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SEPARATION OF PROTEINS IN MOLLUSC SHELLS BY GEL-FILTRATION

Proteins and glycoproteins are involved in biological mineralization processes. For example, collagens in bone structures of vertebrates promote the formation of apatite seeds<sup>1/</sup>, whereas glycoproteins in the exoskeleton of crabs provide a set of highly specific templates for calcite nucleation<sup>2/</sup>. In molluscs, a wide array of structurally different proteins are contained in the shell structures, attesting to the heterogeneity of calcified tissues<sup>3/</sup>.

It has been suggested that independent of the kind of protein participating in crystal-seed formation, the most essential factor, in nucleating a mineral phase appears to be the availability of free carboxyl groups provided by certain acidic amino acids and free amino groups by certain basic amino acids and hexosamines<sup>1-4/</sup>. It is thus inferred that throughout the animal kingdom, Nature adheres to the same principles when it comes to the formation of mineral nuclei.

To test this assumption, mollusc shell tissues of widely different biochemical composition and phylogeny have been studied by means of enzymatic and non-enzymatic degradation techniques and by gel-filtration. Tryptic digests did not result in the dissolution of shell matrix proteins but treatments with urea, hydroxylamine and formic acid degraded the tissues. According to preliminary studies, the hydroxylamine treatment resulted in a cleavage of the protein molecule to units of molecular weight of approximately 20,000 to 80,000<sup>4/</sup>.

The analytical scheme followed during the present investigation is outlined in Figure 1. The decalcified organic tissue was treated with a

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hydroxylamine/6 M Urea solution for 24 hours at 45°C and subsequently with 95% formic acid for 4 hours at 45°C. Each treatment was followed by centrifugation and by gel-filtration of the supernatant, on G-25 Sephadex columns.

A variety of buffer systems were tested and the molality of the buffers (0.1 to 1) did not play a significant role in the efficiency of separation. Although some buffer systems proved to be slightly better than the routinely used borax buffer of pH 9 (hydroxylamine/urea fraction) and formic acid buffer of pH 3.0 (formic acid fraction) the two latter ones interfered least with the subsequent amino acid analysis. The high-molecular fractions (M.W.>5.000) were hydrolyzed and examined for their amino acid composition<sup>4/</sup>. To facilitate a comparison, the amino acid analysis of the original samples and the residues are included in Table 1.

The analytical data indicate that throughout the molluscan phylum the urea/hydroxylamine fraction is consistently enriched in aspartic acid, lysine and amino sugars although this relationship is not necessarily displayed when these three amino compounds are highly concentrated in the original shell. It is tentatively suggested that this peptide fraction contains the active sites for the deposition of the mineral phase and that the remaining part of the proteinaceous matrix in the shells is not involved in the actual calcification. It is reasonable to assume that similar structures are contained in other mineralized tissues such as are found in bones or teeth. A full account on the phylogenetic and chemical aspects of these experiments will be presented elsewhere, together with several hundred amino acid analyses from calcified and uncalcified proteins<sup>5/</sup>.

E. T. Degens, B. W. Johannesson and R. W. Meyer

Department of Chemistry

Woods Hole Oceanographic Institution

Woods Hole, Massachusetts, U.S.A.

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Figure 1 Flow diagram of analytical procedures

