitative polymerase
15 chain reaction (qPCR) to amplify and quantify a species specific target from the
identified species DNA.
3. A method of claim 2 wherein the qPCR step is selected from qPCR using an
intercalating dye and qPCR using a labelled reporter primer or probe.
- 20 4. A method of claim 3 wherein the labelled reporter primer or probe is part of a
fluorescence/quencher reporter system or other fluorescence reporter system in which
amplification of the species specific DNA target results in a reduction or elimination of
fluorescence quenching, or other increase in fluorescence, to result in a detectable
25 fluorescent signal.
5. A method of claim 4 wherein the reporter system comprises a hydrolysis probe, a
molecular beacon probe, a pair of dual hybridization probes, an amplifluor primer
system, a scorpion primer system, a light-upon-extension system or a QZyme primer
30 system.
6. A method of claim 3 wherein the intercalating dye is selected from SYBRGreen and
EvaGreen.
- 35 7. A method of any preceding claim wherein the sample is a food sample, e.g. a meat
sample.

8. A method of any one of the preceding claims wherein the metagenomic target sequence has the same number of copies per genome in each of the species suspected as being present in the sample, so as to further allow for a determination of the relative proportions of the different identified DNAs.
- 5
9. A method of any one of the preceding claims wherein the metagenomic target DNA sequence is a part of the myostatin (MSTN) gene.
10. A method of any preceding claim wherein the species specific target DNA sequence is part of the MSTN gene.
- 10
11. A method of claim 9 or claim 10 wherein the metagenomic target DNA sequence is amplified by a set of conserved primers comprising at least a primer comprising or consisting of the sequence of SEQ ID NO. 1 or SEQ ID NO. 2, and a primer comprising or consisting of the sequence of SEQ ID NO. 3.
- 15
12. A method of claim 11 wherein the metagenomic target DNA sequence is amplified by a set of conserved primers comprising a primer comprising or consisting of the sequence of SEQ ID NO. 1 and a primer comprising or consisting of the sequence of SEQ ID NO. 2 and a primer comprising or consisting of the sequence of SEQ ID NO. 3.
- 20
13. A method of any of claims 10 to 12 wherein at least one of the primers is modified by the addition of an adaptor sequence, a tag or a universal sequence, optionally wherein the set of primers comprises or consists of primers having the sequences of SEQ ID NOs. 4 to 13.
- 25
14. A method of any preceding claim wherein the metagenomic target DNA sequence is sequenced by a process for massively parallel sequencing.
- 30
15. A method of claim 14 wherein the process for massively parallel sequencing is selected from emulsion sequencing, and solid phase sequencing.
- 35
16. A method of any preceding claim wherein the species specific target DNA sequence is amplified by a set of primers and the resulting amplicon is detected by a labelled hybridisation probe, the primers and probes being selected from the following:

- 5 a) primers comprising or consisting of the sequences of SEQ ID NOS. 17 and 18 and a probe comprising or consisting of the sequence of SEQ ID NO. 19 for the quantitation of DNA sequences from pork (*Sus scrofa*); or
- b) primers comprising or consisting of the sequences of SEQ ID NOS. 20 and 16 and a probe comprising or consisting of the sequence of SEQ ID NO. 21 for the quantitation of DNA sequences from chicken (*Gallus gallus*); or
- 10 c) primers comprising or consisting of the sequences of SEQ ID NOS. 22 and 16 and a probe comprising or consisting of the sequence of SEQ ID NO. 23 for the quantitation of DNA sequences from beef (*Bos taurus*); or
- d) primers comprising or consisting of the sequences of SEQ ID NOS. 24 and 16 and a probe comprising or consisting of the sequence of SEQ ID NO. 25 for the quantitation of DNA sequences from sheep (*Ovis aries*); or
- 15 e) primers comprising or consisting of the sequences of SEQ ID NOS. 26 and 27 and a probe comprising or consisting of the sequence of SEQ ID NO. 28 for the quantitation of DNA sequences from horse (*Equus caballus*); or
- f) primers comprising or consisting of the sequences of SEQ ID NOS. 29 and 16 and a probe comprising or consisting of the sequence of SEQ ID NO. 30 for the quantitation of DNA sequences from turkey (*Meleagris gallopavo*); or
- 20 g) primers comprising or consisting of the sequences of SEQ ID NOS. 14 and/or 15 and 16 and a probe comprising or consisting of the sequence of SEQ ID NO. 31 or 32 for the quantitation of DNA from all species in the sample.
- 25 17. A method of claim 16 wherein any one or more of primers having of SEQ ID NOS. 20, 22, 24 or 29 are replaced by a mixture of primers comprising or consisting of the sequences of SEQ ID NOS. 14 and 15.
- 30 18. The use of the primers as defined in claims 11 to 13 together with the primers and probes of claim 16 or 17 for the sequential metagenomic identification and species specific quantitation of DNA in a sample, the selection of species specific primers and probes employed for quantitation being chosen on the basis of the metagenomic identification of species DNA present in the sample.
- 35 19. A use of claim 18 wherein the sample is a food sample, such as a meat sample.
20. A method of any of claims 1 to 15 for the identification and quantification of at least one species specific target sequence in a sample from any one or more of a species

