ation of high-molecular weight proteinase inhibitors from bovine skeletal

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WRY:

and ion exchange chromatography techniques. Purification was concluded by using trypsin-agarose affinity and anti BSA-coupled saffinity. These inhibitors were discriminated on the basis of their efficiency to inactivate trypsin, papain or both. Proteinase with estimated molecular weight of 65 and 60 kDa were thus purified to homogeneity as assessed by SDS-polyacrylamide gel

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the protein as a growing number of investigators have been interested in searching for novel inhibitors in biological fluids or tissues. The protein as inhibitors isolated and identified so far is extremely large.

WSKI and KATO (1980) introduced for the first time a rational nomenclature by grouping these inhibitors into distinct families. This was based on sequence similarity, topological similarity, and mechanism of binding.

le last few years, a series of cysteine proteinases protein inhibitors have also been discovered and characterised (BARRETT et al., and BODE, 1991). The cystatins are tight and reversibly binding inhibitors of the papain-like cysteine proteinases. They form a sequentially homologous proteins subdivided into three families, the stefins, the cystatins and the kininogens. The recently cathelin, a protein inhibitor of cathepsin L indicates that a new family of cysteine proteinase inhibitors may exist (RITONJA et al.,

30. A hibitors might protect the cells from inappropriate endogenous or external proteolysis and could be involved in the control of the responsible for intracellular protein breakdown. There is also growing information about the importance of these inhibitors in decided events such as inflammation, muscle dystrophy, Alzeimer's disease, sclerosis and tumor malignancy.

many studies have been carried out in order to identified proteinase inhibitors in different biological fluids and tissues, few is known in the present study we describe the purification procedure, in bovine skeletal muscle, of three weight proteinase inhibitors.

RIALS AND METHODS:

Gloo and G75 superfine, S-Sepharose, Q-Sepharose and CNBr Activated Sepharose 4B were purchased from Pharmacia Fine Rhzymes (trypsin, papain and chymotrypsin) and substrates (N-CBZ-Phe-Arg 7-amido 4 Methylcoumarin and N-Succinyl-Alamido 4 Methylcoumarin) were obtained from SIGMA Chemical CO. Trypsin affinity column: trypsin insoluble enzyme cross-linked beaded agarose were from SIGMA Chemical CO.

and inhibitors activities: Trypsin and papain were assayed with N-CBZ-Phe-Arg 7-amido 4 Methylcoumarin as substrate by of BARRETT (1980). Chymotrypsin was assayed by measuring N-Succinyl-Ala-Ala-Pro-Phe 7-amido 4 Methylcoumarin (SAWADA, 1983). Inhibitors activities were measured by the decrease in proteolytic activities after preincubation with the inhibitors was expressed in per cent with respect to a control sample in which enzymes were incubated without inhibitor.

Hechophoresis: Electrophoresis on 12,5 % polyacrylamide slab gel was performed according the procedure of LAEMMLI (1980) and with Coomassie Brilliant Blue R-250. Molecular Weight was estimated by comparing mobilities of the bands with those marker proteins: phosphorylase-b (94 kDa), bovine serum albumin (67 kDa), ovalbumin (43 kDa), carbonic anhydrase (30 km arker proteins: phosphorylase-b (94 kDa), bovine serum albumin (67 kDa), ovalbumin (43 kDa), carbonic anhydrase (30 km arker proteins: phosphorylase-b (94 kDa), bovine serum albumin (67 kDa), ovalbumin (43 kDa), carbonic anhydrase (30 km arker proteins: phosphorylase-b (94 kDa), bovine serum albumin (67 kDa), ovalbumin (43 kDa), carbonic anhydrase (30 km arker proteins: phosphorylase-b (94 kDa), bovine serum albumin (67 kDa), ovalbumin (43 kDa), carbonic anhydrase (30 km arker proteins: phosphorylase-b (94 kDa), bovine serum albumin (67 kDa), ovalbumin (43 kDa), carbonic anhydrase (30 km arker proteins: phosphorylase-b (94 kDa), bovine serum albumin (67 kDa), ovalbumin (43 kDa), carbonic anhydrase (30 km arker proteins: phosphorylase-b (94 kDa), bovine serum albumin (67 kDa), ovalbumin (67 kDa)

kDa), soybean trypsin inhibitor (20 kDa) and α lactalbumine (14 kDa).

