Correction of the amino acid sequences of erabutoxins from the venom of the sea snake *Laticauda semifasciata*

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The amino acid sequences of erabutoxins a and b were reinvestigated. The previously reported sequences of Gln-His at positions 6 and 7, and of Pro-Ser at positions 18 and 19 of erabutoxins a and b were corrected to His-Gln and Ser-Pro respectively.

Erabutoxins a, b and c (Ea, Eb and Ec) are neurotoxic proteins, isolated and crystallized by Tamiya & Arai (1966) and by Tamiya & Abe (1972) from the venom of a sea snake, *Laticauda semifasciata*. The amino acid sequences of Ea, Eb and Ec were reported by Sato & Tamiya (1971) and

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by Tamiya & Abe (1972), and correction of the partial sequence was made by Maeda & Tamiya (1977). The X-ray analysis of the molecular structures of crystalline erabutoxins was reported by Low *et al.* (1976), by Tsernoglou & Petsko (1976, 1977) and by Kimball *et al.* (1979). However, there are some inconsistencies concerning the state of histidine-7. On the basis of the X-ray model, which

Fig. 1. Amino acid sequences of erabutoxins a and b

Peptides are shown by named bars (e.g. T_{3Ea}). Symbols used are as follows: →, residue detected by Edman degradation; ←, residue released by carboxypeptidase Y digestion; =, residue confirmed by the amino acid analysis without hydrolysis after the removal of preceding residues by Edman degradation. The one-letter notation for amino acids is given in *Biochem. J.* (1969) 113, 1–4.

follows the sequence data, histidine-7 is exposed to the solvent, whereas the chemical-modification (Sato & Tamiya, 1970) and n.m.r.-spectroscopy (Inagaki *et al.*, 1978, 1981) showed that histidine-7 is buried in the molecule in aqueous solution. We therefore reinvestigated the amino acid sequences of erabutoxins a and b.

Results and discussion

The amino acid composition of the tryptic peptides from reduced and *S*-carboxymethylated Ea and Eb are in agreement with those reported by Sato & Tamiya (1971) and named accordingly. The results of sequence analysis are summarized in Fig. 1.

The sixth and seventh residues of peptide T_{2b}-T₅ from Ea were identified as histidine and glutamine respectively by t.l.c. and by the amino acid analysis after the back-hydrolysis of amino acid phenylthiohydantoin derivatives. The results were also confirmed by direct Edman degradation of reduced and *S*-carboxymethylated Ea. The third and fourth residues of peptide T_{3Ea} were identified as serine and proline respectively.

The sequence analysis of peptide T_{3Eb} confirmed the same *N*-terminal sequence as that of peptide T_{3Ea}.

These results indicate that the amino acid residues at positions 6 and 7, and 18 and 19, of erabutoxins a and b are histidine and glutamine, and serine and proline, respectively (Fig. 1).

The primary structure of the corresponding parts of erabutoxin c was deduced to be the same by homology. Its sequence must therefore also be corrected.

The same sequence correction was also confirmed by the refinement of the X-ray analysis of erabutoxin b crystals (Low *et al.*, 1984).

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