from a genus selected from *Sus*, *Gallus*, *Bos*, *Ovis*, *Equus*, *Meleagris*, *Felis*, *Capra*, *Antilocapra*, *Cervus*, *Anas*, *Anser* and *Coturnix*, for example, *Sus scrofa*, *Gallus gallus*, *Bos Taurus*, *Ovis aries*, *Equus caballus*, *Meleagris gallopavo*, *Felis catus*, *Capra hircus*, *Antilocapra Americana*, *Cervus elaphus*, *Anas platyrhyncho*, *Anser anser* and *Coturnix chinensis*.

5

21. A kit for metagenomic identification of DNA present in a sample, comprising a set of primers for the metagenomic amplification of a metagenomic target sequence in the myostatin gene, said metagenomic target sequence being selected to allow for: i) co-amplification of the metagenomic target DNA sequence from a plurality of species using a set of conserved, common primers; and ii) the identification of species origin of any amplified metagenomic target DNA on the basis of its sequence.
22. A kit of claim 21 wherein the metagenomic target sequence has the same number of copies per genome in each of the species suspected as being present in the sample, so as to further allow for a determination of the relative proportions of the different identified DNAs.
23. A kit of claim 21 or claim 22 wherein the metagenomic target sequence is selected to allow for amplification of DNA from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or 13 different species using a set of conserved, common primers.
24. A kit of any of claims 21 to 23 wherein the set of conserved, common primers includes no more than three primers, for example two or three primers.
25. A kit of any of claims 21 to 24 wherein the set of primers of the kit comprises primers comprising or consisting of the sequence of SEQ ID NO. 1 or SEQ ID NO. 2 and a primer comprising or consisting of the sequence of SEQ ID NO. 3.
26. A kit of claim 25 wherein the set of primers consists of three primers comprising or consisting of the sequences of SEQ ID NO. 1, SEQ ID NO. 2 and SEQ ID NO. 3 respectively.
27. A kit of claim 24 to 26 wherein at least one of the primers is modified by the addition of an adaptor sequence, tag or universal sequence, optionally wherein the set of primers comprises or consists of primers having the sequences of SEQ ID NOs. 4 to 13.

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28. A kit for quantitative PCR analysis of a species specific target sequence in a sample, said kit comprising a set of primers and probes for the amplification and real-time detection of a sequence from the myostatin gene, said sequence being selected to allow for species specific amplification and/or detection.
29. A kit of claim 28 wherein the species specific amplification and/or detection can distinguish between species from a genus selected from *Sus*, *Gallus*, *Bos*, *Ovis*, *Equus*, *Meleagris*, *Felis*, *Capra*, *Antilocapra*, *Cervus*, *Ana*, *Anser* and *Coturnix*, for example, *Sus scrofa*, *Gallus gallus*, *Bos Taurus*, *Ovis aries*, *Equus caballus*, *Meleagris gallopavo*, *Felis catus*, *Capra hircus*, *Antilocapra Americana*, *Cervus elaphus*, *Anas platyrhyncho*, *Anser anser* and *Coturnix chinensis*.
30. A kit of claim 28 wherein the set of primers and probes is selected from at least one of:
- a) primers comprising or consisting of the sequences of SEQ ID NOS. 17 and 18 and a probe comprising or consisting of the sequence of SEQ ID NO. 19 for the quantitation of DNA sequences from pork (*Sus scrofa*); or
 - b) primers comprising or consisting of the sequences of SEQ ID NOS. 20 and 16 and a probe comprising or consisting of the sequence of SEQ ID NO. 21 for the quantitation of DNA sequences from chicken (*Gallus gallus*); or
 - c) primers comprising or consisting of the sequences of SEQ ID NOS. 22 and 16 and a probe comprising or consisting of the sequence of SEQ ID NO. 23 for the quantitation of DNA sequences from beef (*Bos taurus*); or
 - d) primers comprising or consisting of the sequences of SEQ ID NOS. 24 and 16 and a probe comprising or consisting of the sequence of SEQ ID NO. 25 for the quantitation of DNA sequences from sheep (*Ovis aries*); or
 - e) primers comprising or consisting of the sequences of SEQ ID NOS. 26 and 27 and a probe comprising or consisting of the sequence of SEQ ID NO. 28 for the quantitation of DNA sequences from horse (*Equus caballus*); or
 - f) primers comprising or consisting of the sequences of SEQ ID NOS. 29 and 16 and a probe comprising or consisting of the sequence of SEQ ID NO. 30 for the quantitation of DNA sequences from turkey (*Meleagris gallopavo*); or
 - g) primers comprising or consisting of the sequences of SEQ ID NOS. 14 and/or 15 and 16 and a probe comprising or consisting of the sequence of SEQ ID NO. 31 or 32 for the quantitation of DNA from all species in the sample.

