Physicochemical and Functional Properties of Proteins from Prawns (*Metapenaeus dobsoni*)

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Physicochemical and functional properties such as water and fat absorption capacity, foam capacity and stability, and emulsion capacity and stability of proteins from prawn (*Metapenaeus dobsoni*) and composition of meat were investigated. The sedimentation velocity pattern indicated four protein components with $s_{20,w}$ values of 6S (60%), 11S (25%), 14S (10%), and 20S (5%). Gel filtration profile and polyacrylamide gel electrophoresis under native conditions indicated four components. The emission maximum of fluorescence spectrum and the reduced viscosities were 335 nm and 0.4 dL/g, respectively.

INTRODUCTION

Among seafoods, prawns and shrimp are delicacies that contribute about 20% by volume of the world seafood market. Seafoods in general and prawns and shrimps in particular are highly perishable because of their high moisture content, their low connective tissue content, and their high free amino acid content. As a result of alteration in the properties of proteins of fish during frozen storage, textural changes in the muscle occur (Dyer, 1951; Sikorski et al., 1976; Matsumoto, 1979; Jiang and Lee, 1985).

The ability of muscle to retain tissue water or added water and to form emulsion can be attributed to myofibrillar proteins (Hamm, 1986). The economic problem of weight loss during freezing, subsequent storage, and thawing or cooking of meat is related to the water-holding capacity of the muscle.

Though much information is available on the physicochemical and functional properties of proteins of different species of fish, little information is available relative to proteins from prawns. The preservation of prawns, especially that of freshwater prawns (*Macrobrachium rosenbergi*), either by ice or by modified atmosphere or pretreatments, has received some attention (Angel et al., 1985; Passy et al., 1983). The role of myofibrils and enzymic action of muscle of fresh prawns during ice storage has been documented (Papadopoulos et al., 1989; Nip et al., 1985).

Some attempts have been made to understand the physicochemical properties of prawn proteins (Godavaribai et al., 1987). The importance of proteins in storage stability and processing necessitates a deeper understanding of the nature of proteins in prawns.

In the present study, the proteins from prawns (*Metapenaeus dobsoni*) were extracted and the physicochemical and functional properties were evaluated with a view to correlate the properties.

MATERIALS AND METHODS

Sodium chloride and phosphate buffer salts (monobasic and dibasic) were obtained from Sarabhai M. Chemicals; acrylamide, bis(acrylamide), sodium dodecyl sulfate, amido black 10 B, *N*-bromosuccinimide, myosin from chicken muscle, bovine serum albumin, ovalbumin, and lysozyme were obtained from Sigma Chemical Co. Sepharose 4B gel was procured from Pharmacia Fine Chemicals, and *cis*-parinaric acid was obtained from Molecular Probes. Denatured hemoglobin substrate powder was obtained from Worthington Biochemicals, ammonium sulfate, ammonium persulfate, and glycine were procured from E. Merck (India) Ltd., and acetic acid and acetone were from BDH. Spray-dried egg powder was obtained from Animal Products Technology Department, Central Food Technological Research Institute, Mysore, India, and refined groundnut oil of Postman brand was obtained from M/s. Ahmed Oil Mills, Bombay.

Fresh prawns (*M. dobsoni*) caught off the Mangalore coast of India were procured on board and iced immediately in the ratio of 1:1 by weight in a plastic container. The containers were brought to the laboratory within 3 h and re-iced till prawns were peeled and deveined.

Proximate Composition. Moisture, fat, and ash were estimated according to the procedures of the AOAC (1984). Carbohydrate content was determined by the phenol–sulfuric acid method (Montogomery, 1961). All of the experiments were done in triplicate, and the average values are reported. For each trial of proximate analysis about 35 prawns were taken, peeled and deveined. After maceration by pestle and mortar, required quantities were taken for proximate composition analysis. Crude protein in the prawn meat was according to the Kjeldahl method using a Buchi digestion apparatus fitted with an infrared heating system. A factor of 6.25 was used to convert nitrogen to protein.

Nonprotein Nitrogen in Meat. Nonproteinous nitrogen in meat was estimated by the trichloroacetic acid precipitation method (Velankar and Govindan, 1958). To 3.0 g of macerated prawn meat was added 50 mL of 10% trichloroacetic acid (TCA); the mixture was macerated well in a pestle and mortar and allowed to stand for 30 min in refrigerator at 4 °C. The slurry was filtered through Whatman No. 1 filter paper, and nitrogen content in the filtrate was etimated by the Kjeldahl method.