Immunological analysis: Immunodiffusion based on the OUCHTERLONY method (1958) was performed using anti-bovine selections and the selection of the outer to the outer to

Preparation of anti bovine albumin affinity column: Anti-bovine serum albumin (developed in Rabbit) was coupled with column activated Sephanose 4 B according to the contract of the column activated Sephanose 4 B according to the column activated Sephanose 4 B according activated Sepharose 4 B according to the manufacturer's instructions (Pharmacia). Approximately 5 mg antibodies were coupled with each of the Sepharose 4 B according to the manufacturer's instructions (Pharmacia). of the Sepharose beads. The anti BSA-coupled Sepharose 4 B was packed in a column (1 X 5 cm).

Preparation of a crude inhibitor extract: A crude preparation was obtained by extraction from bovine Diaphragma muscle according to ZARAPLet al. (1991) to ZABARI et al (1991).

RESULTS AND DISCUSSION

Gel filtration of the crude inhibitor extract on a Sephadex G100 column (5 x 100 cm) separated four papain inhibiting fractions referred to FI, FII, FIII, FIIII, FIIIII, FIIII, FIIII, FIIIIII, FIIII, FIIII, FIIII, FIIII, FIIII, FIIII, FIIII, FI FI, FII, FIII, FIV (ZABARI et al., 1991). The first active fraction FI eluted near the void volume corresponded to protein with Mr family from 40 to 70 kDa The second fraction FIV: from 40 to 70 kDa. The second fraction FII included proteins with Mr ranging from 30 to 50 kD while FIII exhibited proteins with molecular to 50 kD while FIII exhibited proteins with molecular to 50 kD. The least of the second fraction FII included proteins with molecular to 50 kD while FIII exhibited proteins with molecular to 50 kD. The least of the second fraction FII included proteins with Mr ranging from 30 to 50 kD while FIII exhibited proteins with molecular to 50 kD. The least of the second fraction FII included proteins with Mr ranging from 30 to 50 kD while FIII exhibited proteins with molecular to 50 kD. The least of the second fraction FII included proteins with Mr ranging from 30 to 50 kD while FIII exhibited proteins with molecular to 50 kD. The least of the second fraction FII included proteins with Mr ranging from 30 to 50 kD while FIII exhibited proteins with molecular to 50 kD. The least of the second fraction FII included proteins with molecular to 50 kD. The least of the second fraction FII included proteins with molecular to 50 kD. The least of the second fraction FII included proteins with Mr ranging from 30 to 50 kD while FIII exhibited proteins with Mr ranging from 30 to 50 kD. The least of the second fraction FII included proteins with Mr ranging from 30 to 50 kD while FIII exhibited proteins with Mr ranging from 30 to 50 kD. The least of the second fraction fraction from the second fraction fraction fraction from the second fraction fract weight between 20 and 30 kD. The last fraction FIV, eluted just after myoglobin corresponded to proteins with low molecular weight kDa). In addition to possing FIV FIV. kDa). In addition to papain, FI, FII and FIV inhibited also trypsin and chymotrypsin while FIII show no activity against these sent protein asses. Only the first fraction FI countries and chymotrypsin while FIII show no activity against these sent protein asses. proteinases. Only the first fraction FI containing inhibitors of highest molecular weight was investigated here.

Fraction FI dialysed against acetate sodium buffer pH 5.4 was first loaded on a S-Sepharose column (2.5 x 16 cm) equilibrated with the substitute of the second state buffer. Figure 1 shows that this step separated three inhibitory fractions: non adsorbed material (S₀) and two peaks (S₁, S₂) eluted with 0.5 M linear NaCl gradient. So (New York 1) and the separated three inhibitory fractions: non adsorbed material (S₀) and two peaks (S₁, S₂) eluted with 1.5 miles (S₂, S₂) eluted 0.5 M linear NaCl gradient. S₀ (unretained fraction) and S₁ eluted from the column at about 0.08 M NaCl, inhibited papain and mythereas S₂ eluted at about 0.15 M NaCl, inhibited papain and mythereas S₃ eluted at about 0.15 M NaCl, inhibited papain and mythereas S₄ eluted at about 0.15 M NaCl, inhibited papain and mythereas S₅ eluted at about whereas S_2 eluted at about 0.15 M NaCl inhibited trypsin but not papain. All these fractions show a complex electrophoretic pattern.