31. A kit of claim 30 wherein any one or more of primers having of SEQ ID NOs. 20, 22, 24 or 29 are replaced by a mixture of primers comprising or consisting of the sequences of SEQ ID NOs. 14 and 15.
- 5
32. A kit comprising the features of any of claims 21 to 27 further comprising the features of any one of claims 28 to 31.
- 10
33. A kit of any of claims 21 to 32 further comprising any reagent suitable for use in the metagenomic or qPCR analysis of the DNA content of a sample.


```
Capra hircus      GATGACAGCAGCGACGGCTCCTTGGAAAGACGATGACTACCACGTTACGACGGAACGGTC 480
Equus caballus   GATGACAGCAGTGATGGCTCCTTGGAAAGATGATGATTACCACGGCGACGACGGAACAATC 354
Sus scrofa      GATGACAGCAGTGATGGCTCCTTGGAAAGATGATGATTATCAGCTACGACGGAACGATC 354
** *  ** * * *  ***** * * * *  * * * * *
```

FIGURE 2

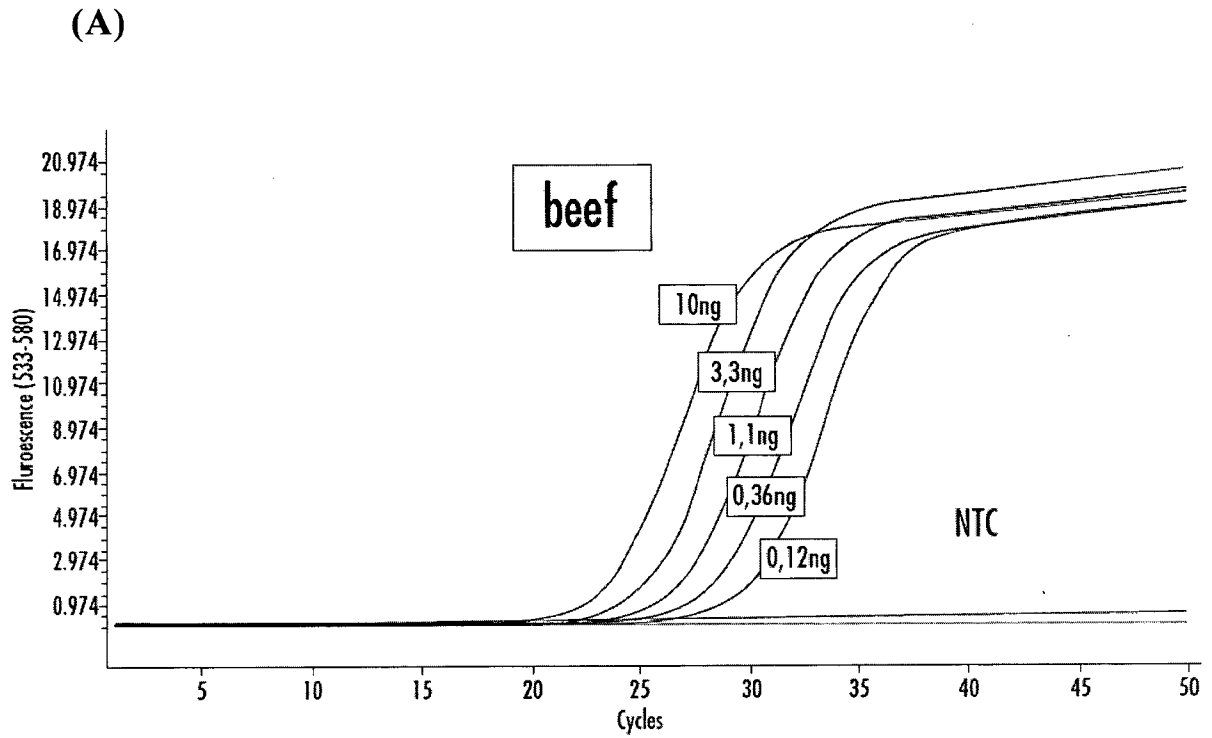
gi Ovis	-----ATGCAAAA <u>CTGCAAATCTTTGTTTATATTTACCT</u> ATTTATGCTGCTTGTGCT	1
gi Capra	AAAACCATGCAAAA <u>CTGCAAATCTTTGTTTATATTTACCT</u> ATTTATGCTGCTTGTGCT	1
gi Bos	AAAACCATGCAAAA <u>CTGCAAATCTTTGTTTATATTTACCT</u> ATTTATGCTGATTGTGCT	1
gi Sus	-----ATGCAAAA <u>CTGCAAATCTTTGTTTATATTTACCT</u> GTTTATGCTGATTGTGCT	1
gi Equus	-----ATGCAAAA <u>CTGCAAATCTTTGTTTATATTTACCT</u> GTTTGTGCTGATTTCTTGGCT	1/2
gi Meleagris	-----ATGCAAAA <u>CTAGCAGCTATGTTTATATTTACCT</u> GTTTCATGCAGATTTTAGTT	1/2
gi Anser	-----ATGCAAAA <u>CTAGCAGCTATGTTTATATTTACCT</u> GTTTCATGCTGATTTTAGTT	1
gi Gallus	-----ATGCAAAA <u>CTAGCAGCTATGTTTATATTTACCT</u> GTTTCATGCAGATCGGGTT	1/2
	***** *	
gi Ovis	GGCCCACTGGATCTGAATGAGAACAGCGAGCAGAAGGAAAATGTGGAAAAAAGGGGCTG	
