Reviewer’s report

Title: A simple HyBeacon probe system enabling high-throughput genotyping of multiple single nucleotide polymorphisms closely positioned in the ovine PRNP gene

Version: Date: 1 2 January 2007

Reviewer: Gabriele Vaccari

Reviewer’s report:

General

Dear editor,

the manuscript “A simple HyBeacon probe system enabling high-throughput genotyping of multiple single nucleotide polymorphisms closely positioned in the ovine PRNP gene” by French and colleagues is an interesting article describing the validation and the improvements of a method used in the genotype prion protein activity applied within the breeding programme for scrapie eradication. The method described could be useful and its characteristic seems to be very interesting from a technical point of view.

Major Compulsory Revisions (that the author must respond to before a decision on publication can be reached)

1) Discussion, page 16-17. Authors referred to experiments testing the output of the assay with rare alleles. I would suggest including these experiments in an additional section of the paper. They would improve the interest of the manuscript and are already done.

Minor Essential Revisions (such as missing labels on figures, or the wrong use of a term, which the author can be trusted to correct)

1) Abstract, Result section. It is probably missing some aminoacid variant successfully detected (ie. M 137, L141 ecc.)
2) Background section. Consider to revise the first sentence “(TSEs), is a degenerative and fatal disease that affects the nervous systems of sheep and goats” with “(TSEs), is a neurodegenerative and fatal disease that affects sheep and goats”.
4) The frequency of alleles or genotypes are reported with the decimal or with the % symbol (see page 12, 13 and 17). Please unify.
5) Results. Codon 141 section. The polymorphism at codon 141 is associate to Nor98 but not referred to as Nor98. Indeed it as been found also in sheep affected by “classical” scrapie.
6) Results. Codon 141 section and throughout the manuscript. I would suggest using the term polymorphisms to indicate a codon with different coded amino acids, not a variant. For instance “melting curve analysis with complementary oligonucleotides predicted that the N138 polymorphism...” consider to change with “... predicted that N at codon 138...” or with equivalent sentence. Same consideration in the last sentence of this section for R143 polymorphism
7) Page 16 last two sentences. See above about polymorphism terminology.

Discretionary Revisions (which the author can choose to ignore)

1) Abstract, Conclusion section. I would suggest consider the term inexpensive and/or to add some additional information on the cost or comparison with other methods on the manuscript.
2) Abstract, Conclusion section. I would suggest consider the sentence starting with “The flexibility ...” and subsequent one. As observed by Authors the method is very powerful however I think that it is the design of the assay and not the technology itself that ensure a correct genotype assignment.
3) Background section. I would suggest revising the 2nd sentence in a more doubting manner.
What next?: Accept after minor essential revisions

Level of interest: An article whose findings are important to those with closely related research interests

Quality of written English: Acceptable

Statistical review: No, the manuscript does not need to be seen by a statistician.

Declaration of competing interests:

I declare that I have no competing interests