Reviewer's report

Title: Differential gene expression associated with postnatal articular cartilage maturation

Version: 1 Date: 6 May 2008

Reviewer: Peter Clegg

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This is an interesting study which whilst somewhat limited, does contain some interesting data and I would support publication.

I have some concerns that the classification/categorization of neonatally upregulated genes is anecdotal and no association with these groups has been performed. An example of this is P9 4th line from the bottom – where the data is described as “seems to have greater up-regulation” - I am surprised that this cannot be proven using some mathematical/statistical method to progress the data from being qualitative to quantitative.

Specific points:

Title: It would be sensible to include the fact that the tissue is equine in the title

Abstract – methods – may be worth putting in age range of animals in methods. It would be nice to indicate that qPCR was performed on only 4 or 5 genes (and possibly include the names of these genes)

Background:

Second paragraph – maybe worth stating which joint Sasono examined (the tibia being a bone..!)

Materials and methods:

No mention of where the cartilage was harvested from (ie which joint and where in the joint). Not clear whether they discarded tissue with cartilage canals. I assume this was done but it isn’t clear.

Primer design: It is not clear whether these primers were human sequences (bought from ABS) and cross reacted with the equine sequence – if this is the case, it should be mentioned. The efficiencies are quite a broad range (0.9 - 1.2) and are greater than some commentators have deemed to be acceptable - This should be discussed. It would be interesting to know whether any of the housekeeping genes featured in the microarray and whether they showed differences between different aged tissues.

What was the selection criteria for the 5 genes selected for qPCR analysis – it would be nice to see some hypothesis on why these were chosen (from 544 candidates) – why is data for fibronectin not mentioned in results or fig 4, whilst it is mentioned in methods

Quantification of housekeeping genes stability - Would this stability been better
proven using one of the housekeeping gene algorithms, such as Genenorm or Normfinder?!

Discussion – some genes discussed which are not mentioned in results, nor proven by qPCR – such as NID2 – why is this discussed in such detail – it seems to be a bit out of context?

**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