

Rabbit muscle proteomics: a great leap forward

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Abstract

The rabbit is an important species as both a production animal and as a model organism in physiology, pharmaceutical and numerous other studies. Similar to other species, the rabbit skeletal muscle proteome has been characterized, first using 2DE mapping and more recently using high-throughput shotgun proteomics. This article is a commentary on “Shotgun proteomics analysis of the sarcoplasmic reticulum preparations from rabbit skeletal muscle”, recently published in proteomics. Herein, we present the reasons why the manuscript is of high relevance to three major fields: farm animal, rabbit and muscle/meat proteomics.

Key words: Rabbit, Muscle Proteome, Sarcoplasmic reticulum, Physiology

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Main text

Similarly to the pig[1], the rabbit (*Oryctolagus cuniculus*) is one of the most versatile and interesting domesticated species. In fact, rabbits are used for a multiplicity of purposes: from meat production animals in Mediterranean Europe to a worldwide generalized use in the pharmaceutical industry as an animal research model. In addition the rabbit genome is considered a sequenced genome, albeit further annotation seems to be needed. Paradoxically, and given its importance, the rabbit is seldom a subject of proteomics-based research, with the exception of a few specific areas related to skeletal and cardiac muscle physiology[2].

The characterization of a particular proteome is a difficult task that depends to a great extent on the approach and, above all, on how complete are databases used in protein identification. Recent years have witnessed an increase in proteome characterization papers. In fact from the earlier works, typically two-dimensional electrophoresis maps depicting the position of a few proteins in a 2DE gel, we have moved from high-throughput shotgun proteomics, able to identify and allocate to a given tissue or fluid a considerable number of proteins. In the farm animal proteomics community, although several years behind other areas, this was also the natural evolution and we have passed from generalist 2DE maps [3,4] to very complete and specific lists of frequently several thousands of proteins [5]. Concerning the rabbit skeletal muscle proteome, a similar evolution was recorded, from the first 2DE mapping[6] to this novel manuscript by Liu and co-workers[7].

Despite their necessity and usefulness, proteome characterizations are often poorly perceived by the non-proteomics scientific community. In fact, descriptions such as “never-ending list of proteins” and “lack of practical use” are often applied to such studies. As a consequence, leading proteomics journals tend to favor the publication of proteome maps in the form of short communications or dataset briefs.

The manuscript to which this commentary refers is in fact a proteome characterization exercise. Nevertheless, it is far from being a simple and long list of proteins. In fact, the manuscript by Liu et al. [7] presents for the first time an updated proteomic analysis of the sarcoplasmic reticulum in the rabbit skeletal muscle. The authors have applied a rather innovative shotgun proteomics approach based on one-dimensional electrophoresis followed by an automated LC-MS/MS on a hybrid linear ion trap (LTQ) – Orbitrap instrument. Using this approach, the authors were able to identify nearly 500 different proteins, approximately 10 times the number achieved roughly five years ago using 2DE and MALDI MS[6].

Customarily, the authors have thoroughly classified the proteins according to their role: metabolism (16%), biological oxidation (15%), cell death and defense (1.5%), signaling (13%), transporters and channels (11%), protein synthesis (7%), protein targeting (6%), protease (2.6%) and surprisingly only 6% of proteins related to contraction and roughly 20% of proteins with unknown function. The last two classifications are perhaps the most striking, indicating that the rabbit's muscle sarcoplasmic reticulum proteome is much larger than the world of majorly represented proteins and that there is an impressive number of nearly 100 proteins without a known described role. In addition, the authors were able to identify several proteins such as RyR1, calsequestrin, junctin and triadin, as well as several proteins such as mitofusin 2, inositol triphosphate receptor and voltage dependent anion channel that are implicated in the links between the mitochondria and the ER.

The results obtained in "Shotgun proteomics analysis of the sarcoplasmic reticulum preparations from rabbit skeletal muscle" has therefore a number of appealing reasons to justify reading it, from the in-depth level of the analysis and the number of proteins found in these separations to the several proteins that were found without an attributed role, something which is not so frequent in a (nearly) sequenced organism.

Nonetheless, the rabbit is a model species. In accordance, the data published by Liu and co-workers will therefore be extremely useful to understand muscle biochemistry and physiology, successfully complementing mouse and rat models from a human biology perspective. Naturally, the relevance of Liu and co-workers findings makes also a bridge with animal science, repeating not only the physiology angle previously mentioned but also from a point of view in line with the importance of muscle characteristics and their relevance to post-mortem changes and meat science, meat product quality and safety[8,9] making it of utmost relevance in the field of animal science. In fact, the relevance to animal science is perhaps one of its most appealing and relevant aspects, as for this particular field, shotgun proteomics is rarely accessible to researchers, making this manuscript of particular relevance.

Finally, it is worthy to note the origin of this manuscript, from outside the European and North American regions, and confirming China and Asia as a continuously growing major pole for proteomics research, in this case for muscle proteomics and its role in muscle physiology.

As stated above, "Shotgun proteomics analysis of the sarcoplasmic reticulum preparations from rabbit skeletal muscle" is considered to be a very interesting article which

could be easily classify as a “must read” paper in farm animal, rabbit and muscle physiology proteomics. Indeed a great leap forward.

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References

- [1] De Almeida, A.M., Bendixen, E., Pig proteomics: a review of a species in the crossroad between biomedical and food sciences. *Journal of proteomics* 2012, 75, 4296–314.
- [2] Miller, I., Rogel-Gaillard, C., Fontanesi, L., Spina, D., Almeida, A.M., The rabbit as an experimental and production animal: from Genomics to Proteomics. *Current Protein and Peptide Science* (in press).
- [3] Bouley, J., Chambon, C., Picard, B., Mapping of bovine skeletal muscle proteins using two-dimensional gel electrophoresis and mass spectrometry. *Proteomics* 2004, 4, 1811–24.
- [4] Chaze, T., Bouley, J., Chambon, C., Barboiron, C., Picard, B., Mapping of alkaline proteins in bovine skeletal muscle. *Proteomics* 2006, 6, 2571–5.
- [5] Reinhardt, T.A., Lippolis, J.D., Nonnecke, B.J., Sacco, R.E., Bovine milk exosome proteome. *Journal of Proteomics* 2012, 75, 1486–1492.
- [6] Almeida, A.M., Campos, A., Van Harten, S., Cardoso, L.A., Coelho, A.V., Establishment of a proteomic reference map for the gastrocnemius muscle in the rabbit (*Oryctolagus cuniculus*). *Research in veterinary science* 2009, 87, 196–9.
- [7] Liu, Z., Du, X., Yin, C., Chang, Z., Shotgun proteomic analysis of sarcoplasmic reticulum preparations from rabbit skeletal muscle. *Proteomics* (in press).

- [8] Paredi, G., Raboni, S., Bendixen, E., De Almeida, A.M., Mozzarelli, A., “Muscle to meat” molecular events and technological transformations: the proteomics insight. *Journal of proteomics* 2012, 75, 4275–89.
- [9] Paredi, G., Sentandreu, M.-A., Mozzarelli, A., Fadda, S., et al., Muscle and meat: New horizons and applications for proteomics on a farm to fork perspective. *Journal of proteomics* 2013 (in press).