gi Capra	GGCCCACTGGATCTGAATGAGAACAGCGAGCAGAAGGAAAATGTGGAAAAAAGGGGCTG	
gi Bos	GGCCCACTGGATCTGAATGAGAACAGCGAGCAGAAGGAAAATGTGGAAAAAAGGGGCTG	
gi Sus	<u>GGTCCCCTGGATCTGAATGAGAACAGCGAGCAGAAGGAAAATGTGGAAAAAAGGGGCTG</u>	1
gi Equus	<u>GGTCCAGTGGATCTAAATGAGAACAGCGAGCAGAAGGAAAATGTGGAAAAAAGGGGCTG</u>	2
gi Meleagris	<u>CATCCGGTGGCTCTTGATGGCAGTAGTCAGCCACAGAGAACGCTGAAAAAGACGGACTG</u>	2
gi Anser	<u>GATCCGGTGGCTCTTGATGACGGTAGTCAGCCACAGAGAACGCTGAAAAAGATGGACTG</u>	
gi Gallus	<u>GATCCAGTGGCTCTGGATGGCAGTAGTCAGCCACAGAGAACGCTGAAAAAGACGGACTG</u>	2
	* *	
gi Ovis	TGTAATG <u>CATGCTTGTGGAGACAAAACAATAAAATCCT</u> CAAGACTAGAAGCCATAAAAAATC	2
gi Capra	TGTAATGCATGCTTGTGGAGACAAAACAATAAAATCCTCAAGACTAGAAGCCATAAAAAATC	2
gi Bos	TGTAATGCAT <u>TGTTTGTGGAGGCAAAAACACTACATCCT</u> CAAGACTAGAAGCCATAAAAAATC	
gi Sus	<u>TGTAATGCATGTATGTGGAGACAAAACAATAAAATCCT</u> CAAGACTAGAAGCCATAAAAAAT	2
gi Equus	TGCAATGCATGTACTTGGAGACAAAACAATAAAATCCTCAAGAATAGAAGCCATAAAAAAT	
gi Meleagris	TGCAATGCTTGCAAGTGGAGACAGAATAACAATAAAATCCTCCAGAATAGAAGCCATAAAAAAT	
gi Anser	TGCAATGCTTGACATGGAGACAGAATAACAATAAAATCCTCCAGAATAGAAGCCATAAAAAAT	
gi Gallus	TGCAATGCTTGACGTGGAGACAGAATAACAATAAAATCCTCCAGAATAGAAGCCATAAAAAAT	
	* *	
gi Ovis	CAATCCTCAGTAAGCTTCGCCTGGAAACAGCTCCTAACATCAGCAAAGATGCTATAAGA	
gi Capra	CAATCCTCAGTAAGCTTCGCCTGGAAACAGCTCCTAACATCAGCAAAGATGCTATAAGA	
gi Bos	CAATCCTCAGTAAACTTCGCCTGGAAACAGCTCCTAACATCAGCAAAGATGCTATCAGA	
gi Sus	CAATCCTCAGTAAACTTCGCCTGGAAACAGCTCCTAACATCAGCAAAGATGCTATAAGA	
gi Equus	CAGATCCTCAGTAAACTTCGCCTGGAAACAGCTCCTAACATCAGCAAAGATGCTATTAGA	
