MYOFIBRILLAR PROTEINS PROFILES EVOLUTION IN DRY-CURED HAM

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INTRODUCTION

We pretended to analyse in this study, in each sample of dry cured ham, and in the muscles *biceps femoris* (BF) and *semimembranosus* (SM), the electrophoretical profiles of myofibrillar proteins relatively comparable.

The different types of pork leg muscle have *in vivo* functions a little distincts and certainly that the turnover of the hundreds of varied proteins that are to be found in each one of them will have very proper features according to the genetical line of the animals, the feeding regime, the husbandry, etc (1).

The modulation of this protein renovation will be essentially attributable to the enzymatic systems intracellular and of the extracelular matrix. After slaughter of the animals, coincidingly normally with a peak of protein turnover in a perspective of protein deposition increase, it will be the enzymatic systems both from the citosolic type and of the lisosomal type and adittionally some of the extracellular space that will condition the proteolysis.

MATERIALS AND METHODS

A set of dry cured hams was let evoluted until they accomplished 15 months of preparation. During this period going between 2 and 15 months we determined in each sample and in the two types of muscle (*biceps femoris*, BF, and *semimembranosus*, SM) the profile of myofibrillar proteins (2).

Profile of Myofibrillar Proteins (2):

Experimental part:

The protein extract was performed after two distinct areas: muscle *biceps femoris* and muscle *semimembranosus*. Each sample was treated after the following scheme: all samples were subjected to an electrophoresis with SDS in gel gradient with polyacrylamide between 5 and 20%.

Treatment and analysis of the electrophoretic results:

Gels were scanned with an appropriate software Gel-Compar from Applied Maths, capable of normalizing the individual tracks and substracting a certain basal line that enables the clustering of samples according to the similarity of their electrophoretic patterns that determines the molecular masses and the relative quantities of each band.



Outline of the protein extraction procedure

The software allows additionaly the generation of data bases from electrophoretic tracks and their algorithms of clustering possibilitate the comparison of a certain band or of an unknown track against the data base generated, allowing for the identification of that band or of its homology percentage with the selected track.

Graphics of electrophoretic profiles:

To make easier the reading and interpretation of the results obtained, the different fractions separated by electrophoresis were united in seven groups and were graphed as bars attending to each percentage in each group. Accordingly the first group includes the fractions with molecular weights between 0 and 20, highlighting the percentage that the group represents, the second group includes fractions between 20 and 40, the third group between 40 and 60, the fourth group between 60 and 80, the fifth group between 80 and 100, the sixth group between 100 and 120 and the seventh group between 120 and 200 or 120 and 300 or 400.

RESULTS DISCUSSION

The proteolysis profiles corresponding to myofibrillar proteins is scarcely reproducible from sample to sample, although it sketches a certain tendency for the fractions with molecular masses 40-60 KDa are the most important percentually in SM muscles, while in the BF muscles this higher importance falls in fractions 10-20 and 20-40 KDa. The fractions 120-200 KDa sometimes are in large quantities and othertimes in infimate quantities or even inexistant.





CONCLUSIONS

In the two types of muscles the proteolysis do not cause breakdown uniform and reproducible of the substract (ham) between 2 and 15 months old.

We admit that probably the degree of proteolysis going on in the muscles at the moment of slaughter of the animals it is the more important factor as responsible by the profile of myofibrillar proteins until 15 months of age of the dry cured hams.

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