Extraction of Protein from Prawn. Proteins from fresh or frozen or freeze-dried prawns were extracted with phosphate buffer (pH 7.8, 0.03 M) containing 1 M sodium chloride. This buffer will be referred to herein as extraction buffer (EB). The ratio of prawn meat to buffer was 1:7. Homogenization was carried out at 4 °C in Virtis homogenizer Model 60K, fitted with a variable-speed regulator and a macroshaft with four blades. Homogenization was done at 5000 rpm for 2 min. The slurry was centrifuged in a Sorvall RC-5B refrigerated centrifuge at 3500*g* for 45 min (4 °C). The supernatant was further centrifuged in a Hitachi 55-P2 refrigerated preparative ultracentrifuge at 10000*g* for 60 min at 4 °C since the debris after being centrifuged at low speed would still contribute to the turbidity of the protein solution. The clear supernatant was used for all studies after determination of the protein concentration.

Determination of Protein Concentration. The protein concentration of extracted sample was determined both by absorbance value in the ultraviolet region and by Kjeldahl nitrogen (AOAC, 1984). The absorbance value was obtained by correlating the nitrogen content of the protein extract by the Kjeldahl method to absorbance at 275 nm in a Shimadzu UV 150–02 spectrophotometer. A plot of protein concentration vs

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absorbance at 275 nm was obtained from which the absorbance factor of 11.05 ± 0.10 for $E^{1\%}_{1cm,275nm}$ was obtained.

Fluorescence Spectra. The fluorescence excitation and emission spectra of the protein solution were recorded in an Aminco-Bowman spectrofluorometer at 27 °C. Clear protein solution having an absorbance of 0.10–0.15 at 275 nm in extraction buffer was used in all experiments. The excitation spectra were recorded from 200 to 300 nm with emission fixed at 336 nm. The excitation maximum was fixed at 280 nm for maximum emission intensity. The emission spectra were measured in the range 300–400 nm with excitation at 280 nm. All measurements of fluorescence were monitored 10 s after excitation at 27 ± 0.5 °C.

Polyacrylamide Gel Electrophoresis (PAGE). Polyacrylamide gel electrophoresis was carried out using 10 cm × 0.5 cm glass tubes with polyacrylamide gels containing 9% acrylamide and 0.3% *N,N'*-methylenebis(acrylamide) along with 0.15% TEMED and 0.025% ammonium persulfate. The gels were prerun in respective buffers before the sample was loaded, and the run was performed in constant current mode of 3 mA per tube using an LKB powerpack according to the method of Davis (1964).

Sodium Dodecyl Sulfate (SDS)–Polyacrylamide Gel Electrophoresis. The preparation of gel and running conditions were the same as described for ordinary PAGE. The running buffer contained 0.03 M phosphate buffer, 0.1% SDS, and 0.1% 2-mercaptoethanol. After each run, gels were soaked in 10% acetic acid to remove SDS and then stained in Coomassie blue and destained by standard procedure. Standard proteins myosin, bovine serum albumin, and ovalbumin, and lysozyme were used as markers. The relative mobility of each protein band was calculated by the method of Weber and Osborn (1969). The molecular weights of the proteins were calculated from the calibration curve.

Gel Filtration. Gel filtration of total proteins from prawns was performed using Sepharose 4B gel. The degassed gel was equilibrated with extraction buffer and then packed in a column of dimension 1.8 cm × 100 cm by gravity. The bed volume (V_t) of the column was 247 mL and the void volume (V_0) 87 mL. The void volume was determined using Blue dextran 2000. A known amount of the protein (50–60 mg) was loaded to the column and eluted with EB. Fractions of 3.0–3.5 mL were collected using a programmable Pharmacia Frac-300 fraction collector interfaced with peristaltic pump P-1. The absorbance of each fraction was monitored at 275 nm using a Shimadzu UV 150–02 double-beam spectrophotometer. The ratio of elution volume (V_e) of the fraction vs void volume (V_0) of the column was calculated and plotted against absorbance at 275 nm to obtain the gel filtration pattern.

