

Isolation and structures of peptide hormones from the silkworm *Bombyx mori*: bombyxins – peptides structurally related to insulin

Akinori SUZUKI, Hiromichi NAGASAWA and Hironori ISHIZAKI*

Department of Agricultural Chemistry, University of Tokyo, Tokyo 113, JAPAN

*Faculty of Science, Nagoya University, Nagoya 464, JAPAN

Abstract - Bombyxins have been isolated from the heads silkworm, *Bombyx mori*, and stimulate the adult formation of the debrained pupae of *Samia cynthia ricini*. The amino acid sequence of bombyxins has suggested that bombyxins are the first insulin-related peptides isolated from the invertebrate animal.

INTRODUCTION

In 1917, Kopec first described the endocrinological function of insect brain in the metamorphosis. Until early-1950's, the role of a brain hormone, prothoracicotrophic hormone (PTTH), in the insect metamorphosis had been established. In 1958, Kobayashi and Kirimura reported that the adult formation of brainless pupae of *Bombyx mori* was ocured by injecting the brain extract of *Bombyx* pupae. Soon after that, Ichikawa and Ishizaki showed that the extract of *Bombyx* pupal brains provoked the adult formation of the brainless dormant pupae of *Samia cynthia ricini* and that the active principle should be proteinic. In early-1970's, we have started colaborating to isolate PTTH active to the brainless *Samia* pupae (ref. 1). Starting with large amounts of the silkworm heads, we have succeeded in isolating PTTH active to *Samia* pupae in 1982 (ref. 2). In the course of purification of PTTH, we have confirmed that the extract of *Bombyx* heads contains two species-specific PTTHs, one (temporarily termed 22k-PTTH) is active to the brainless *Bombyx* pupae and other (recently termed bombyxin) active to the debrained *Samia* pupae (ref. 3). Recently, we have isolated three molecular species of bombyxins, bombyxin-I, -II and -III, and determined the whole amino acid sequence of bombyxin-II, which is suggested to be the first insulin-related peptide isolated from the invertebrate animal (ref. 4 and 5).

ISOLATION AND CHARACTERIZATION

For purification of bombyxins, the bioassay was made by using the brainless dormant pupae of *S. cynthia ricini* and the titers of bombyxins were quantified by *Samia* unit; one *Samia* unit was defined as the minimal dose of bombyxins necessary to cause the adult formation in an assay pupa (ref. 1). The starting materials for extracting bombyxins were the adult heads of *B. mori*, which were easily collected in large amounts by a simple operation cutting the heads with a razor blade.

The purification procedure is summerized in Fig. 1 (ref. 6). The first 8 steps consisted of simple precipitations, by which we could overcome the disadvantage of using the whole heads of *Bombyx* adults as starting materials in stead of the brains, and from step 9 to 14 the conventional chromatographieere used. The final step was a reversed phase high performance liquid chromatography (HPLC) using Partisil ODS-3 column to afford the isolation of bombyxin-I. Bombyxin-II and -III were also isolated by a reversed phase HPLC using Develosil ODS-5 column. The yields of bombyxin-I, -II and -III were 50, 36 and 63 ug, respectively, from about 650,000 *Bombyx* adult heads and each bombyxin was active to a brainless *Samia* pupa at a dose of 0.1 to 0.4 ng (0.1 to 0.4 ng/*Samia* unit). Then, the overall purification was about 1.7×10^6 fold. When 5 to 500 pg of bombyxin was added to 100 ul of the culture medium of a prothoracic gland taken out freshly ecdysed *Samia* pupa, the ecdyson release from the prothoracic gland was markedly increased, three times as much as that of control.

Bombyxins were suggested to be heterodimeric peptides connected by disulfide bonds with molecular weight of 4 to 5 kDa. The amino terminal amino acid sequences of bombyxins were determined by a gas phase protein sequencer and cystein residues were confirmed through sequencing the S-carboxamide methyl derivatives, indicating the homology in these bombyxins.

The replacement of amino acid residues in these bombyxins occurs in such a way that the hydrophylic and hydrophobic nature of amino acid residues is retained at their respective positions and the biological function of bombyxins can tolerate these amino acid substitution, because three bombyxins show almost same level of biological activity (ref. 4).

