Report for "Comparative proteomics analysis reveals the difference during antler regeneration stage between red deer and sika deer"

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General remarks

In this manuscript, the authors compares the antler regeneration stage from two species of deer, at the proteomic level. The methods they used (protein extraction, LC-MS/MS, label-freee quantification) are well suited for the study. However the design of the study is questionable, mainly because the objectives of the study are unclear. They stated that they wanted to "unveil the distinctive differences of antler regeneration between sika deer and red deer". But the authors never explained why this difference matter. Is there any morphological differences between the antlers of this two species ? Is the timing of the regeneration different? Later in the discussion it seems that the authors described the proteins involves in the regeneration rather than making a comparison between the species. If the aim of the study was to identify proteins involved in the regeneration stage, wouldn't have been better to compare between antlers at regeneration stage vs antlers at rest (for the same species)? Furthermore, are the authors sure that the antlers of both species are at the same regeneration stage? Also English language should be checked, especially the use of the word proteome (e.g.: l. 59-60, 63, 84,130-131,295). In my opinion, it will be suitable for publication after a major change in the presentation of the study and some minors changes listed below.

Specific remarks

Introduction

The introduction is a bit short and I would appreciate a description of the two species studied, what are their main differences and similarities, why comparing them?

l. 32-36 While comparing antlers and bovid horns seems to make sense for non-specialist like myself, it is a bit odd to start by comparing them then stating that they are completely different organs. Why introducing horns?

l. 59-60 What kind of differences? From which study? This part should be largely developed.

l. 62-72 This part should be rewritten by clarifying the objectives. The reference to genome of red deer belongs to material and methods.

Material and Methods

101 What was the quantity of proteins injected into the LC-MS/MS?

120-121 What software was used for the differential analysis? What kind of test was used (ANOVA, t-test...)? Were protein abundances normalized ?

Results

l. 145 146 typo error (differences)

l. 152-153 I don't understand this sentence

l. 143-153 I have trouble doing the maths of the identified proteins. 578 proteins identified were shared by both species (l.147), 114 only identified in sika deer (l. 148) and 19 only in red deer (l.149). 578 + 114 + 19 = 711 proteins. At l. 143 the authors stated that 1060 proteins were identified, am I missing something here? Is there other proteins identified or some redundancy in the data?

Figure 1 In this figure 579 proteins are identified in both species (whereas 578 at l. 147)

Table 1 Fix the legend (Differentially expressed proteins involved in **ribosome** pathway)

Table 1-4 Maybe you can merge all the tables into one with 4 categories?

l. 188 Why is there 180 DEPs here? I thought only 47 proteins were differentially expressed (l. 150-151)

Discussion

The discussion describes well the proteins involved, with background on mutation and disease but differences between species is, in my opinion, not thoroughly discussed.

l. 195-251 The high abundance of ATP8 in red deer (Table 1) is not discussed. Why is it more abundant in red deer?

l. 297-298 Could this mean that antlers are at different stages of the regeneration process?