Anion exchange chromatography on O-Sepharose:

-S₀ (unabsorbed material from S-Sepharose) was dialysed towards 0.05 M pipperazine-formic acid buffer, pH 4.0. The dialysed sampled to the column equilibrated in the same buffer. The dialysed samples (S applied to the column equilibrated in the same buffer. The inhibitory activity was recovered into two fractions: the unabsorbed proteins and a peak (SoO₂) eluted within the linear transfer towards 0.05 M pipperazine-formic acid buffer, pH 4.0. The dialyses applied to the column equilibrated in the same buffer. The inhibitory activity was recovered into two fractions: the unabsorbed proteins and a peak (SoO₂) eluted within the linear transfer towards 0.05 M pipperazine-formic acid buffer, pH 4.0. The dialyses applied to the column equilibrated in the same buffer. and a peak (S₀Q₁) eluted within the linear gradient at 0.15 M NaCl (Figure 2). Both fractions showed inhibitory activity against participation and chymotrypsin and chymotrypsin. On SDS-PAGE S. O. 1 trypsin and chymotrypsin. On SDS-PAGE, S₀Q₀ showed several bands emerging at position between 40 and 70 kDa. Further studies of fraction are under progress. S₀Q₀ analysed by SDS PAGE. fraction are under progress. S₀Q₁ analysed by SDS-PAGE showed one band with a molecular weight of about 65 kDa. S₁ and S₂ were dialysed towards 0.03 M Tris-HCl buffer pH 8 and were separately loaded on Q-Sepharose equilibrated in this buffer.

-From S1 we obtained a single peak (S₁Q) inhibiting both papain and trypsin and eluted with 0.25 M NaCl (Figure 3). SDS-PAGE shows bands with a Mr of 40 and 60 kDa, respectively.

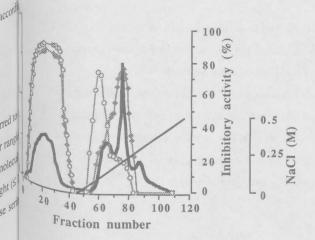
-From S_2 we also obtained a single peak (S_2Q) inhibiting only trypsin and eluted with 0.2 M NaCl (Figure 4). SDS-PAGE show one bands around 25 kDa.

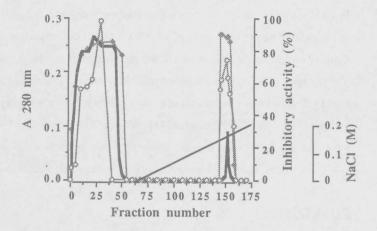
cm) equilibrated with a solution of 0.03 M Tris-HCl buffer, pH 8, containing 0.4 M NaCl. For each fraction (S₁Q and S₂Q) only inhibitory peak was obtained which was estimated in each inhibitory peak was obtained which was estimated in each case to have a molecular weight of 60 kDa by comparison with elution of the standard proteins: bovine albumin (Mr 68 kDa), egg albumic (Mr standard proteins: bovine albumin (Mr 68 kDa), egg albumin (Mr 43 kDa), pepsin (Mr 35 kDa) and soybean trypsin inhibitor (Mr 40 kDa). The homogeneity of both inhibitors was examined by polynomia. The homogeneity of both inhibitors was examined by polyacrylamide gel electrophoresis. A single band with molecular weight of 60 kDa obtained from each inhibitory fractions.

In order to determine whether both inhibitory activities (against papain and trypsin) associated with the S₁Q 60 kDa inhibitor are brought only one protein, this Sephadex G75 fraction was loaded on a trypsin. only one protein, this Sephadex G75 fraction was loaded on a trypsin agarose affinity column ($0.5 \times 2 \text{ cm}$) equilibrated in Tris-HCl buffer agarose. Chromatography of fraction FI on S-Sepharose.

