Published in the Slovak Republic
European Journal of Molecular Biotechnology
Has been issued since 2013.
E-ISSN: 2409-1332
2019, 7(1): 17-24

DOI: 10.13187/ejmb.2019.1.17
www.ejournal8.com

Grouping of Proteins Comprised in the Lungs Proteome by Physico-Chemical and Functional Properties of *Bos Taurus* and *Sus Scrofa*

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Abstract

The article is concerned with lungs proteome analysis of live-stock animals (*Bos Taurus* and *Sus scrofa*) with further proteins grouping by their physico-chemical and functional properties. Primary information of proteins comprised in the lungs proteomes of *Bos Taurus* and *Sus scrofa* was obtained from the UniProt database, taking into account the functional properties received from Gene Ontology database. The analysis revealed several thousand annotated proteins used for further grouping: by the chemical nature of their prosthetic groups, their localization in relation to the cell and functional properties. Consequently, we found a predominance of phosphoproteins in the lungs proteome, exceeding by almost 2 and 10 times the number of proteins related to glycoproteins and lipoproteins, respectively. Protein analysis by their localization in relation to the cell reveals a predominance of membrane and intracellular proteins. Practically significant proteins were extracellular proteins. Maximum function diversity of proteins comprised in the lungs proteome was in *Bos Taurus* - 741, *Sus scrofa* – 379. Therefore, lungs proteins of *Bos Taurus* are more promising for the industrial production than *Sus Scrofa's* ones. The obtained data can be used as a basis for the development or optimization of protein isolation methods for the pharmaceutical and biotechnology industries demands in future.

Keywords: proteome, databases, UniProt, Gene Ontology, physico-chemical properties, *Bos Taurus*, *Sus scrofa*.

1. Introduction

Lungs of live-stock animals such as cows and pigs are the product of secondary meat processing in animal husbandry. Accordingly, discussions on rational use concerning thesecondary animal products processing are under way (Faustino et al., 2019). Currently pharmaceutical and biotechnological products of the proteins isolated from the live-stock animals lungs are used. For example, one of the medicines is Calfactant, which contains surfactant proteins B and C (Ga et al., 2015; Bayat et al., 2015; Speer et al., 2013; Chen et al., 2016), and medicines, which contain Aprotinin (Baoukina et al., 2010; Mahdy et al., 2004; Wagener et al., 2008; Jegadeesan et al., 2016). Nevertheless apart from surfactant-associated proteins in the lungs, there are other promising proteins which can be used in the new therapeutic strategies development.

Complete proteome analysis based on functional and physico-chemical properties with the further development of protein isolation and purification methods is required with the purpose of finding promising proteins (Qoronfleh, 2004; Thysen et al., 2015). Particular difficulties may arise in the process of cellular and membrane-bound animal proteins isolation and purification from whole cells extracts. Regardless of the reason for the particular protein isolation and purification,

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the general stages are basically the same. Nevertheless applying of methods certain modifications to specific problems, such as protein insolubility and the loss of its activity, which can be encountered during the isolation and purification processes, is necessary due to the protein properties. Accordingly, the physico-chemical properties analysis of proteins comprised in the live-stock animals lungs proteome, will enable the development of isolation methods.

In connection with the above, the aim of the study was creation a grouping of proteins by functional and physico-chemical properties comprised in the lungs proteome of *Sus scrofa* and *Bos Taurus*.

2. Materials and methods

Grouping of proteins comprised in the lungs proteome of live-stock animals *Sus scrofa* (pig) and *Bos Taurus* (bovine) was executed by the chemical nature of prosthetic groups, physiological nature and their localization in relation to the cell, and by their functions. The search and analysis of the lungs proteomes was executed using the UniProt database (https://www.uniprot.org). The grouping included only annotated proteins.

Grouping of proteins by the prosthetic groups chemical nature was carried out due to their belonging to glycoproteins [KW-0325], lipoproteins [KW-0449] and phosphoproteins [KW-0597]. Grouping by localization of the target proteins in relation to the cell was carried out using the synonymic construct «Subcellular location» with the key words: cytoplasm «(Cytoplasm [SL-0086])» and cytosol («Cytosol»), membrane («Membrane»), extracellular protein («Extracellular»).