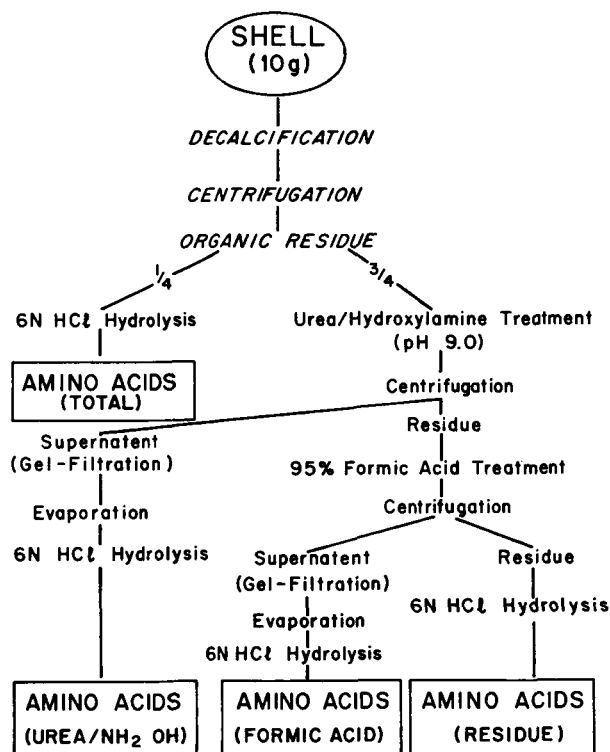


TABLE 1 A

## AMINO ACID COMPOSITION OF MOLLUSC SHELL PROTEINS AND ISOLATED PEPTIDE/PROTEIN FRACTIONS - (IN RESIDUES PER 1000)

	CRYPTOCHITON			NAUTILUS			HALIOTIS			ACHATINELLA		
	TOTAL NH <sub>2</sub> OH	FORMIC ACID	RESIDUE	TOTAL NH <sub>2</sub> OH	FORMIC ACID	RESIDUE	TOTAL NH <sub>2</sub> OH	FORMIC ACID	RESIDUE	TOTAL NH <sub>2</sub> OH	FORMIC ACID	RESIDUE
*	(2)	(1)	(2)	(3)	(1)	(2)	(3)	(1)	(2)	(4)	(1)	(2)
ASPARTIC ACID	117	118	118	85	70	89	186	160	70	64	185	36
THREONINE	58	62	71	19	23	38	43	32	23	23	53	12
SERINE	75	49	77	113	109	55	101	144	159	35	79	53
GLUTAMIC ACID	103	103	111	52	59	56	50	32	72	42	131	27
PROLINE	105	136	120	10	5	53	36	37	9	61	52	63
GLYCINE	128	122	139	296	255	270	212	350	135	365	156	417
ALANINE	100	75	86	223	248	69	163	63	252	40	86	53
CYSTINE	19	12	25	9	7	21	3	-	12	3	1	18
VALINE	50	51	65	16	20	23	22	21	35	69	53	92
METHIONINE	16	15	25	5	5	1	4	2	1	5	3	1
ISOLEUCINE	31	33	30	15	18	16	12	12	13	58	32	63
LEUCINE	52	46	68	27	27	24	29	27	26	99	68	75
TYROSINE	23	19	16	13	9	38	20	6	12	13	10	14
PHENYLALANINE	39	38	29	59	61	58	31	29	69	64	36	59
OH-LYSINE	-	-	-	1	1	1	1	1	1	-	-	-
LYSINE	24	28	16	3	4	28	19	45	21	41	51	12
HISTIDINE	6	18	14	3	2	14	3	1	1	3	2	2
ARGININE	54	75	34	51	77	22	65	38	104	15	2	3
PROTEIN												
HEXOSAMINES	1.11	7.12	0.87	121	661	43	33	35	36	92	67	302
PER CENT PROTEIN IN TOTAL SHELL	2.87			2.24			1.12			0.68		

\* Number in parentheses indicate the number of individual analyses.

TABLE 1 B

## AMINO ACID COMPOSITION OF MOLLUSC SHELL PROTEINS AND ISOLATED PEPTIDE/PROTEIN FRACTIONS - (IN RESIDUES PER 1000)

	MYTILUS		AEQUIPECTEN		MERCENARIA		LAEVICARDIUM	
	TOTAL UREA/ NH <sub>2</sub> OH	FORMIC ACID	TOTAL UREA/ NH <sub>2</sub> OH	FORMIC ACID	TOTAL UREA/ NH <sub>2</sub> OH	FORMIC ACID	TOTAL UREA/ NH <sub>2</sub> OH	FORMIC ACID
	(2)	(1)	(4)	(1)	(4)	(1)	(4)	(1)
	(5)	(2)	(4)	(1)	(4)	(1)	(4)	(1)
ASPARTIC ACID	95	159	296	340	148	196	125	141
THREONINE	19	56	36	15	47	54	57	28
SERINE	93	86	186	218	75	102	58	127
GLUTAMIC ACID	36	84	59	57	71	84	90	53
PROLINE	20	82	23	21	128	91	87	66
GLYCINE	357	226	214	211	146	103	195	227
ALANINE	183	84	62	44	70	57	68	81
CYSTINE	13	13	12	9	21	24	90	97
VALINE	27	36	18	15	32	35	56	16
METHIONINE	7	9	6	1	14	12	25	1
ISOLEUCINE	15	24	12	8	24	22	31	6
LEUCINE	49	52	25	19	35	35	44	54
TYROSINE	34	13	5	4	42	41	17	15
PHENYLALANINE	15	16	8	6	33	29	20	29
OH - LYSINE			1	1				
LYSINE	14	46	26	23	68	69	24	31
HISTIDINE	4	2	3	5	5	22	5	16
ARGININE	19	12	8	3	41	24	10	12
PROTEIN								
HEXOSAMINES	394	37	856	61	102	45	179	48
PERCENT PROTEIN IN TOTAL SHELL	0.91		0.25		0.28		0.54	
				n.d.			128	250

\* Number in parentheses indicate the number of individual analyses.