Applied on a S-Sepharose column (16 x 2.5) equilibrated in adject at a sodium buffer pH 5.4. Proteins were eluted with a dient of 0 - 0.5 M NaCl in the same buffer at a flow rate of 3 A 280 nm papain inhibition %

Figure 2: Chromatography on Q-Sepharose of fraction S1 Fraction S2 was applied on a Q-Sepharose column equilibrated in 0.05 M pipperazine formic acid buffer, pH 4. Proteins were eluted with a linear gradient of NaCl (0 - 0.2 M) in the same buffer at a flow rate of 3 ml/min. A 280 nm ______ trypsin inhibition % ______





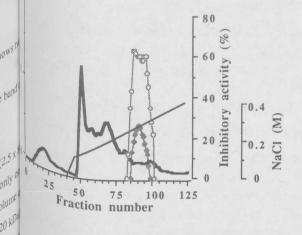
Chromatography of fraction S1 on Q-Sepharose.

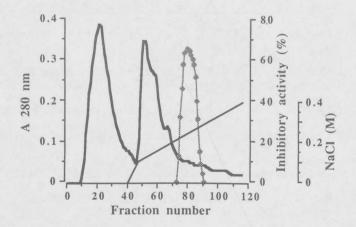
In 0.03 M Tris-HCl buffer, pH 8.0. Proteins were eluted stadient at a flow rate of 3 ml/min and 4.5 ml fractions trypsin inhibition %;

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8 and unbound proteins were eluted with the same buffer. In the unbound fraction, only the papain inhibiting activity was recovereds, a tribition clearly decreased and which clearly decreased and the same buffer. which clearly desmonstrate that papain and trypsin inhibitory activities were brought by different proteins. However, we did not succeed to the contract of the papain and trypsin inhibitory activities were brought by different proteins. our attempt to eluate the bound trypsin inhibitory activity even after an extensive washing of the column with 25 mM HCl. Two reasons of the column with 25 account for this failure: (1) the inhibitor was unstable at acidic pH and could not be detected or (2) because the protein inhibitor binds tight the column, itt was not release in such conditions. These two assumptions have not yet been tested.

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Chromatography on anti BSA-coupled Sepharose 4 B:

In the first steps of the purification procedure we noted the presence of bovine serum albumin in most active inhibitory fraction. Immunodiffusion performed using anti-BSA revealed contamination by BSA of most purified inhibitory fractions. In order to eliminate samples where therefore run on an efficient

The presence of BSA, a major serum protein, in these fractions suggested that some of these inhibitors might originate from contaminate from c blood a finding supported by a set of evidence showing the plasma origin of albumin found in muscle tissue (HEILIG and PETTE, 1989). reviewed by LASKOWSKI and KATO (1980) and TRAVIS and SALVESEN (1983), plasma contains a number of proteinase inhibitors where been extensively investigated in the containing and the co have been extensively investigated. Hence, it would be important to focuse the present work on inhibitors which exist within muscle cell this respect, tissue specificity as well as cellular localisation will be investigated by immunochemical methods.

Endogenous cysteine and serine proteinases are probably the most active muscle proteinases responsible for intracellular protein degradation.

The present study report the purification of four distinction of the protein degradation degradation of the protein degradation The present study report the purification of four distinct inhibitors of these proteinases. The 65 kDa protein inhibitor inactivates both costs and serine proteinases. Among the three other muscle inhibitor. and serine proteinases. Among the three other muscle inhibitor (each with a Mr of 60 kDa), two of them inhibit only trypsin and the last distribution inactivate only papain. The purified inhibitors are be inactivate only papain. The purified inhibitors can be compared with muscle inhibitors of serine type (WAXMAN and KREBS, 1978; KHULLING) et al., 1984); cysteine type (SCHWARTZ and BIRD, 1976).

This work confirm the great complexity of the muscle equipment in proteinase inhibitors already suggested in earlier studies conducted in laboratory (OUALL et al. 1986, ZADADA). laboratory (OUALI et al., 1986, ZABARI et al., 1991). Further investigations are needed in order to improve our knowledge about possible function, their target enzymes as well as their al. possible function, their target enzymes as well as their relationship with the protein inhibitors isolated from various tissues and fluids.

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