- 648,000 Male adult Bombyx heads (fw. 4.86 kg)
1. Acetone powder
 2. Washing with 80% ethanol
 3. Extraction with 2% saline
 4. Heat treatment
 5. Ppt. with 80% satd. ammonium sulfate
 6. Ppt. with 50-75% acetone
 7. ppt. with 90% satd. picric acid
 8. Ppt. with 80% acetone
 9. Sephadex G-50 (fine)
 10. DEAE-Sepharose CL-6B (stepwise)
 11. SP-Sephadex C-25 (stepwise)
 12. Sephadex G-50 (superfine)
 13. DEAE-Sepharose CL-6B (gradient)
 14. Sephadex G-50 (superfine)
 15. Reversed phase HPLC (gradient)
- Bombyxin-I (50 ug)
 Bombyxin-II (36 ug)
 Bombyxin-III (63 ug)

Fig. 1 Purification procedure of bombyxin-I, -II and -III

	1	10	20
Bombyxin-I	G V V D E C C F R P C T L D V L L S Y C		
Bombyxin-II	G I V D E C C L R P C S V D V L L S Y C		
Bombyxin-III	G V V D E C C L Q P C T ? D V V A T Y C		

Fig. 2 Amino terminal amino acid sequences of bombyxin-I, -II and -III

AMINO ACID SEQUENCE OF BOMBYXIN-II

Bombyxin-II was reductively alkylated to yield the carboxamide methyl derivative, which was separated into two peptides, A and B chain peptides, by HPLC, indicating that bombyxin-II was a heterodimeric peptide, in which A and B chains were connected with disulfide bonds. The amino acid sequences of A and B chain peptides were determined by the combination of enzymatic digestion with trypsin, α -chymotrypsin and pyroglutaminase, and sequencing the resulted fragmental peptides (ref. 5). The carboxyl terminal amino acid sequences of both peptides were confirmed by the results of carboxypeptidase A digestion.

A chain

	1	10	20
Human insulin	G I V E Q C C T S I C S L Y E L E N Y C N		
Bombyxin-II	G I V D E C C L R P C S V D V L L S Y C		

B chain

	1	10	20
Human insulin	F Y N Q H L C G S H L V E A L Y L V C G E R		
Bombyxin-II	X Q P Q A V H T Y C G R H L A R T L A D L C W E A		

X: pyroglutamic acid

G F F Y T P K T
G V D

Fig. 3 Amino acid sequences of bombyxin-II and human insulin

To determine the mode of disulfide bonds, bombyxin-II was digested with thermolysin to give five fragments, Th1 - 5. Since Th4 and 5 contained only one disulfide bond, the disulfide bond, A₂₀- B₂₂, was unequivocally established. Because Th3 contained two disulfide bonds, there were three possible structures, (a), (b) and (c), for Th3. All of these three peptides were synthesized and compared with Th3 by HPLC, indicating that Th3 was coeluted with peptide (b). Thus the disulfide bonds were established to be A₆ - A₁₁ and A₇ - B₁₀ and the whole amino acid sequence of bombyxin-II was determined along with the mode of three disulfide bonds, which was exactly the same as that of insulin (ref. 7).

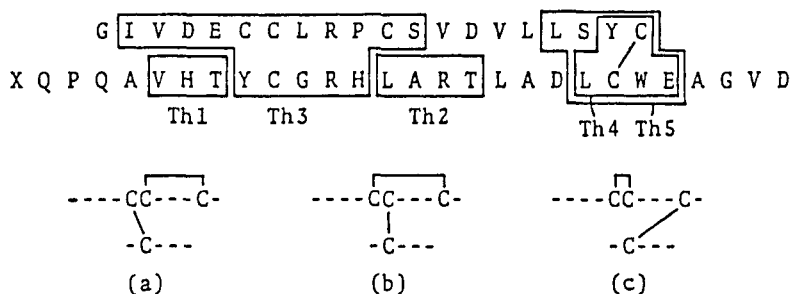


Fig. 4 Thermolysin digestion of bombyxin-II and possible structures for the fragmental peptide, Th3

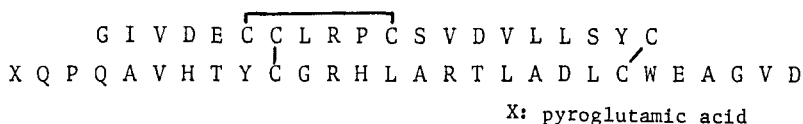


Fig. 5 The whole amino acid sequence of bombyxin-II

The synthesis of bombyxin-II was attempted to confirm its amino acid sequence. The protected A and B chain peptides were synthesized by a peptide synthesizer of Applied Biosystems. After deblocking, the free A and B chain peptides were combined, reduced with dithiothreitol and reoxidized with air to afford bombyxin-II in a yield of 4%. The peptide maps of the thermolysin digests of the natural and synthetic bombyxin-II were completely identical. Further the synthetic bombyxin-II showed almost the same activity to the assay pupae as the natural one. Thus the amino acid sequence of bombyxin-II was synthetically confirmed (ref. 7).

