Infrared Spectra and X-ray Examination of the Complex Albumin Human with UO_2^{2+}

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Abstract: Reaction dioxouranium (VI) UO_2^{2+} ion with human serum albumin was prepared: human albumin with uranium UO_2^{2+} ion and the X-ray method of investigation of these complexes. The authors have shown that Human Albumin may be used to remove highly toxic uranyl UO_2^{2+} ions.

Key words: Albumin serum human, dioxouranium (VI) UO_2^{2+} ion, X-ray, complex.

1. Introduction

Human serum albumin is the most abundant protein in human blood plasma. It is produced in the liver. Albumin constitutes about half of the blood serum protein. It is soluble and monomeric. Albumin transports hormones, fatty acids, and other compounds, buffers pH, and maintains osmotic pressure, among other functions. Albumin is synthesized in the liver as a prealbumin, which has an N-terminal peptide, which is removed before the protein is released from occurring rough endoplasmic reticulum human. The product, proalbumin, is in turn cleaved in the Golgi vesicles to produce the secreted albumin.

The approximate sequence of human serum albumin is:

MKWVTFISLL FLFSAYSRG VFRRDAHKSE
VAHRFKDLGE ENFKALVLIA FAQYLQQCPF
EDHVKL VNEV TEFAKTCVAD ESAENC DKSL
HTLFGDKLCT VATLRETYGE MADCCAKQEP
ERNECFLQHK DDNPNLPRLV RPEVDVMCTA
FHDNEETFLK KYLYEIARRH PYFYAPELLF
FAKRYKAAFT ECCQAADKAA CLLPKLDEL R

DEGKASSAKQ RLKCASLQKF GERAFAKAWAV
ARLSQRFPKA EFAEVSKLVT DLTKVHTECC
HGDLLCADD RADLAKYICE NQDSISSKLK
ECCEKPLLEK SHCIAEVEND EMPADLPSLA
ADFVESKDVC KNYAEAKDVF LGMFLYEYAR
RHPDYSVLL LRLAKTYETT LEKCCAAADP
HECYAKVFDE FKPLVEEPQN LIKQNC ELF E
QLGEYKFQNA LLVRYTKKVP QVSTPTLVEV
SRNLGKVGSK CCKHPEAKRM PCAEDYLSVV
LNQLCVLHEK TPVSDRVTKC CTESLVNRRP
CFSALEVDET YVPKEFNAET FTFHADICTL
SEKERQIKKQ TALVELVKHK PKATKEQLKA
VMDDFAAFVE KCKKADDKET CFAEEGKKLV
AASQAALGL.

The italicized first 24 amino acids are signal and propeptide portions are not observed in the translation, and transported protein but present in the gene. There are 609 amino acids in this sequence with only 585 amino acids in the final product observed in the blood.

In work [1] has been studied chemical and biological insights into uranium-induced apoptosis of rat hepatic cell line. Uranium release into the environment is a threat to human health, and the mechanisms of cytotoxicity caused by uranium are not well-understood. To improve our understanding in this respect, the authors herein evaluate the effects of

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uranium exposure on normal rat hepatic BRL cells. As revealed by SEM (scanning electron microscopy) and TEM (transmission electron microscope) analyses, uranyl nitrate was found to be transformed into uranyl phosphate particles in the medium and taken up by BRL cells in an endocytotic uptake manner, which presumably initiates apoptosis of the cell, although soluble uranyl ion may also be toxic. The apoptosis of BRL cells upon uranium exposure was also confirmed by both the acridine orange and ethidium bromide double staining assay and the Annexin V/propidium iodide double staining assay. Further studies revealed that uranium induced the loss of mitochondrial membrane potential in a dose-dependent manner. Moreover, the uranium-induced apoptosis was found to be associated with the activation of caspase-3, caspase-8 and caspase-9, indicating both a mitochondria-dependent signaling pathway and a death receptor pathway by a crosstalk. This study provides new chemical and biological insights into the mechanism of uranium toxicity toward hepatic cells, which will help seek approaches for biological remediation of uranium.

2. Experimental Sections

Dioxouranium (VI) (UO_2^{2+}) cation was used as nitrate salts. Albumin human was used as disodium salt. Reaction dioxouranium (VI) UO_2^{2+} ion with human serum albumin was prepared: human albumin with

uranium UO_2^{2+} ion and the X-ray method of investigation of these complexes.