gi Meleagris	CAATCCTCAGCAAAGCTTCGCCTGGAAACAGCTCCTAACATCAGCAAAGATGCTATAAGA	
gi Anser	CAATCCTCAGCAAAGCTTCGCCTGGAAACAGCTCCTAACATCAGCAAAGATGCTATAAGA	
gi Gallus	CAATCCTCAGCAAAGCTTCGCCTGGAAACAGCTCCTAACATCAGCAAAGATGCTATAAGA	
	* *	
gi Ovis	CAACTTTTGCCCAAGGCTCCTCCACTCCG <u>GGAACTGATTGATC</u> AGTACGATGTCCAGAGA	2
gi Capra	CAACTTTTGCCCAAGGCTCCTCCACTCCG <u>GGAACTGATTGATC</u> AGTACGATGTCCAGAGA	2
gi Bos	CAACTTTTGCCCAAGGCTCCTCCACTCCG <u>GGAACTGATTGATC</u> AGTACGATGTCCAGAGA	2
gi Sus	CAACTTTTGCCCAAGGCTCCTCCACTCCG <u>GGAACTGATTGATC</u> AGTACGATGTCCAGAGA	2
gi Equus	CAACTTTTGCCCAAGGCTCCTCCACTCCG <u>GGAACTGATTGATC</u> AGTACGATGTCCAGAGA	2
gi Meleagris	CAACTTTTACCCAAAGCTCCTCCGCTGCA <u>GGAACTGATTGATC</u> AGTATGAGTCCAGAGA	2
gi Anser	CAACTTTTACCCAAAGCTCCTCCACTTACA <u>GGAACTGATTGATC</u> AGTATGAGTCCAGAGA	2
gi Gallus	CAGCTTTTACCCAAAGCTCCTCCACTGCA <u>GGAACTGATTGATC</u> AGTATGATGTCCAGAGG	2
	* *	
	normalizer probe	
gi Ovis	GATGACAGCAGCGACGGCTCCTTTGGAAGACGATGACTACCAGTTACGACGGAAACGGTC	3
gi Capra	GATGACAGCAGCGACGGCTCCTTTGGAAGACGATGACTACCAGTTACGACGGAAACGGTC	3
gi Bos	GATGCCAGCAGTGACGGCTCCTTTGGAAGACGATGACTACCAGTTACGACGGAAACGGTC	3
gi Sus	GATGACAGCAGTGATGGCTCCTTTGGAAGATGATGATTA <u>CACGCTACGACGGAAACGATC</u>	3
gi Equus	GATGACAGCAGTGATGGCTCCTTTGGAAGATGATGATTA <u>CACGCTACGACGGAAACGATC</u>	3
gi Meleagris	GACGACAGTAGCGATGGCTCCTTTGGAAGACGATGACTATCATGCCACAACCGAAACGATT	3
gi Anser	GATGACAGTAGCGATGGCTCCTTTGGAAGACGATGACTATCATGCCACAACCGAAACGATT	3
gi Gallus	GACGACAGTAGCGATGGCTCCTTTGGAAGACGATGACTATCATGCCACAACCGAGACGATT	3
	* *	

