CLONING, YEAST EXPRESSION, PURIFICATION AND BIOLOGICAL ACTIVITY OF THE EXTENSION REGION OF THE SOYBEAN 7S GLOBULIN ALFA' SUBUNIT INVOLVED IN HEP G2 CELL CHOLESTEROL HOMEOSTASIS

The present invention refers to a recombinant α' fragment of the soybean 7S globulin corresponding to the N-terminal hydrophilic fragment of the natural α' subunit, to a process for its preparation and to compositions containing it as an active ingredient useful for controlling the cholesterol and triglyceride homeostasis.

BACKGROUND OF THE INVENTION

The role of dietary soybean proteins in the control of lipidemic levels of hypercholesterolemic patients is a widely accepted issue [1]. In previous studies [2-4], the direct involvement of one subunit of the soybean 7S globulin, the α' subunit, in the up-regulation of the LDL-receptor was demonstrated in *in vitro* and *in vivo* systems, suggesting that biologically active (poly)peptides, capable of modulating cholesterol homeostasis, are likely to be produced by cell enzyme processing.

The native 7S globulin is composed of three randomly assorted polypeptide chains, the α', α and β subunits [5], encoded by different genes. The mature α' (Accession N. P11827 UniProtKB/Swiss-Prot database) and α chains (Accession N. P13916 UniProtKB/Swiss-Prot database) share an extended N-terminal region of about 145 amino acid residues which is missing in the β subunit (Accession N. P25974 UniProtKB/Swiss-Prot database). Based on the peculiar amino acid sequence of the α' extension region, this subunit was purified by metal affinity chromatography and orally administered to hypercholesterolemic rats, thus allowing to show both its plasma lipid-lowering properties and up-regulation of liver β-VLDL receptors [4]. On the

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other hand, since the molecular weight of the α' subunit is around 71 kDa [6], it seems unlikely that it may cross *in vivo* the intestinal barrier with no modification.

For this reason, our research has been directed to seeking the amino acid sequence/s of α' subunit responsible for the pharmacological effect. Since the core regions of the three subunits have more similar amino acid sequences, it is conceivable that the biological activity should reside in one or more (poly)peptides of the extension region. In principle, the localized but significant amino acid differences between the extension regions of the α' and α chains would limit the number of peptides responsible for the biological activity.

From these previous statements, the first strategy pursued was to test the effect of both polypeptides in Hep G2 cells, obtained from the *in vitro* digestion (pepsin/trypsin) of Croksoy^{R}70, an isoflavone-free soybean concentrate routinely employed in the dietary treatment of hypercholesterolemic patients [7-8], and synthetic peptides, corresponding to specific amino acid sequences that differed between the 7S soybean globulin subunits, on the LDL-receptor (LDL-R) modulation. The results obtained in these studies pointed out that a marked LDL-R up-regulation could be induced in HepG2 cells exposed to enzyme digestion products of Croksoy^{R}70 with MW ranging from 3,000 to 20,000 Da, as well as to a small synthetic peptide (2,271 Da) from 7S soybean globulin added to cells at a concentration of 10^{-4}M [9]. The study obtained with small peptides is still currently under investigation and have not been conclusive so far [10].

The cholesterol and triglyceride lowering capacity of soybean proteins is a consolidated issue. The soybean protein diet is currently the most potent dietary tool for treating hypercholesterolemic patients, thus providing a unique opportunity for the management of adults and very young subjects. Moreover,

it is clearly established that the plasma cholesterol reduction is greater in patients having a high baseline degree of cholesterolemia [14].

The hypothesis that proteins *per se* reduce blood cholesterol arose from experimental studies indicating that a shift from animal to plant proteins in the diet activates the LDL receptor system in the liver of laboratory animals [15], as well as in circulating lymphomonocytes of hypercholesterolemic patients [16]. To identify the soybean protein components responsible for the cholesterol lowering effect, *in vitro* studies were carried out with a human hepatoma cell line that is highly sensitive to factors regulating LDL-receptor expression and cholesterol biosynthesis/breakdown. The purified α' subunit from the 7S soybean globulin was found to up-regulate LDL-receptors in Hep G2 cells [3] and this finding was confirmed in cholesterol-fed rats [4]. Although these data support the hypothesis that the protein moiety is responsible for the observed biological effect, arguments may be raised to α' chain *in vivo* biological fate, since peptides and amino acids are normally produced by the action of gastric and/or intestinal proteolytic enzymes. However, an increasing number of animal and plant (poly)peptides is being claimed to play relevant regulatory functions, often attributed to anti-oxidant, anti-proliferative and anti-inflammatory effects [17]. As far as soybean is concerned, experimental evidence clearly indicates the possibility that peptides and even small compact proteins, such as the Bowman-Birk inhibitor, may be adsorbed [18], thus eliciting a number of effects, including anti-cancer, anti-inflammatory, radio-protective ones [19]. Also genetically modified soybean (poly)peptides have been shown to trigger biological responses, such as hypotensive effects [20]. Recently, a LDL-R transcription stimulating peptide (FVVNATSN), deriving from the 7S globulin β chain, has been identified from a soybean hydrolysate prepared by a protease from *Bacillus amyloliquefaciens* and then by chemical synthesis [21]. In this case,

an increased LDL-R transcription (+148%) was detected in Hep G2 cells exposed to the peptide at a concentration of 100 μM. Other peptides arising from the 11 S globulin have been shown to exert similar but lower activity [21].