3. Results and Discussion

In work [1] has been studied structural consequences of Binding of UO_2^{2+} to Apotransferrin.

It has been established that transferrin binds a variety of metals. These include toxic uranyl ions which form rather stable uranyl-transferrin derivatives. The authors determined the extent to which the iron binding sites might accommodate the peculiar topographic profile of the uranyl ion and the consequences of its binding on protein conformation. Indeed, metal intake via endocytosis of the transferrin/transferring receptor depends on the adequate coordination of the metal in its site, which controls protein conformation and receptor binding. Using UV-vis and Fourier transform infrared difference spectroscopy coupled to a microdialysis system, the authors showed that at both metal binding sites two tyrosines are uranyl ligands, while histidine does not participate with its coordination sphere. Analysis by circular dichroism and DSC (differential scanning calorimetry) showed major differences between structural changes associated with interactions of iron or uranyl with apotransferrin. Uranyl coordination reduces the level of protein stabilization compared to iron, but this may be simply related to partial lobe closure. The lack of interaction between

Fig. 1 Structural consequences of binding of Fe^{3+} and UO_2^{2+} to Apotransferrin.

uranyl-TF and its receptor was shown by flow cytometry using Alexa 488-labeled holotransferrin. The authors propose a structural model summarizing our conclusion that the uranyl-TF complex adopts an open conformation that is not appropriate for optimal binding to the transferrin receptor.

In work [2] has been studied UO_2^{2+} uptake by proteins. The capture of uranyl, UO_2^{2+} , by a recently engineered protein with high selectivity and femtomolar sensitivity has been examined by a combination of density functional theory, molecular dynamics, and free-energy simulations. It was found that UO_2^{2+} is coordinated to five carboxylate oxygen atoms from four amino acid residues of the SUP (super uranyl binding protein). A network of hydrogen bonds between the amino acid residues coordinated to UO_2^{2+} and residues in its second coordination sphere also affects the protein's uranyl binding affinity. Free-energy simulations show how UO_2^{2+} capture is governed by the nature of the amino acid residues in the binding site, the integrity and strength of the second-sphere hydrogen bond network, and the number of water molecules in the first coordination sphere. Alteration of any of these three factors through mutations generally results in a reduction of the binding free energy of UO_2^{2+} to the aqueous protein as well as of the difference between the binding free energies of UO_2^{2+} and other ions (Ca^{2+} , Cu^{2+} , Mg^{2+} , and Zn^{2+}), a proxy for the protein's selectivity over these ions. The results of the free-energy simulations confirmed the previously reported experimental results and allowed us to discover a mutant of SUP,

specifically the GLU64ASP mutant, that not only binds UO_2^{2+} more strongly than SUP but that is also more selective for UO_2^{2+} over other ions. The predictions from the computations were confirmed experimentally [3-5].

Analysis of the complex albumin human with uranium UO_2^{2+} ion was performed by X-ray microanalysis. Instrument: electron probe microanalyzer. Brand: Superprobe 733, Japan Electron Optics Laboratories, Japan.

The analysis of the elemental composition of the resulting of the microsphere magnetic catalyst with salts of Thorium and Uranium was performed using energy-dispersive spectrometer Energy Oxford Instruments, England, established by electron probe microanalyzer Superprobe 733 at an accelerating voltage of 25 kV and a probe current of 25 nA.

Figs. 2 and 3 show the laboratory unit and X-ray spectrum of the complex albumin human with UO_2^{2+} .

Table 1 shows the elemental composition of the complex albumin human with UO_2^{2+} ion.

Fig. 4 shows IR spectrum of the complex albumin human with UO_2^{2+} .

Thus, the authors obtained a complex of albumin human with uranium UO_2^{2+} ions and IR spectra and X-ray method to explore these complexes.

4. Conclusions

Interaction of dioxouranium (VI) UO_2^{2+} ion with albumin human was obtained a complex of adenosine with uranium UO_2^{2+} ion and X-ray method to explore these complexes.

Fig. 2 Obtain a complex of albumin human with UO_2^{2+} .

Fig. 3 X-ray spectrum of the complex albumin human with UO_2^{2+} .

Table 1 Elemental composition of the complex albumin human with UO_2^{2+} .

Compound	C	H	O	N	S	P	U
Unit, %	33.06	0.02	22.04	19.28	0.08	0.42	0.36

Fig. 4 IR spectrum of the complex albumin human with UO_2^{2+} .

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