Forward primer 1

Reverse primer 3

Taqman probe 2

FIGURE 3



(B)

Error: 0.0143
Efficiency: 1.968
Slope: -3.400
YIntercept: 30.48
Link: 3.802

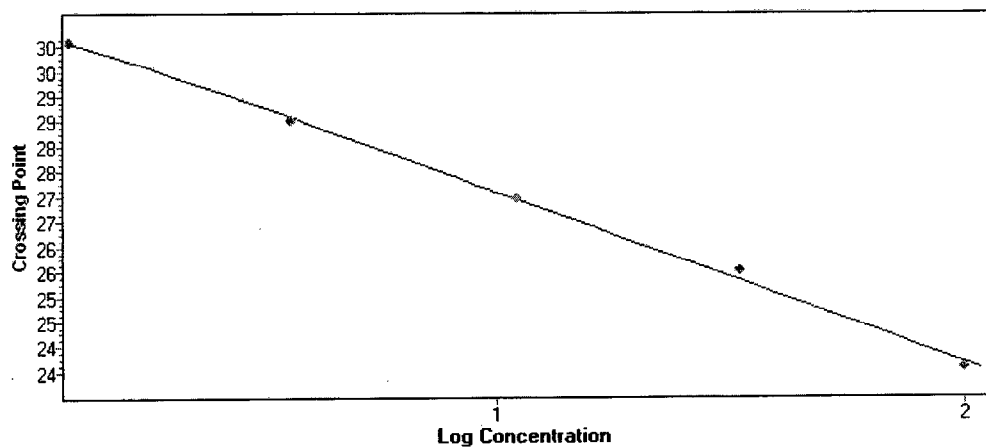