Advanced search query was used in the UniProt database with the inclusion of the identification numbers of the Gene Ontology database (https://www.ebi.ac.uk/QuickGO/) for the purpose of grouping by functional properties. Search of identification GO numbers was carried out using synonymic constructs «lung». The next step was determination of the most common Gene Ontology identification numbers in the lungs proteome.

Excel (Microsoft Office, USA) was used in building summary tables based on the results of analysis and grouping. The tables included the following elements: organism name, Uniprot ID, prosthetic groups chemical nature, physiological property (enzyme/receptor), their localization in relation to the cell and functions.

3. Results and discussion

As a result of the UniProt database bioinformatic analysis, 472 annotated proteins of *Bos taurus* and 193 – of *Sus scrofa* comprised in the lungs proteome were obtained. After the analysis of the received proteins, they were assorted by the prosthetic groups chemical nature for *Bos taurus* (Table 1) and *Sus scrofa* (Table 2)

Table 1. Grouping of proteins comprised in the lungs proteome of *Bos Taurus* by the prosthetic groups chemical nature

Glycoproteins (158)
P35246, O46406, Q8SPU5, Q0VCX4, Q2KJH1, P30922, P21758, Q3T0I2, F1MMS9, P79391, P21809, P24627, Q5E9P3, O19116, Q9XT49, Q06599, P21214, P79331, O97827, Q28044, Q10741, Q17QB3, O97831, P42891, O77783, P25930, P39873, F1MJW3, A5D7U4, P51867, Q1JQA4,Q32KP1, A6QLF8,Q3ZBV0, Q704V6, Q0VCF5, Q3T0Q2,Q9GLX9, A7YWH9,Q3SZE3, Q9TQZ3, Q28173, Q2KJ39, A4D7S0, Q3ZBN5, Q2HJ17, Q0II78, Q3ZBH3, Q3LUH2,Q9XSK2, Q2KIV9, Q5E9E3, P85521, P46626, Q5EA66, O77802, P22444, P10730, Q8SPF8, O77750, P35350, Q1RMR1, A2VDP5, Q11126, Q2KIX5, P21450, Q95M17, Q0VCS6, P11052, A6QP79, B9VR26, P32749, A6QLI0, Q5EA62, P98133, P56541, A6QLZ7, A5D7H3, A7MB63, Q29RT9, Q95122, Q9MZ08, P26201, Q5E9X0, Q0VCA0, P14769, Q5E9H1, P58354, P04651, Q0VCP3, Q32PI9, P31096, Q8SPJ1, Q58D34, Q58D84, P50291, P26892, P20959, Q05716, Q28028, P52173, A7MB64, Q5J316, Q9MYY0, P30546, Q5BIM9, Q1JQB3, Q28034, Q8SQG8, Q6UC88, Q3T181, P79345, Q0P5F0, P81265, P13909, Q2KJ15, A7MBJ4, Q3MI05, **P15781**, P21793, O62664, Q8WMP9, Q9TTY5, Q9MYW0, Q1LZE9, P45478, Q1JQA0, P30931, Q06807, P20414, Q6QUN5, Q32L50, **Q6RXL1**, A0JNP2, A0JNN2 P55270, Q2KJH6, Q05588, P48616, P02784, P55918, O77836, O77482, Q04790, Q148L1, A5PK45, P32592 Q862A9, P53712, Q0VCJ8, Q769I5, Q5EA06, Q92180, P80746, Q9XT56, A2VE13, Q148M6, Q8HXQ5