Sedimentation Velocity. Sedimentation velocity experiments were performed using a Spinco Model E analytical ultracentrifuge fitted with a rotor temperature indicator control unit and phase plate schlieren optics. A standard 12-mm 4° sector Kel-F centerpiece cell was used for all runs. The concentration of protein solution used was 1.5–2.0%, and the runs were performed at 59 780 rpm at 27 °C. Photographs were taken at regular time intervals. $s_{20,w}$ values were calculated according to the procedure described by Schachman (1959). The percentage fractions were estimated by enlarged tracings using a Gaertner microcomparator M-2000. Johnston–Ogston corrections were not applied for the percentage fraction calculated.

Viscosity. Viscosity measurements were made using an Ostwald viscometer at 25.0 ± 0.1 °C. Distilled water, buffer solutions, and protein solutions were passed through sintered glass filters (G-1 grade) to remove any dust and floating particles. Solutions of 5 mL were equilibrated to the viscometer bath temperature. Reduced viscosity of the protein was calculated according to the procedures of Yang (1961) and Bradbury (1970). The reduced viscosity was determined from extrapolation of viscosity values at different protein concentrations to zero protein concentration.

Measurement of Enzyme Activities. Adenosine triphosphatase (ATPase) activity in the muscle extract was estimated by the method of Perry (1955). Inorganic phosphorus was estimated in the filtrate by the method of Taussky and Shorr (1953). Proteolytic activity of protein of prawn was estimated by the method described by Wojotowicz and Odense (1972). The substrate denatured hemoglobin was used at a concentration of 1.5% in 0.1 M acetate buffer (pH 4.1). To 2 mL of hemoglobin solution was added 1 mL of prawn protein extract in extraction buffer, and the mixture was incubated at 37 °C in a Queue incubator-shaker at 140 rpm for 30 min. The reaction was stopped by addition of 3 mL of 10% trichloroacetic acid. The liberated tyrosine was estimated by Folin–Ciocalteu reagent. A standard curve of tyrosine was generated using tyrosine hydrochloride, and the proteolytic activity was expressed as micromoles of tyrosine liberated per milligram of protein per hour.

Amino Acid Analysis. Amino acid analysis was carried out in an LKB 9-151 Alpha-plus amino acid analyzer. The protein extract was dialyzed against distilled water to remove sodium chloride and buffer salts, lyophilized, and used for hydrolysis. Forty micrograms of lyophilized material was hydrolyzed with 6 N HCl for 22 h at 110 °C and the hydrolysate prepared for loading on the column according to the method of Moore and Stein (1963). Tryptophan in prawn meat was estimated by the *N*-bromosuccinimide method (Spande and Witkop, 1967) and expressed as percentage weight of protein. The analysis was done in both native and denatured condition.

Hydrophobicity Measurements. Average hydrophobicity was calculated from amino acid composition by the method of Bigelow (1967). Surface hydrophobicity measurements were carried out using *cis*-parinaric acid as a fluorescence probe as outlined by Kato and Nakai (1980).

Freeze-Drying of Prawns. Fresh prawns were peeled, the alimentary system was removed, and the prawns were cleaned and frozen to −20 °C and immediately freeze-dried in a Virtis freeze mobile 6 freeze-dryer till the moisture content was less than 3%. The freeze-dried samples were powdered for further experimentation or stored at −20 °C under desiccated conditions till further use. In some of the experimental procedures, the use of freeze-dried samples is a necessity according to the protocols such as water absorption and fat absorption capacities.

Functional Properties. *Nitrogen Solubility Index.* About 15–20 prawns were peeled and deveined and cut into small pieces. To 7.0 g of prawn meat was added 50 mL of 0.03 M phosphate buffer, pH 7.8, containing sodium chloride concentration in the range of 0.1–1.5 M. The proteins were extracted as described under Extraction of Protein from Prawns. Solubilized nitrogen in the supernatant was determined by the Kjeldahl method and the percent protein solubilized calculated.

Foam Capacity and Foam Stability. Foam capacity (FC) was determined by the method of Lawhon et al. (1972). Foam capacity was expressed as percent volume increase due to foam as compared to the initial volume. Foam stability (FS) was estimated by the method of Ahmed and Schmidt (1979).

Water Absorption Capacity. Water absorption capacity (WAC) of freeze-dried material was determined by the method of Sosulski (1962) and expressed as grams of water per gram of dried material.

Fat Absorption Capacity. Fat absorption capacity (FAC) of the freeze-dried material was estimated according to the method of Lin et al. (1974). The FAC of freeze-dried material was expressed as grams of oil per gram of dried material.