FIGURE 4

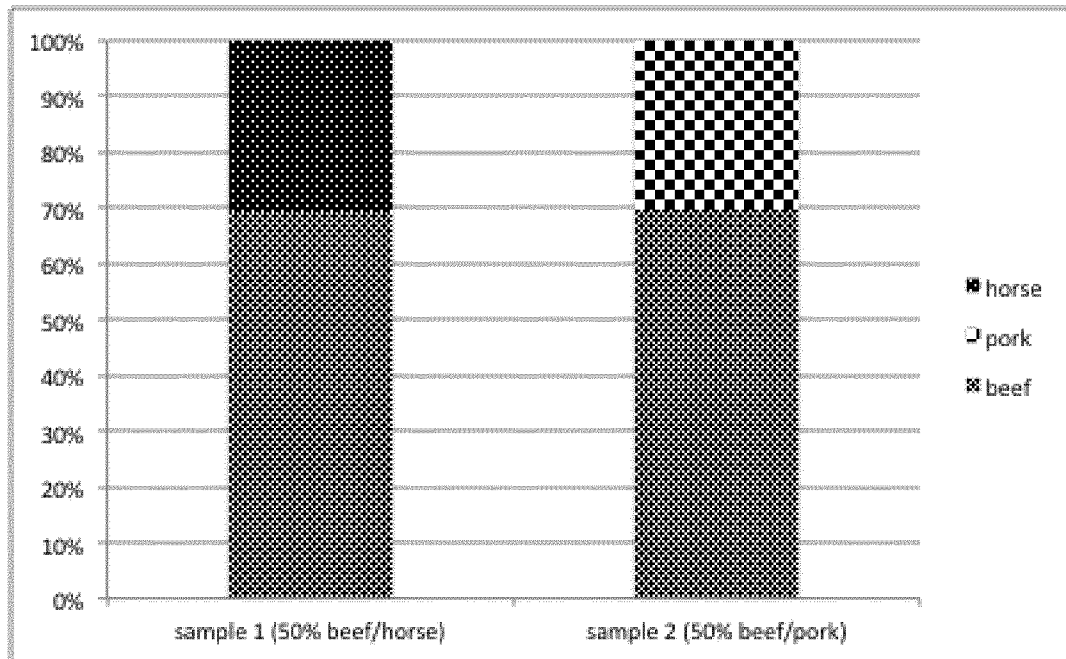


FIGURE 5

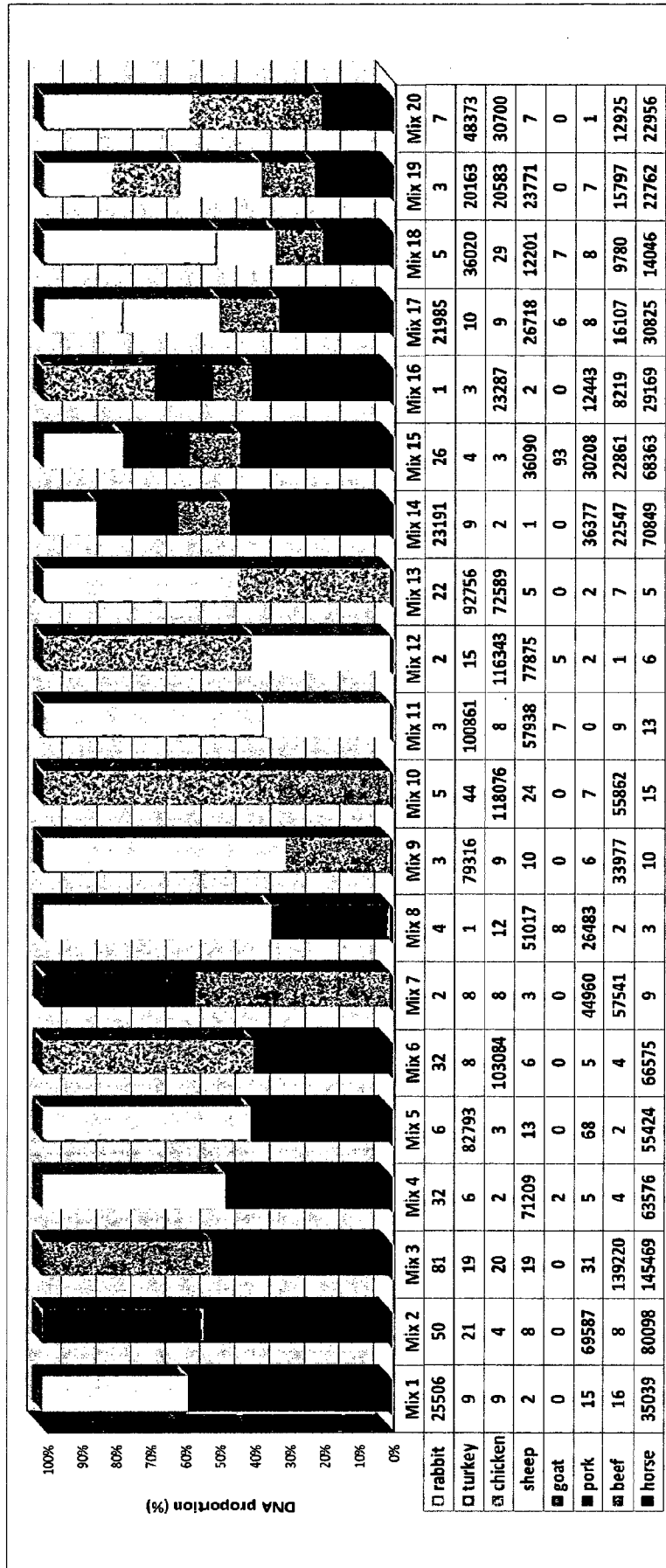
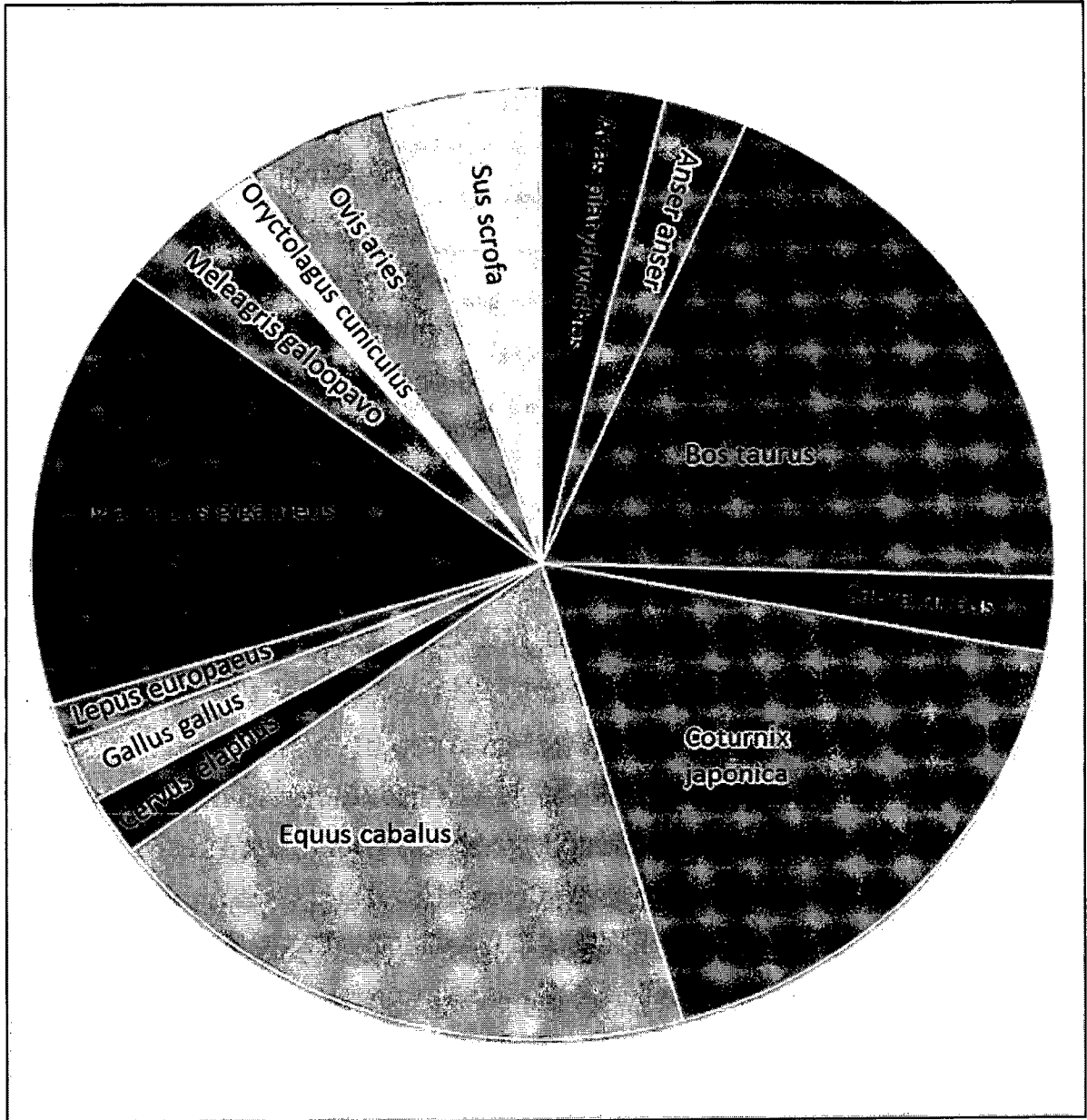