Lipoproteins (34)
P28088, F1MMS9, P79391, Q5E9P3, Q06599, P11023, P79132, Q28044, Q2KJ93, P26201, P60519, Q8SQG8, P84080, Q3ZBW5, O77750, Q2HJ17, Q04790, Q95122, P30931, P24275, A4D7S0, Q05588, P46626, Q9XSK2, Q58DW6, P50154, Q3ZBH3, Q1JPA0, Q5E9X0, Q5E9F0, P29105, **P15783**, Q58DS9, Q5EA55
Phosphoproteins (203)
P28088, Q0VCX4, Q2KJH1, P00516, O77834, P21758, P48644, P67868, F1MMS9, Q05717, Q28156, Q5E9P3, Q3T0E7, Q9XT49, Q06599,Q28021, O18971, P11023, P79132, Q66WT7, O97827, Q17R13, Q28044, Q10741, P21146, P17870, Q56K14, Q3T0L7, P61257, F1MJW3, A5D7U4, Q5E9F5, Q3ZBV0,Q0VC58, Q5E988, Q148E7, P50227, Q3ZC34, A7YWH9, A7YY57, Q3SZE3, Q3ZBW5,Q0P5H5, Q3T003, Q0VCC0, Q2HJ17, Q3SZX4, A4FV37,Q2KI22, Q0VCN0,Q765N9, Q1LZF8,A2VDY3, O02754, Q5E9J5, P02817, A4FV29,A2VDP1, P85521, P04272, P21398, Q3T013, Q17QW1, O77750, P48034, P35350, P24275, O97831, A5D7D1,Q9N0W2, P31976, A4IFD2, A5D7A0, P42891, Q2KIT4,Q29S22, Q2KIX5, P21450, P68103, A5D7U0, Q92176,B9VR26, Q2KJ93, Q08E26, P32749, O46382, Q2KIC2,Q8HYW0, P55052, A6QLZ5, P98133, Q0VCQ1, A5D7H3,P25930, Q2KJ36, Q3B7L5, Q9MZ08, Q3T0A6, P19803,P60519, Q1KZG4, Q3SZH7,Q17QE2, A7E3Q8, Q32PI9, P31096, Q8SPJ1, Q5E9E2,Q1LZ74, Q08E02, Q58D84, P03969, P43249, A7YWP4,P26892, P20959, Q05716, Q3ZC46, P30546, Q28034,A4FV08, A0JND2, Q08DU9, Q0VCL6, Q3B7N9, Q3T181, Q2HJ49, Q3T0C8, P81265,O46404, A7MBJ4,E1BM58, Q8MJG1, A6H772, Q66LN0,Q9XT96, Q8WN55,Q9BGI1, Q0P5J0, Q2HJG5, A2VDK6, Q9MYW0, O97681, P21752, O18883, Q8HYY4, P55859,Q32PF3, Q2KJ28, Q3T0T1,Q3ZBP3, Q3ZBF7, Q27967,Q3MHG1, Q05B92,Q9GMB8, Q3ZBT5, Q06807, P20414,Q2KIC8, Q3T0D7, A5D7K1, Q3SWZ6, P82915, Q2HJ86,A3KMV1, Q2KI99, Q2KJH6, E1BJD1, Q1JQE0, P67808,P48616, Q9BEG9, Q32LP7, Q2KJE0, Q2KJA1, Q3T0Q8,F1MJM0, P46196, Q0VCF9, O77836, Q9GLE4, Q04790,Q0VBZ5, Q8MKF0, Q5EAE5, P32592, Q29S21, Q5GJ77,P53712, Q2KI23, Q769I5, P11017, Q9BDR7, P01966,Q9XT56, P02070, A1A4R1, Q0VBY8, Q148M6, Q27966, Q28824, Q8HXQ5

