COMPARATIVE CHARACTERISTICS OF UBIQUITIN PROTEIN IN HUMANS AND PULMONARY FRESHWATER MOLLUSKS

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Proteases probably originated in the earliest stages of protein evolution as simple destructive enzymes necessary for protein catabolism and amino acid generation in primitive organisms. The current success of research in this group of ancient enzymes is due mainly to a large collection of findings demonstrating their relevance in the management of numerous biological processes in all living organisms.

Thus, proteases regulate the fate, localization and activity of many proteins, modulate protein-protein interactions, create new biologically active molecules, contribute to the processing of cellular information, generate, transduce and amplify molecular signals. As a direct result of these multiple actions, proteases affect DNA replication and transcription, cell proliferation and differentiation, tissue morphogenesis and remodeling, heat shock and deployed protein responses, angiogenesis, neurogenesis, ovulation, fertilization, wound repair, stem cell mobilization, hemostasis, blood clotting, inflammation, immunity, autophagy, aging, necrosis and apoptosis.

Finally, proteases are also important tools of the biotechnology industry because of their usefulness as biochemical reagents or in the production of numerous products [1].

Protein modifications provide cells with exquisite temporal and spatial control of protein function. Ubiquitin is one of the most important modifiers, serving both to target hundreds of proteins for rapid degradation by the proteasome and as a dynamic signaling agent regulating the function of covalently bound proteins. The diverse effects of ubiquitylation reflect the Assembly of structurally different ubiquitin chains on target proteins. The resulting ubiquitin code is interpreted by an extensive family of ubiquitin receptors [3].

In all tissues of living organisms, most intracellular proteins are degraded by the ubiquitin-proteasome pathway (UPP). This regulated type of proteolysis plays the most important role in cellular signaling [2].

The relevance of the study is associated with the search for organisms that can be sources of these cells and tissues for the production of proteolytic enzymes for use in practical needs (biopharmaceuticals, cosmetics, nutrition).

As a possible source for the production of proteolytic enzymes, the mollusks widely distributed in the waters of Europe – *Planorbarius corneus* (coil horn) and *Lymnaea stagnalis* (common pond), the closest relative of which is the well-studied *Biomphalaria glabrata* [4].

The aim of this work was a comparative analysis of the degree of homology of proteolytic enzymes in humans and pulmonary freshwater mollusks.

Material and method. The paper uses bioinformatic approaches based on the use of different servers: the search and selection of nucleotide sequences encoding human proteins was carried out on the server https://www.ensembl.org; search for homologous sequences for mollusks was carried out on the server https://www.ncbi.nlm.nih.gov using the BLAST resource.

Nucleotide and amino acid sequences of ubiquitin protein for human and pulmonary freshwater mollusks were used for the analysis.

Findings and their discussion. In the human genome, ubiquitin is encoded by 4 genes. But for mollusks, 1 gene was found, which when aligned with each of the 4 human genes gave different percentages of homology.

As a result of the work done, the following indicators were established: Expected value, Identities, Query coverage.

Enzyme	Type of sequence	Expected value	Identities	Query coverage
UBB (Biomphalaria)	NS[1]	6e-180	81%	56%
	AAS[2]	5e-162	99%	100%
UBB (Lymnaea)	NS	2e-59	82%	55%
	AAS	8e-50	100%	99%
UBC (Biomphalaria)	NS	0.0	79%	93%
	AAS	0.0	100%	96%
UBC (Lymnaea)	NS	5e-64	84%	93%
	AAS	1e-45	100%	93%
UBA52 (Biomphalaria)	NS	3e-89	79%	68%
	AAS	8e-87	94%	67%
UBA52 (Lymnaea)	NS	1e-59	82%	39%
	AAS	3e-50	100%	40%
RPS27A (Biomphalaria)	NS	3e-120	81%	43%
	AAS	7e-80	93%	43%
RPS27A (Lymnaea)	NS	1e-112	80%	43%
	AAS	2e-81	93%	43%

Ubiquitin is a small (8.6 kDa) regulatory protein found in most tissues of eukaryotic organisms. Four genes in the human genome code for ubiquitin: UBB, UBC, UBA52 and RPS27A.

In a comparative analysis of these four genes, the following data were obtained for *Biomphalaria glabrata*. UBB – homology on nucleotide sequence – 81%, on amino acid sequence – 99%. UBC – homology on nucleotide sequence – 79%, on amino acid sequence – 100%. UBA52 – homology on nucleotide sequence – 79%, on amino acid sequence – 94%. RPS27A – homology on nucleotide sequence – 81%, on amino acid sequence – 93%.

[1] nucleotide sequence;
[2] amino acid sequence.

For *Lymnaea stagnalis*, slightly different data were obtained. UBB – homology on nucleotide sequence – 82%, on amino acid sequence – 100%. UBC – homology on nucleotide sequence – 84%, on amino acid sequence – 100%. UBA52 – homology on nucleotide sequence – 82%, on amino acid sequence – 100%. RPS27A – nucleotide sequence homology – 80%, amino acid homology – 93%.

Conclusions. The homology of this enzyme by nucleotide sequences in humans and pulmonary freshwater mollusks is within 79-81 % (*Biomphalaria glabrata*) and 80-84% (*Lymnaea stagnalis*).

The practical significance of the high degree of homology of proteolytic enzymes in humans and freshwater lung mollusks justifies the formation of aquaculture of mollusks to obtain from their tissues protein enzymatic preparations of proteolytic action in the biopharmaceutical, cosmetic and food industries.

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JUNIPERUS COMMUNIS L. SEEDS MORPHOLOGY AND THEIR ANALYZE

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Gymnosperms seeds have dense seed coat. A membranous structure – nucellus remainder – is situated under it. The remaining volume of the seed is occupied by the thelom gametophyte which had been transformed into the nutrient tissue and by the embryo which is located in a special chamber. The embryo consists of a root, a stalk, cotyledons and a bud. The embryo is connected with the nutrient tissue by a suspensior which departs from the embryo root [1].

There are various methods of studying the viability and internal structure of seeds: organoleptic (based on the external characteristics of the seeds), chemical (non-stratified seeds are stained with 0.05% indigo carmine aqueous solution),