FIGURE 6



INTERNATIONAL SEARCH REPORT

International application No.

PCT/EP2014/078179

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:
- a. forming part of the international application as filed:
- in the form of an Annex C/ST.25 text file.
 - on paper or in the form of an image file.
- b. furnished together with the international application under PCT Rule 13ter.1(a) for the purposes of international search only in the form of an Annex C/ST.25 text file.
- c. furnished subsequent to the international filing date for the purposes of international search only:
- in the form of an Annex C/ST.25 text file (Rule 13ter.1(a)).
 - on paper or in the form of an image file (Rule 13ter.1(b) and Administrative Instructions, Section 713).
2. In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that forming part of the application as filed or does not go beyond the application as filed, as appropriate, were furnished.
3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2014/078179

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12Q1/68
ADD.
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)
C12Q
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)
EPO-Internal

C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2006/099617 A1 (SHIH YANG-CHIH [TW] ET AL) 11 May 2006 (2006-05-11) abstract paragraphs [0034], [0036], [0039], [0041], [0041], [0044], [0046], [0047]; tables 1,23	1-33
A	WO 2011/023950 A1 (WYETH CORP [GB]; BAIGENT SUSAN [GB]; NAIR VENUGOPAL [GB]; LE GALLUDEC) 3 March 2011 (2011-03-03) abstract	1-33
A	WO 2012/056227 A2 (OXITEC LTD [GB]; FU GUOLIANG [GB]) 3 May 2012 (2012-05-03) abstract; claim 1	1-33

Further documents are listed in the continuation of Box C. See patent family annex.

* Special categories of cited documents :

"A" 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
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"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 11 May 2015	Date of mailing of the international search report 22/05/2015
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Name and mailing address of the ISA/ European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Authorized officer Celler, Jakub
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INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No PCT/EP2014/078179

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