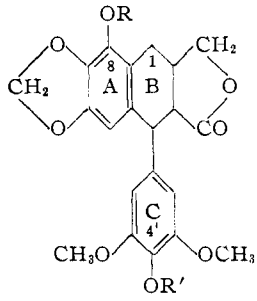
The results of our analysis of the degradation-reactions and of the methylation indicate that the new glucoside has the structure 8-O(-β-D-glucopyranosyl)-α-peltatin (Ia).



Ia, α-peltatin-β-D-glucoside (R = glucose residue, R′ = H)
Ib, α-peltatin (R = R′ = H)
II, β-peltatin-β-D-glucoside (R = glucose residue, R′ = CH_3)

The three lignane compounds occurring in the resin fraction of the American plant *Podophyllum peltatum L., viz.*, podophyllotoxin, β-peltatin and α-peltatin, are thus also present in the form of glucosides. The glucoside described here also exhibits antimitotic activity. Details of the isolation and properties will be published shortly in *Helvetica Chimica Acta*.

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STUDIES ON ADRENOCORTICOTROPIN. XI. A PRELIMINARY COMPARISON OF CORTICOTROPIN-A WITH β-CORTICOTROPIN

Sir:

The recent publication[1] of a tentative structure for β-corticotropin, prompts us to report the status of our work on corticotropin-A. Since the two materials are from the same source but isolated by different techniques, it will be of interest to determine the differences, if any, between them.

In previous publications we have shown the first nine positions at the amino end,[2] and the last eleven positions at the carboxyl end[3] of corticotropin-A. These sequences are identical with those published by the Cyanamid group for β-ACTH. Additionally, in our publication on the carboxyl end, we proposed tentatively a further sequence of seven amino acids. This sequence, with the addition of a residue of tyrosine,[4] we now believe to be correct. The corrected sequence is shown in Table I, positions 21–28. Although the Cyanamid

(1) P. H. Bell, THIS JOURNAL, **76**, 5565 (1954).
(2) W. F. White and W. A. Landmann, *ibid.*, **77**, 771 (1955).
(3) W. F. White, *ibid.*, **76**, 4194 (1954).
(4) In our early work tyrosine (and methionine) was destroyed during acid hydrolysis of fractions isolated by paper chromatography. In later work this difficulty was eliminated by carefully washing the paper with dilute formic acid before use.