BOMBYXINS BELONG TO INSULIN FAMILY PEPTIDES

The most striking feature of bombyxins is the homology with insulin; the homology in A chain is approximately 50% and that of B chain about 40%. In addition, the mode of three disulfide bonds are completely identical with each other and the hydrophobic core residues in bombyxin-II, A₂ (Ile), A₁₆ (Leu), B₁₄ (Leu) and B₁₈ (Leu), are also identical with those of insulin. The glycine residues, which may contribute to the fold of peptide chains, at A₁, B₁₁ and B₂₆ in bombyxin-II is homologous with those of insulin. Based upon these facts, a three dimensional model of bombyxin-II has been constructed using computer graphics, showing that bombyxin-II can assume an insulin-like tertiary structure (ref. 8). Recently the gene coding a bombyxin has been cloned using a *Bombyx* gene library and synthetic DNA probe and the DNA sequence of the bombyxin gene indicates that bombyxin are bio-synthesized in the form of prepropeptide followed by post-translational processing (ref. 9). Thus bombyxins can be considered to be a member of the insulin family peptides. In spite of considerable homology, insulin was inactive to the adult formation of brainless *Samia* pupa even at a dose of 1 ug, 10⁴ times as much as the minimal active dose of bombyxins, and bombyxins failed to react with guinea pig antibody of porcine insulin. Bombyxins and insulin family peptides might have arisen from a common ancestral gene, which must be considerably conserved during the evolution to insects and mammals with different functions. From this view point, it is worthy of note that the presence of the gene coding an insulin-related peptide in Molluscan, termed molluscan insulin-related peptide (MIP) has recently been reported irrespective of the biological functions (ref. 10).

Acknowledgements

Authors wish to thank Emeritus Professor Saburo TAMURA, The University of Tokyo, for his unfailing encouragement. This work was partly supported by grants from the Ministry of Education, Science and Culture of Japan.

REFERENCES

1. H. Ishizaki and A. Suzuki, 'Neurohormonal Techniques in Insects', ed. T. A. Miller, pp244-276, Springer-Verlag, New York (1980).
2. A. Suzuki, H. Nagasawa, H. Kataoka, Y. Hori, A. Isogai, S. Tamura, F. Guo, X. Zhong, H. Ishizaki, M. Fujishita and A. Mizoguchi, Agric. Biol. Chem., **46**, 1107-1109 (1982).
3. H. Ishizaki, A. Mizoguchi, M. Fujishita, A. Suzuki, T. Moriya, H. Ooka, H. Kataoka, A. Isogai, H. Nagasawa, S. Tamura and A. Suzuki, Devel. Growth and Differ., **25**, 593-600 (1983).
4. H. Nagasawa, H. Kataoka, A. Isogai, S. Tamura, A. Suzuki, H. Ishizaki, A. Mizoguchi, Y. Fujishita and A. Suzuki, Science, **226**, 1344-1345 (1984).
5. H. Nagasawa, H. Kataoka, A. Isogai, S. Tamura, A. Suzuki, A. Mizoguchi, Y. Fujiwara, A. Suzuki, S. Y. Takahashi and H. Ishizaki, Proc. Natl. Acad. Sci., USA, **83**, 5840-5843 (1986).
6. H. Nagasawa, H. Kataoka, Y. Hori, A. Isogai, S. Tamura, A. Suzuki, F. Guo, X. Zhong, A. Mizoguchi, M. Fujishita, S. Y. Takahasghi, E. Ohnishi and H. Ishizaki, Gen. Comp. Endocrinol., **53**, 143-152 (1984).
7. H. Nagasawa, K. Maruyama, B. Sato, H. Hietter, H. Kataoka, A. Isogai, S. Tamura, H. Ishizaki, T. Semba and A. Suzuki, 'Peptide Chemistry 1987', ed. T. Shiba and S. Sakakibara, pp123-126, Protein Research Foundation, Osaka (1988).
8. H. Jhoti, A. N. McLeod, T. L. Blundell, H. Ishizaki, H. Nagasawa and A. Suzuki, FEBS Letters, **219**, 419-425 (1987).
9. M. Iwami, et al., in preparation.
10. A. B. Smit, E. V. Vreugdenhil, R. H. M. Ebberink, W. P. M. Geraerts, J. Klotwijkstra, and J. Joosse, Nature, **331**, 535-538 (1988).