Note: surfactant-associated proteins are highlighted in bold

Table 2. Grouping of proteins comprised in the lungs proteome of *Sus scrofa* by the prosthetic groups chemical nature

Glycoproteins (78)
Q9N1X4, Q5XW65, Q29411, P23563, P09858, O77633, O46427, Q28997, Q764M9, P20735, Q29055, Q6RHW4, Q5I2M3, P07200, P02543, Q02745, P21692, P53714, Q5U9S1, O02671, Q1W675, Q8SQ34, Q95L12, P52649, O97763, Q9MYU4, P26445, Q6KEQ9, Q75ZH0, Q9TUQ3, Q764N2, Q5PXD3, Q3ZDR4, Q95252, Q8HYN8, 8WN93,A9Y006, A8W649, Q2VL90, Q8MIB3, P30555, Q10982, Q9MYZ9, P35463, Q58D68, Q29010, B1PHQ8, B6CVD7,Q9TV36, Q29121, F1S584, Q29243, O62680, P14082, P50127, Q29042, A7UHZ5, Q95J68, A2BD09, Q8WNW3,Q9MYM5, P18430, Q29056, P01219, B3SP85, P79335, Q9XSD4, Q9N2D1, Q95242, Q6TYI6, Q5MNU5, **P49874**, Q28983, Q9GJR5, P01232, P79385, Q01580, Q1RPR6
Lipoproteins (16)
Q007T2, P23563, Q4LE85, Q52NJ, Q28997, Q007T5, P00592, P26234, Q6RVA9, Q06AU3, P3546, Q58D68, Q95252, O62680, P30555, Q8HYN8
Phosphoproteins (93)
Q29529, Q007T2, O62807, P19619, Q29073, Q19S50, P23563, P63053, O46374, Q4LE85, A5D9M6, A5GFW1, O77633, Q28997, Q764M9, I3LM39, Q8WNV7, Q2VIU1, Q9TUB2, Q9TU45, B8XX90, P26234, P02543,P21692,Q9XT90,P53714,Q2YGT9,Q95342,P80220,C5HGF3,F1SR90,A5GFW7,Q2HY40, P21753,Q95274,Q3S853,A5GFN6,Q06AU3,A5GFW5,Q6RVA9,P35750,Q764N2,Q5PXD3,Q8WN 93,O19004,Q2VL90,P30555,Q9MYZ9,P35463,Q58D68,Q29010,P13222,P67872,P52649, B1PHQ8,P04574,B6CVD7,Q9TV36,F1S584,P52650,Q29243,B0KYV5,Q5PXT2,P12675,Q7YR76, Q8WNW3,P60662,Q8MJ49,Q29024,Q1W675,P18430,A0FIN4,P80031,P61291,Q9TSX9,Q6R2V 0,Q95242,P67937,Q4VYA0,I3L5V6,Q6QAP7,Q5MNU5,Q767L7,P00339,O02671,Q9GJR5,Q8MJ 39,Q9XSZ6,P01965,P02067,P62802, Q71LE2,Q29122

Note: surfactant-associated proteins are highlighted in bold

As a result of the proteins grouping by their localization in relation to the cell, there was a significant predominance of proteins associated with membranes both in *Bos taurus* (Table 4), and *Sus scrofa* (Table 3).

Table 3. Grouping of proteins comprised in the lungs proteome of *Sus scrofa* by the localization in relation to the cell

Cytoplasm (60)
Q29411, Q007T2,O62807, P19619,Q29073, Q19S50,P63053, A5D9M6,A5GFW1, Q6QAQ1,Q007T5, I3LM39, P16469, Q2VIU1,Q9TUB2, B8XX90,P26234, P02543,Q9XT90, Q9N1F5,Q29122, P35750,P00339, Q9TSX9, P26889, Q06AU3,Q2YGT9, P83884,Q95342, P80310,P80220, F1SR90,Q2IA00, P35323,Q2HY40, P21753, Q95274, P46405,Q3S853, A5GFN6,A5GFW5, A3QRX8,P04574, Q29243,D2SW95, B0KYV5,Q5PXT2, Q8WNW3,Q8MJ49, Q29024,Q8MJD6, A0FIN4,P80031, P61291,Q6R2V0, P67937,I3L5V6, Q28999, Q767L7, P12309
Membrane (82)
Q007T2, P19619, P23563, Q4LE85,Q52NJ1, O77633,Q28997, Q007T5,Q764M9, I3LM39,P20735, P16469,Q9TU45, Q5I2M3,B8XX90, P26234,Q02745, Q9XT90,P53714, Q9XSZ6,Q29122, O02671,Q1W675, Q8SQ34,P35750, Q6RVA9,P80310, P26445,C5HGF3, F1SR90,Q3S853, Q6KEQ9,Q06AU3, Q75ZH0,Q764N2, Q5PXD3,Q3ZDR4, Q95252,Q35916, Q8HYN8,Q8WN93, A9Y006,A8W649, Q2VL90,Q30C86, Q8MIB3,P30555, Q10982,Q9MYZ9, P35463, Q9MYU4, Q58D68, Q29010,P52649, B1PHQ8,P04574, B6CVD7,Q29121, F1S584,P52650, Q29243,O46420, Q29036,D2SW95, O62680,P50127, Q29042,B0KYV5, Q8WNW3, Q9XSD4,Q767L9, Q95242,Q6TYI6, Q5MNU5, P47787,O97562, Q28983,Q9GJR5, P79385,Q01580, Q1RPR6,P82126

Extracellular space (12)
Q9N1X4,Q29411,P19619,P09858,P07200,P21692,Q29243,Q9TV36,Q01580, P45846, **P49874**, Q29042

