9 strains of *Salmonella* (1.9%) were resistant to extended-spectrum cephalosporins. According the beta-lactamase inhibitor susceptibility tests, five of them were classified as ESBL-producers, 4 strains — as AmpC-producers. ESBL CTX-M was detected in strains of *S.* Haifa isolated from chicken samples and *S.* Derby isolated from the imported pork heart. AmpC cephalosporinase CMY was produced by two strains of *S.* Kentucky, isolated in 2006 and 2009 from imported poultry products, as well as two *S.* Dublin isolated in 2005 from the internal organs of a fallen calf and cow.

In opportunistic bacteria (*E. coli* and *Klebsiella* spp.) 22 strains were resistant to extended spectrum cephalosporins, 15 of them produced ESBL according the beta-lactamase inhibitor susceptibility tests. The class of detected β-lactamases was established in 11 strains. In *K. pneumoniae* and *K. ozenae* isolated from the milk of cows sick with mastitis ESBL CTX-M1 were detected. In *E. coli* isolated from calves suffering from diarrhea, was detected ESBL CTX-M1 and CTX-M9. So, our study has confirmed the circulation of *Salmonella* and other *Enterobacteriaceae* strains resistant to clinical significant antibiotics (fluoroquinolones and cefalosporines) in animal farms.

9.34 doi: 10.15789/2220-7619-2018-4-9.34

DATA ANALYSIS OF MASS-SPECTRAL *KLEBSIELLA PNEUMONIAE* PROFILES TO PREDICT OF CARBAPENEM-RESISTANT STRAINS

E.V. Zueva, N.V. Mikhailov, I.V. Likhachev, L.A. Kraeva, S.A. Egorova, A.A. Totolian

St. Petersburg Pasteur Institute, St. Petersburg, Russia Federation

The increase of the number of enterobacteria with resistance to carbapenems has become a global problem. A rapid method for predicting resistance to carbapenems is needed, the results of which will be obtained even before the sensitivity to antibiotics is determined. In recent years, has been developing the trend, related to the increase in the MALDI-TOF mass spectrometry potential by bioinformatic approach to typing bacteria at the level of strains.

The study's aim was the data analysis of the *K. pneumoniae* mass spectra for protein biomarker discovery that make it possible to predict the detection of strains with OXA-48 and NDM-1 carbapenemase activity.

We used archived spectra obtained for the routine identification of isolates from hospital patients of St. Petersburg in 2015–2017. Digital data of 67 raw spectra, selected by identification results at the *K. pneumoniae* species level, were exported to the "BioNumerics" software. The created classifier was used to identify of new seven OXA-48 and eight NDM-1 strains pre-characterized by PCR, and 16 sensitive to meropenem *K. pneumoniae* strains. The biomarker peaks were designated by comparing their molecular weights with the data of plasmid proteins *K. pneumoniae* in the NCBI and UniProtKB bases with using the ExPASy portal.

The cluster analysis results of 67 spectra were used to create a model, that consist of six classes. The aggregate efficiency of the classifier was 89.6%. The spectra of group #4 had a marker peak m/z = 5996 Da, which was comparable in molecular weight to the protein pKF140-142 of plasmid pKF3-140. The marker peak m/z = 6096 of group #2 was designated as a plasmid protein according it coincidence on molecular weight with the protein UUU_02980 of plasmid pKPt2. Sixteen sensitive strains were mainly classified in group #2, but their spectra lacked a plasmid peak m/z = 6096. Eight NDM-1 strains were assigned to different groups, however their spectra showed either the peak of the plasmid protein m/z = 6096 or the peak m/z = 5936 which was also identified as a plasmid protein according to the protein of the outer membrane receptor protein of the plasmid pF77. All OXA-48 strains were assigned to group #4 and their spectra contained the peak of the plasmid protein m/z = 5996.

It has been suggested that the mass spectra of carbapenem-resistant *K. pneumoniae* strains may contain peaks attributed to the plasmid-encoded proteins. Such small plasmid proteins, which molecular weight don't correspond to the carbapenemases, even so, can appear as predict biomarkers of carbapenemase activity of strains.