Emulsion Capacity. Emulsion capacity (EC) of prawn proteins was determined by the method of Pearce and Kinsella (1978). Prawn proteins were extracted in phosphate buffer (0.03 M, pH 7.8) and then used for EC measurements after the protein concentration was determined according to the Kjeldahl method (AOAC, 1984). Emulsion capacity was expressed as milliliters of oil per gram of protein.

Emulsion Stability. Emulsion stability (ES) of the protein solution was evaluated by the method of Paulson and Tung (1988). ES was expressed as time taken to reach half of the initial reading of absorbance at 500 nm, measured in a Shimadzu 150 UV-02 double-beam spectrophotometer.

RESULTS AND DISCUSSION

Proximate Composition. The proximate composition along with some of the physicochemical data of prawn and its proteins are given in Table 1. All of these values are fairly comparable to reported values in the literature for fish and/or krill (Shenoy and James, 1972). Salt-soluble

Table 1. Chemical Composition, Enzymic Activities, and Hydrophobicity Values of Proteins of Prawn Meat

component	composition
moisture (g kg^{-1})	777 ± 8
protein content (g kg^{-1})	188.7 ± 2.5
fat (g kg^{-1})	10.2 ± 1.5
salt-soluble protein (as % of total protein)	80.2 ± 1.0
nonprotein nitrogen (g kg^{-1})	5.4 ± 0.2
total carbohydrate (g kg^{-1})	0.8 ± 0.2
ash (g kg^{-1})	29.5 ± 3.0
ATPase activity [μg of inorganic phosphorus (mg of protein)$^{-1}$ min^{-1}]	0.625
proteolytic activity [μmol of tyrosine (mg of protein)$^{-1}$ h^{-1}]	0.700
average hydrophobicity (cal/res)	910
surface hydrophobicity	93

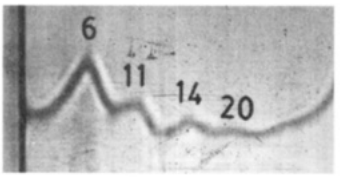

Figure 1. Sedimentation velocity pattern of fresh prawn protein extract in extraction buffer consisting of 0.03 M PB, 1 M NaCl, pH 7.8. A protein concentration of 1.5% was used in the experiment, and the photograph was taken at a bar angle of 55° and 60 min after two-thirds machine spread was reached.

protein fractions accounted for 80–82% of total proteins. This value is slightly lower than for certain fresh fishes, which have values of 85–90% of total proteins. The value of nonprotein nitrogen (NPN) in prawn meat is about 17% of total nitrogen. In most teleost fishes of Indian origin the NPN accounts for 10–12% of total nitrogen (Velankar and Govindan, 1958).

The total carbohydrate content in the protein extract is less than 0.1%. The ash content of prawns (3%) is almost the same as in other marine fishes.

The ATPase activity of the protein extract is 0.625 μg of inorganic phosphorus min^{-1} (mg of protein)$^{-1}$. The monitoring of ATPase activity of muscle protein will give an indication of the ability of myosin to bind to other muscle components.

Although it is suspected that the cathepsins/proteolytic enzymes of muscles are responsible for many autolytic changes, the extent to which these enzymes are responsible for post-mortem changes that occur in fish and shellfish during processing and storage is not very clear.

Physicochemical Properties. The sedimentation velocity patterns indicate four protein components with $s_{20,w}$ values of 6S, 11S, 14S, and 20S constituting 60%, 25%, 10%, and 5%, respectively (Figure 1). The 6S component appears to be the major component followed by the 11S component. The sedimentation coefficient of myosine from various sources such as cod, tuna, and tilapa has a value in the range 6.0–6.5S (Connell, 1954, 1958, 1963; Chung et al., 1967; Takashi et al., 1974). In the present study, the major protein correlates to myosin fraction of other species. With time of storage the pattern varies considerably, and care is taken to extract proteins from the fresh prawn for analysis of data.