Note: surfactant-associated proteins are highlighted in bold

Table 4. Grouping of proteins comprised in the lungs proteome of *Bos Taurus* by the localization in relation to the cell

Cytoplasm (125)
Q0VCX4, P00516, O77834, P30922, P48644,P16068, Q08E39, P79105,Q28021, O18971, P11023, Q66WT7, P62739, P21146, P17870, P48034, P31976, P18203, Q92176, Q2KJ93, Q3B7L5, P79135, Q8SPJ1, Q08E02, P43249, Q3ZC46, Q4U5R4, P50227 , Q0P5H5, Q0VCC0, Q3SZX4, A4FV37, Q2KI22, Q27971, O02751, A2VE78, Q3SX44, Q58CQ2, O18737, P84080, Q17QW1, P63258, A5D7D1, A2VDX7, Q2KIT4, Q2KIX5, P68103, Q95M17, A5D7U0, Q0VCQ0, Q08E26, O46382, P55052, Q2KJ36, Q3SZT6, P19803, P19687, Q1KZG4, O18879, Q3SZH7, Q17QE2, A7E3Q8, F1N152, Q8MJD5, P68265, A4FV08, Q2HJ49, Q0VCN1, Q5E9B6, Q3T0C8, P05980, E1BM58, Q3T0E7, A6H772, Q66LN0, P52897, Q9BGI1, Q0VCW6, A2VE79, Q2HJG5, A2VDK6, P21752, O18883, Q8HYY4, P55859, Q3T0T1, Q0VCJ7, O02739, Q5BIR5, Q3ZBF7, Q9GMB8, Q17QV3, Q06807, Q3ZCC8, Q3MHL6, Q2KIC8, Q28050, P28782, A5D7K1, Q3SWZ6, Q2HJ86, P55270, Q2KI99, Q0VCI2, P67808, P48616, Q5E969, Q3MHQ4, Q32LP7, Q2KJA1, P46196, Q9GLE4, Q8MKF0, Q5EAE5, A5PKK7, Q148C9 ,Q58DS6, Q56JY0, Q28035, P11017, Q9N0V4, Q3T0K9, Q148M6, Q27966, Q28824
Membrane (195)
P28088, Q0VCX4,P21758, F1MMS9, P79391, Q5E9P3, Q08E39, P79105, Q9XT49, Q06599, Q28021, P11023, P79132, Q66WT7, Q7SIB2, O97827, Q17R13, Q28044, Q10741, P21146, P17870, P04272, O97831, P31976, P42891, P18203, F1MJW3, A5D7U4, Q3SYU3, Q5EA70, P51867, Q1JQA4, Q32KP1, A6QLF8, Q3ZBV0, Q704V6, A0JNK6, Q0VC58, Q0VCF5, Q3T0Q2, Q8HZT6, A7YWH9, Q3SZE3, Q9TQZ3, Q28173, Q3ZBW5, Q0P5H5, Q58DW6, Q3SZI5, Q2HJ17, Q0II78, A4FV37, Q2KI22, Q3ZBH3, Q27971, Q3LUH2, Q0VCN0, Q765N9, Q2HJ22, Q29442, Q9XSK2, Q1LZF8, A2VDY3, Q5E9J5, O18737, P84080, P85521, P46626, P10730, P21398, Q3T013, Q17QW1, O77750, P35350, P24275, Q148F2, Q1JPA0, Q9N0W2, A2VDP5, Q11126, A5D7A0, Q2KIT4, Q2KIX5, P21450, P68103, Q0VCS6, A6QP79, Q92176, B9VR26, Q2KJ93, Q0VCQ0, O46382, A6QPI4, O77783, P55052, A4IFP3, A5D7H3, P25930, Q2HJ66, A7MB63, Q29RT9, Q3SZT6, Q95122, Q9MZ08, P26201, Q3ZCD0, Q5E9X0, Q01888, P14769, Q5E9F0, P58354,Q0P5F3, Q32PI9, P79135, Q5E972, Q1RMT9, Q3SYT0, Q8SPJ1, P43249, F1N152, Q5I3B2, A7MB64, Q5J316, Q9MYY0, P30546, Q5BIM9, Q1JQB3, Q8SQG8, P29105, Q24JY7, Q6UC88, Q3T181, Q2HJ49, Q0P5F0, P81265, A7MBJ4, E1BM58, A6H7B8, Q0VCC1, Q66LN0, Q9XT96, O62664, Q95L14, Q8WMP9, Q58DS9, Q9TTY5, Q2HJG5, Q9MYW0, O97681, Q27979, Q3MHG1, P30931, Q0IIE5, Q3ZBT5, Q06807, Q6QUN5, Q2KIC8, P28782, Q1LZB3, P55270, Q2KI99, Q0VCI2, Q05588, A1A4L0, A1A4J8, Q2KJA1, P81103, P46196, O77836, Q9GLE4, Q6IED8, Q04790, Q8MKF0, Q5EAE5, Q6QRN8, Q148L1, P32592, Q862A9, Q5GJ77, P53712, Q769I5, A4IF94, P50154, Q5EA06, O18756, Q92180, Q9BDR7, P80746, Q5EA55, Q9XT56, A2VE13, Q95J56, Q148M6, Q27966, Q8HXQ5
Extracellular space (24)
P35246, O46406, Q2KJH1, P30922, P21809, P21214. P79331, Q7SIB2, P04272, P21793, P98133, A4D7S0, P02817, Q29442, **P15781**, **Q6RXL1**, Q9GLX9, **P15783**, O18739, Q5EA62, P55918, Q3ZBN5, Q32L50, **P00974**