TABLE I

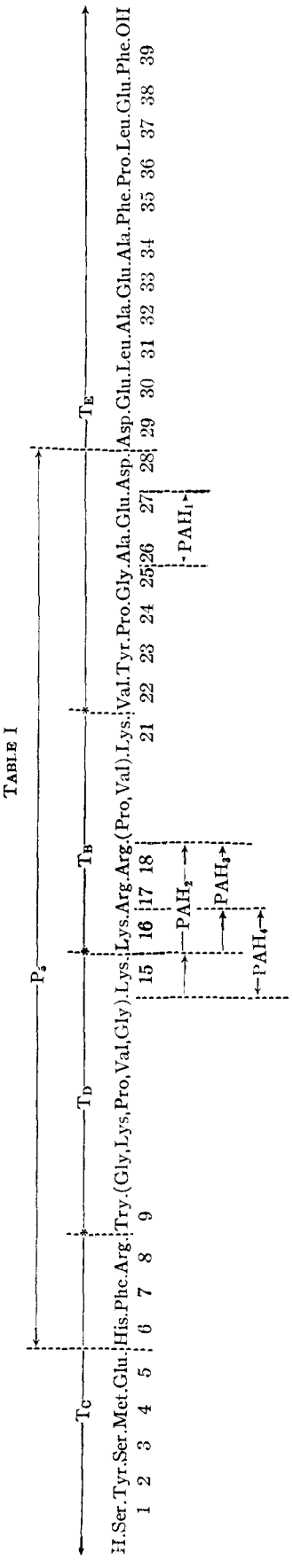

TABLE II

Peptide No.	Rf Part.[a]	Rf 2-But.-NH3[b]	Rf W & W[c]	Iono-graphy dist., cm.[d]	Amino Acids on Complete Acid Hydrolysis[e]	N-Terminal Determination	C-Terminal Determination	Structure
PAH_1	0.34	Glu	...	−6.0	Ala,Glu	DNFB: Ala	...	Ala.Glu
T_D	.26	Tyr	...	...	Gly_2Lys_2Pro,Val	Aminopeptidase[f]: Try	Carboxypeptidase: Lys	Try(Gly_2Lys,Pro,Val)Lys
T_B	.05–.10	Zero	0.85xLys	...	Lys_2Arg_2Pro,Val	Aminopeptidase: Lys,Arg_2	Carboxypeptidase: Lys	(Lys,Arg,Arg)(Pro,Val)Lys
PAH_2	.05	Zero	.66xLys	...	Lys,Arg	DNFB: Both bis-DNP-Lys and ε-DNP-Lys	...	Lys(Lys,Arg,Arg)
PAH_3	.03	Glu-	.57xLys	...	Lys_2Arg	DNFB: Both bis-DNP-Lys and ε-DNP-Lys	...	Lys (Lys,Arg)
PAH_4	.05	Glu	.75xLys	...	Lys	DNFB: Both bis-DNP-Lys and ε-DNP-Lys	...	Lys.Lys

[a] *n*-Butanol–water–acetic acid (4:5:1). [b] 2-Butanol–ammonia (3:1). The R_f's are given in terms of the nearest amino acid. [c] *n*-Butanol–acetic acid–water–pyridine (30:6:24:20), S. G. Waley and J. Watson, *Biochem. J.*, **55**, 328 (1953). Since the system is used in an extended run, the R_f's are given with reference to the R_f of lysine. [d] 20 hours at 100 volts on Whatman 3 paper in 0.1 *N* ammonium acetate buffer (*p*H 6.6). As reference, glutamic acid moved −9.4 cm. [e] The subscripts indicate the number of residues of the amino acid as shown by quantitative measurement. [f] Aminopeptidase preparation made according to E. L. Smith, *J. Biol. Chem.*, **153**, 627 (1944).

group has indicated an area of uncertainty in this region, there is an obvious difference in the two structures involving, in its simplest terms, an interposition of a glycine and an alanine residue.

Our evidence for the sequence in this region is primarily from the stepwise hydantoin reaction. Application of a modification of the Edman procedure[5] to the long chain C-terminal tryptic peptide (T_E, Table I) gave the sequence as shown from position 22 to 28. Further confirmation of part of the sequence was obtained by the isolation of the dipeptide Ala.Glu (PAH_1, Tables I and II) from the products of partial acid hydrolysis of peptide P_5.[6]

In attempting to close the gap between the two ends of corticotropin-A, we have concentrated on a study of the products of tryptic digestion. In addition to the N-terminal octapeptide (T_C, Table I) and the long-chain C-terminal fragment (T_E), our chromatograms of the tryptic digests show only two other prominent fragments. These, with their chemical and enzymatic characteristics, are shown in Table II. Since tryptophan had previously[7] been shown to occur in an Arg.Try sequence, fragment T_D obviously fitted next to T_C, leaving T_B to fill the final gap between T_D and T_E. Because of the possibility of transpeptidation during the tryptic digestion, we sought confirmation of the multiple basic amino acid sequence. Three peptides which were isolated from the products of partial acid hydrolysis, as shown in Table I (PAH_2, PAH_3, PAH_4), provided the desired overlap.

Thus it appears that the backbones of corticotropin-A and β-ACTH are very similar, with only the seven uncertain residues in our structure and the three uncertain ones in β-ACTH as possible differences. A further point of difference rests in the amide linkages. β-ACTH has been shown to possess only one such linkage, on the Glu residue located ten positions from the carboxyl end. We have not yet made a systematic investigation of the amide linkages in corticotropin-A, but with the procedures used to date, no evidence has been obtained that any of the acidic residues is in the amide form.