The gel filtration profile of the proteins on Sepharose 4B gel is shown in Figure 2. The pattern indicates two major components, with one fraction eluting at V_e/V_o = 1.15 and another major fraction eluting at V_e/V_o = 2.8. The gel filtrations of protein extract from sea bass croaker and krill exhibit very similar profiles, suggesting a close relationship between these marine species (Ummemoto and Kanna, 1970; Seki and Arai, 1974). However, a single

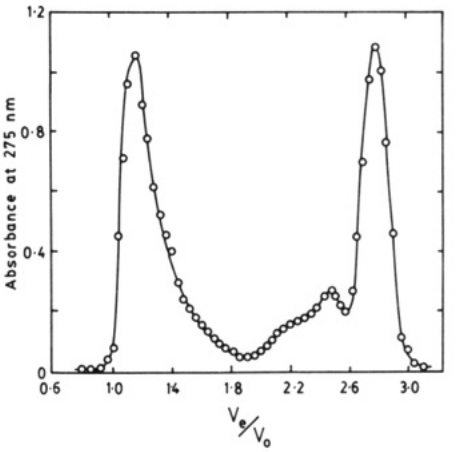

Figure 2. Gel filtration pattern of fresh prawn protein extract on Sepharose 4B gel in extraction buffer consisting of 0.03 M PB, 1 M NaCl, pH 7.8. The proteins were eluted with the same buffer, and fractions of 3.5 mL were collected.

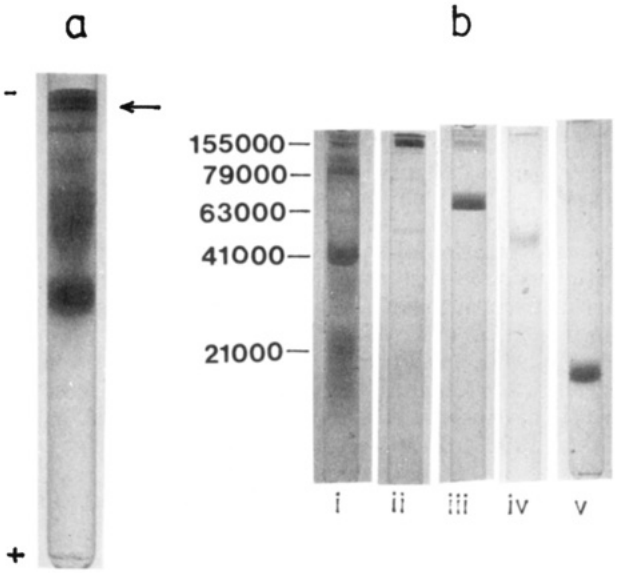

Figure 3. PAGE and SDS–PAGE of fresh prawn protein extract. (a) Native PAGE. The running buffer contained 0.03 M PB, 0.1% 2-mercaptoethanol, pH 7.8. The protein was extracted with PB 0.03 M, pH 7.8. (b) SDS–PAGE pattern of prawn protein along with standard protein markers. The running buffer contained 0.03 M PB, pH 7.8, 0.1% 2-mercaptoethanol, and 0.1% SDS. (i) Prawn protein; (ii) myosin from chicken muscle; (iii) bovine serum albumin; (iv) ovalbumin; (v) lysozyme. Preparation of sample is described under Materials and Methods.

peak in gel filtration does not necessarily indicate a single species of protein.

The page pattern indicates four major bands of fairly similar intensity and three faint bands (Figure 3a). It has been shown in several fish species that the PAGE pattern indicates the presence of light and heavy chains of myosin in the protein extract (Seki, 1976). The two major protein fractions (indicated by arrows in Figure 3a) may be myosin molecules.

The SDS–PAGE pattern of total protein extract indicates several bands showing complexity of proteins from prawn under totally denatured and reduced conditions (Figure 3b). The molecular weight of each band of prawn protein along with those of standard proteins are given in Figure 3b. The bands having molecular weights of 155 000 and 123 000 may be grouped as the heavy chain of myosin.

The reduced viscosity (η_{red}) as a function of protein concentration is shown in Figure 4. The dependence of η_{red} on protein concentration is seen with a positive slope,

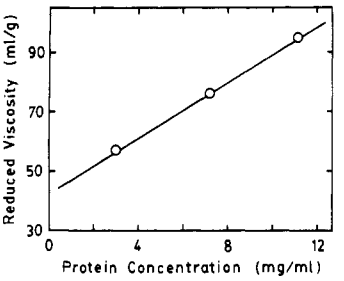

Figure 4. Reduced viscosity (η_{red}) as a function of protein concentration of fresh prawn protein extract in extraction buffer consisting of 0.03 M PB, pH 7.8, in 1 M NaCl. Viscosity was measured at 25 ± 0.1 °C.