Note: surfactant-associated proteins and aprotinin are highlighted in bold

Thereby, correlation between cytoplasmic proteins, associated with the membrane and located in the extracellular space, is almost the same both in *Bos taurus* and *Sus scrofa*. Proteins with practical significance are represented by glycoproteins/lipoproteins and they are located in the extracellular space, upon a detailed proteins exploration, for example, P35246 – Pulmonary surfactant-associated protein D and P00974 – Pancreatic trypsin inhibitor (Aprotinin).

As a result of the search for identification numbers, associated with the proteins functional properties in Gene Ontology, 31 identifiers were found. Only 8 of them are associated with proteins

comprised in the lungs proteome of *Bos Taurus* and *Sus scrofa*: GO:0061033, GO:0030324, GO:0060437, GO:0060428, GO:0060487, GO:0048286, GO:0060449, GO:0060501.

Consequently, the most common proteins functions, presented in Figure 1, were revealed.

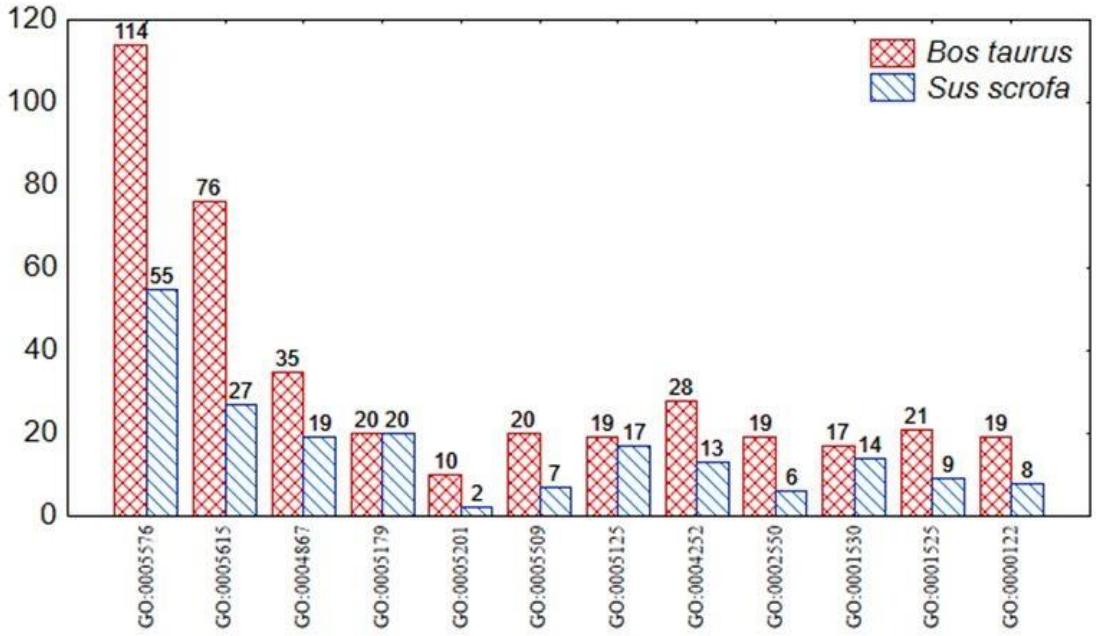

Fig. 1. The most frequently occurring functional properties of proteins, comprised in the lungs proteome of *Bos Taurus* and *Sus scrofa*, according to Gene Ontology