The central line of Table I shows the sequence of corticotropin-A as we know it at the present time. The fragments referred to for the first time in this paper are indicated by the dotted lines and arrows.

Acknowledgment.—The authors wish to acknowledge the technical assistance of Mr. A. M. Gross.

(5) W. A. Landmann, M. P. Drake and J. Dillaha, THIS JOURNAL, **75**, 3638 (1953). The authors also wish to acknowledge help from unpublished manuscripts made available by Dr. J. I. Harris, The Carlsberg Labs., Copenhagen, Denmark.

(6) This fragment is formed by 24-hour peptic digestion of corticotropin-A. By this treatment five amino acid residues are split off the amino end and eleven off the carboxyl end. The remaining portion of the molecule (P_5) is separated from the smaller fragments by means of its immobility in the two chromatographic solvent systems used throughout our work (*cf.* ref. 2).

(7) W. F. White and W. A. Landmann, THIS JOURNAL, **76**, 4193 (1954).

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RECEIVED FEBRUARY 4, 1955

BOOK REVIEWS

The Elementary Chemical Composition of Marine Organisms. By A. P. VINOGRADOV, Vernadsky Laboratory for Geochemical Problems, Moscow, U.S.S.R. Translated from Vinogradov's original Russian by Julia Efron and Jane K. Setlow, with bibliography edited and newly enlarged by Virginia W. Odum, for the Survey of Existing Knowledge of Biogeochemistry, American Museum of Natural History, Sears Foundation for Marine Research, Yale University, New Haven, Connecticut. 1953. xiv + 647 pp., 370 tables. 24.5 × 31.5 cm. Price, $17.00.

It is quite natural that sooner or later someone would bring together and evaluate the vast number of elemental analyses of living things that, for more than a century and a half, have preoccupied chemists and biologists working at the simplest contact of their two sciences. To the biogeochemist such a compilation has now become a necessity, and it is the great merit of Professor Vinogradov's compendium that it summarizes and tabulates most of what has been written on the elemental composition of living matter, threading the whole together with a discerning discussion.

The aim of Vinogradov's enquiry is ultimately to provide insight to the geochemical roles of living matter, and the primary data sought are precise determinations of the elementary compositions of organisms living in the sea. It is regrettable, from Vinogradov's point of view, that relatively few analyses have been made of whole organisms. Even where this has been done, relatively few elements have been investigated in any single research. Indeed an analysis of a plant, for example, is quite generally viewed as "complete" if it includes some 9 or 10 elements; comparable analyses of animals are ordinarily still less inclusive. However there seems no lack of limited elemental analyses of the parts of organisms, and it is chiefly from these that Vinogradov has drawn this first comprehensive account of the elemental composition of marine life. This account is necessarily very approximate, for many of the data are old (perhaps a third having been collected before 1900), there is scant attention to measures of the reliability of chemical determinations, and for the most part potentially significant biological variables, such as age, sex, symbiont associations, season of capture, and so on, remain unassessed. Vinogradov is of course acutely conscious of all this, and his book may be expected to prove a marked influence in bringing about an over-all improvement in research of this sort.

Following a brief introduction that comments on the history of the subject, on the nature of the analytical data, and on the elemental composition of sea water and of living matter, there are 18 chapters that survey the elementary composition of particular marine organisms. Each chapter is devoted to a more or less coherent taxonomic assemblage of organisms; collectively they deal with flowering plants, algae, bacteria, protozoa, most kinds of invertebrate animals and fish. These chapters are topically subdivided to the degree that analytical information or knowledge of special biological aspects warrants, and for this reason they are of very unequal length. Thus, of the 586 pages of text and tables, nearly 60% is devoted to algae (139 pp.), molluscs (104 pp.) and fish (105 pp.). Four other chapters dis-