Table 2. Amino Acid Composition of Proteins from Prawn

amino acid	g of amino acid/ 100 g of protein	amino acid	g of amino acid/ 100 g of protein
lysine	9.85	alanine	5.77
histidine	1.04	valine	4.43
arginine	7.92	methionine	3.41
aspartic acid	11.58	isoleucine	4.48
threonine	4.58	leucine	7.75
serine	5.04	tyrosine	4.22
glutamic acid	16.89	phenylalanine	4.27
proline	3.71	tryptophan[a]	1.06
glycine	4.00		

[a] Tryptophan was estimated by the method of Spande and Witkop (1967) under denaturing conditions of 8 M urea.

and extrapolation of the results to zero protein concentration leads to a value of 0.4 ± 0.03 dL/g. The values for myosin from various sources such as carp, cod, and rabbit range from 1.2 to 2.2 dL/g (Takashi et al., 1970; Connell, 1954; Webber and Portzhel, 1952). There are studies in the literature for which the values of intrinsic viscosity of myosin have been reported to be as high as 2.17 dL/g (Van Holde, 1985). This large variation of values possibly indicates the conformational transition occurring in myosin, leading to structural hierarchy of the assembled molecules which profoundly affects the viscosity of proteins. In the present study, the reduced viscosity measurements were done on the total proteins, and the presence of other components such as carbohydrates that were coextracted may also play a role in viscosity measurements.

The amino acid composition of the total protein fractions of prawn is shown in Table 2. The protein appears to be rich in both aspartic and glutamic acids with 17% and 12%, respectively. The results indicate the acidic nature of protein. The values of amino acids compare well with the amino acid composition of krill which possibly is related to prawn species in the evolutionary tree (Suyama et al., 1965). The sweetness of the prawn muscle has been attributed to free glycine (Konosu and Yamaguchi, 1982). In the present study the glycine content of muscle is 4.0 g/100 g.

Figure 5 shows the fluorescence excitation and emission spectra of prawn proteins. The spectrum indicates an excitation maximum at 280 nm, and the emission spectrum indicates maximum at 335 nm. The fluorescence emission maximum at 335 nm in proteins generally arises due to tryptophanyl residues. Even though tyrosyl residues also fluoresce at this wavelength, the tryptophanyl residues predominate over tyrosyl residues and are generally measured. Tryptophan or its amide has a fluorescence maximum at 350 nm in water and at 325–328 nm in low dielectric constant solvents (Shifrin et al., 1971; Teale, 1960). The emission maximum of prawn proteins at 335 nm possibly indicates, on average, tryptophanyl residues

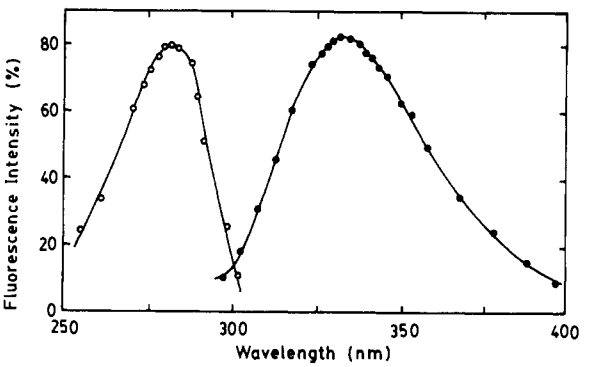

Figure 5. Fluorescence excitation spectrum (in the range 250–310 nm) and emission spectrum (in the range 300–400 nm) of fresh prawn protein (0.09 mg/mL).

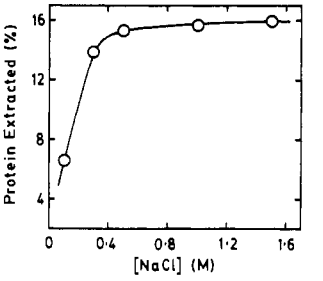

Figure 6. Nitrogen solubility profile of fresh prawn proteins as a function of NaCl concentration in 0.03 M PB, pH 7.8. The points in the curve are averages of three values, and the number of prawns used for each concentration was 15–20.

that are partly exposed to bulk solvent in the pH and salt condition of experiment. Monitoring the fate of tryptophanyl residues at 335 nm in the fluorescence spectroscopy of prawn protein may prove to be useful in the study of the denaturation of this class of proteins.

