The study of the main porcine muscle proteins and its modifications

P-02.3-01

A. Akhremko[I]

[I]V.M. Gorbatov Federal Research Center for Food Systems of RAS, Moscow, Russia

In recent years, the volume and scale of meat production is in trend to be arisen. This tendency causes serious investigations, which can be successfully attributed to livestock farming. Porcine muscle tissues was studies, as well as functional structural proteins were identified, including their modifications. 2D PAGE was carried out by O'Farrell method; scanned with Bio-5000 plus (Serva, Germany) images were analyzed with ImageMaster™ 2D Platinum software (GE Healthcare, Switzerland); protein fractions were identification by MALDI-TOF MS.
A comparative analysis of 2-DE muscle samples using the software showed that on about 300 spots were detected on each gel. 56 standard protein fractions were observed in samples with various geographical origin, breed, age, as well as in samples with different technological processing and storage conditions of muscle tissue. Major proteins belonged to tropomyosin family, myosin structural light chains, phosphorylated myosin light chains, isoforms of muscle enolase and creatine phosphokinase, aldolase A, glyceraldehyde-3-phosphate dehydrogenase and myoglobins, stress-induced phosphoprotein, pyridoxine isoform, diethanolamine phosphate binding protein, troponin I and phosphoglyceratmutase.
The most dynamic changes caused by various factors (storage conditions, degree of autolysis, breed, age) were concerned the following protein fractions: myosin light chains (21.5 kDa), tropomyosin chains (33.5 kDa), pyruvate dehydrogenase components (33.5 kDa), creatine kinase (41.0 kDa) and enolase beta (46.0 kDa). This work was supported by RFBR, project number 19-316-90056.