Maximum function diversity of proteins comprised in the lungs proteome is in *Bos Taurus* – 741, *Sus scrofa* – 379. Predominately, there are proteins excreted into the extracellular space, and proteins involved in the endopeptidase activity regulation process. Proteins related to group GO: 0004867 get involved in cell adhesion, extracellular matrix formation. Among the proteins of GO: 0005615 group, there were founded proteins-regulators of cell differentiation and proliferation, transport proteins and lipoproteins and proteins associated with lipids. Proteins involved in cell adhesion were founded in both the GO: 0005576 and GO: 0005615 groups. Proteins of GO: 0004867 group are inhibitors of metalloproteinases, serine and trypsin proteases, chymotrypsin, thrombin and express endopeptidase activity. Collagen and proteoglycan chains are also frequently occurring proteins.

Accordingly, the isolation of proteins from the lungs of *Bos Taurus* for the purpose of exploration will be more effective, than from the lungs of *Sus Scrofa*. The major part of the proteins is hydrophobic and interacts with lipids or is lipoproteins, what should be taken into account in isolation and purification.

As for the molecular weight, the correlation between proteins functions of GO: 0005576 and GO: 0005615 groups were not found. Proteins of GO:0004867 can be divided by mass into three groups:

1. Structural proteins involved in the synthesis and fixation of hyaluronic acid in the extracellular space: have the largest molecular weight – 100-104 kDa.

2. Hydrophobic proteins, which are responsible for the proteinase inhibitors transport, – 44–46 kDa.

3. Proteases inhibitors (trypsin, acrosin, plasmin, serine protease) – 6-14 kDa.

Consequently, proteins separation by molecular weight using electrophoresis can be the basis for their division by functional properties.

Maximum number of proteins of *Bos Taurus* and *Sus scrofa* depending on their localization in relation to the cell is membrane ones. They are divided into peripheral and integral membrane proteins, which are associated to varying degrees with the phospholipid bilayer. Peripheral membrane proteins can be dissociated using relatively mild techniques that break the electrostatic

or hydrogen bonds between the peripheral proteins and the membrane, without total membrane disruption. For this purpose buffers containing high salts are used as they decrease electrostatic interactions between proteins and charged lipids. Chaotropic ions disrupt hydrophobic bonds present in the membrane surface and promote the transfer of hydrophobic groups from non-polar environment to the aqueous phase (Pandey et al., 2016).

In order to solubilise integral membrane proteins, it is necessary to disrupt the lipid bilayer, which may be achieved with organic solvents.

In the proteins distribution, depending on prosthetic groups, the majority was represented by phosphoproteins. Ion-exchange chromatography or chromatofocusing, affinity chromatography with immobilized metals are used for proteins isolation and purification (Adamczyk et al., 2001).

In previous studies, surfactant-associated proteins and Aprotinin, which have practical importance, were discovered in the result of proteome analysis using virtual screening. Knowledge about physico-chemical, physiological properties and information about pulmonary proteins localization in relation to the cell can help to predict the possibility of practically significant proteins isolation and purification.

4. Conclusion

Knowledge of physico-chemical properties are necessary for isolation potentially significant proteins from the lungs. Frequently occurring lungs proteins are phosphoproteins and lipoproteins, located on cell membranes, or secreted into the extracellular space. This feature should be taken into account in the proteins isolation, and isolate the proteome in two stages – with the extraction of hydrophobic, and hydrophilic proteins from the lungs.

The proteome analysis performed in this work will allow to create a strategy for the isolation and purification of proteins mainly from the lungs of *Bos Taurus*, as this organism has maximum functional diversity of proteins and the largest number of annotated proteins in physico-chemical properties.

5. Acknowledgments

This work was supported by the Russian Foundation for Basic Research (RFBR) Project no. 18-44-343003 “Complex potentially bioactive molecules isolation, based on the study of cattle lungs proteome”

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