Functional Properties. The functional properties of prawn meat are a result of the nature and quality of proteins present in them. The functional properties, which are generally dominated by surface properties, of proteins can be used for evaluating the quality of the protein in the meat by measurements such as nitrogen solubility index, hydration and fat absorption parameters, and foaming and emulsification properties. The properties of water absorption and fat absorption capacities were evaluated with freeze-dried and powdered samples from fresh prawns.

In Figure 6 is shown the nitrogen solubility index of fresh prawn as a function of NaCl concentration. The solubility increases very rapidly up to 0.3 M NaCl, above which there is a slight increase in solubility tapering at 1 M NaCl. Hence, for most studies 1.0 M NaCl was used for extraction of proteins present in prawn.

The WAC of freeze-dried and powdered prawn meat is 4.96 ± 0.3 g of water/g of dried material (Table 3). This value of WAC is relatively higher compared to many other protein sources of both vegetable and animal origin (Kinsella, 1976). However, in the dehydrated prawn, the protein content is nearly 92%. This probably overrides all other properties and could play an important role in the hydration phenomenon in prawn.

As shown in Table 3, the FAC of freeze-dried and powdered prawn meat is 6.7 ± 0.1 g of oil/g of dried powder. This is high compared to that of egg powder which was found to be 2.19 ± 0.3 g of oil/g. As compared to alfalfa leaf protein and other vegetable and squid muscle proteins, the FAC of prawn meat is high.

The EC and ES of prawn protein was found to be 114 mL/g of protein, and 22 min, respectively (Table 3). As

Table 3. Functional Properties of Prawn Meat and Proteins Extracted[a] from It and of Egg Protein Extract

functional property	total prawn from prawn meat	egg protein total extract
water absorption capacity[b] [g of water (g of dried powder)$^{-1}$]	4.96 ± 0.30	2.54 ± 0.20
fat absorption capacity[b] [g of oil (g of dried powder)$^{-1}$]	6.70 ± 0.10	2.19 ± 0.30
foam capacity (%)	57 ± 2.50	101 ± 3.0
foam stability (%) (foam capacity after 30 min)	92 ± 1.50	98.5 ± 1.0
emulsion capacity[a] (mL of oil (g of protein)$^{-1}$]	114 ± 0.70	110 ± 1.0
emulsion stability[a] (min)	22 ± 2	14 ± 1

[a] The EC and ES were determined on the extracted protein. The concentration of protein used was 11.5 mg/mL. [b] Freeze-dried samples.

compared to those of egg protein, the EC and ES values of prawn protein are higher. If one compares the foaming capacity values of both prawn protein and egg protein (Table 3), it is clear that the foam capacity is nearly half in the case of prawn, where the value of egg protein is 101 ± 3. However, the foam stability values are comparable between the two samples. One possible reason for higher values may be the higher solubility of proteins in the buffer system used. In comparison to the EC values of other marine fishes such as cod and sea bass, prawn protein has a higher EC value.

The correlation of structural properties with functional parameters is to be done with great caution since the behavior of an individual protein will vary as a function of several solution conditions. The proteins from prawn separate into four components in analytical ultracentrifuge with sedimentation coefficients of 6S, 11S, 14S, and 20S. The proteins also separate into two major components and two minor components on gel filtration and polyacrylamide gel electrophoresis. The tryptophanyl residues in prawns, as evidenced by the fluorescence spectrum (Figure 5), are partly exposed to bulk solvent. The estimation of tryptophan by the *N*-bromosuccinimide method in the native (0.2%) and denatured proteins (1.06%) supports such an observation. The viscosity of protein is also very high, partly contributed by the polymerization property of macromolecules in the system. The pattern of total protein is fairly comparable with that of other species such as krill which is reported in the literature.

The functional properties of prawn meat as well as its protein extract when compared with those of egg, after normalizing for the protein content of both, give an indication that foam capacity of prawn is much less as compared to foam capacity and stability of egg protein (Table 3). The water and fat absorption of freeze-dried prawn show nearly 2 and 3 times the values, respectively, as compared to freeze-dried whole egg. The nature of surface hydrophobicity of prawn protein would possibly decide the value of foaming as well as emulsifying properties (Table 1).

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Received for review September 9, 1993. Accepted October 26, 1993.[⊗]

[⊗] Abstract published in *Advance ACS Abstracts*, December 1, 1993.