It would be desirable to make available shorter polypeptides maintaining or even improving the biological properties of the full length protein.

DESCRIPTION OF THE INVENTION

It has now been found that the so-called α' Extension Region of Soybean 7S Globulin corresponding to the N-terminal side thereof has advantageous biological activity and proved to be even more effective on LDL uptake and degradation than the full size α' chain.

The invention provides therefore said α' Extension Region, which will be hereinafter referred to as eα', as well as a process for its preparation by cloning, yeast expression and purification of the recombinant polypeptide containing the N-terminal extension region of the soybean α'subunit.

To this purpose the heterologous expression of the N-terminal fragment of the α' chain was undertaken. The objective was achieved in secretion-competent yeast cells of yeast *Pichia pastoris*. The recombinant polypeptide was purified and its biological activity assessed in HepG2 cells. By the use of this biotechnological approach, adequate amounts of the recombinant polypeptide could be obtained to be tested in *in vitro* trials and also in *in vivo* experiments.

DESCRIPTION OF THE FIGURES

Fig. 1 Overview of the pPICZαB-eα' construct. Expression of eα' is driven by the AOX (Alcohol OXidase) methanol-inducible promoter (5'AOX1); the α-Mating Factor (α-MF) promotes secretion of the recombinant protein to the medium; AOX1 TT: AOX transcription termination

region. *Sh ble* gene confers resistance to zeocin; pUC Ori: origin of replication for high number plasmid copy in *E. coli*. The other abbreviations refer to the cleavage positions of restriction enzymes; bp: base pair.

Fig. 2 Sequence alignment of the recombinant polypeptide (eα') and wild type soybean α' subunit. Stars indicate identical amino acid residues in the two sequences.

Fig.2A Sequence of the recombinant polypeptide (eα)' (SEQ ID1)

Fig.2B Sequence of the wild type soybean α' subunit (SEQ ID2)

Fig. 3A. SDS-PAGE under reducing conditions of recombinant *Pichia pastoris* culture:

Lane M: Molecular Weight Marker

Lane 1: TCA-precipitated culture supernatant (cell free) before induction with methanol.

Lane 2: TCA-precipitated culture supernatant (cell free) after 1h of induction with methanol.

Lane 3: TCA-precipitated culture supernatant (cell free) after 8h of induction with methanol.

Lane 4: TCA-precipitated culture supernatant (cell free) after 19h of induction with methanol.

Lane 5: TCA-precipitated culture supernatant (cell free) after 25h of induction with methanol.

Fig. 3B. SDS-PAGE under reducing conditions of eα' purification steps:

Lane M: Molecular Weight Marker

Lane 1: lyophilized powder of fermentation broth

Lane 2: DEAE-cellulose 150 mM NaCl eluted fraction

Lane 3: DEAE-cellulose 250 mM NaCl eluted fraction

DETAILED DESCRIPTION OF THE INVENTION

The invention will now be described in detail in the following

experimental section.

Materials and Methods

Yeast, bacterial strains and chemicals. *Pichia pastoris* X33 (WT) strain (Invitrogen, San Diego, CA) was used for yeast expression. The bacterial strain utilized for genetic manipulations was *E. coli* XL1-Blue (Invitrogen, San Diego, CA). Restriction enzymes Pst I and Xba I were purchased from Roche (Indianapolis, IN), Sac I from Fermentas (Ontario, Canada) Taq DNA polymerase was purchased from Invitrogen (San Diego, CA). Zeocin was purchased from Invivogen (San Diego, CA). The oligonucleotides for PCR were obtained from Primm (Milano, Italy). Peptone, tryptone, yeast extract and agar were purchased from Becton Dickinson and Company (Sparks, MD). Glucose and Sorbitol were purchased from Sigma (St. Louis MO). Dialysis Membranes were purchased from Spectrum Laboratories (Rancho Dominguez, CA). DEAE resin was purchased from Whatman (Maidstone, England). NiNTA resin was purchased from Qiagen (Hilden, Germany). Symmetry C4 HPLC Column was purchased from Waters (Milford, MA).

Other chemicals were reagent grade from Sigma (St. Luis, MO) or from Merck (Darmstadt, Germany).

Media and growth conditions. *P. pastoris* X33 strain was cultured in YPD (Yeast Peptone Dextrose) complete medium (2% peptone, 1% yeast extract, 2% glucose). The Mut^+ transformants were selected in plates containing YPD, agar 1.5%, 100 mg/mL zeocin. All yeast cultures were maintained at 30°C. For heterologous protein detection, Zeo^r-Mut^+ transformants were cultured to an optical density of 5 at 600 nm in YPS (Yeast Peptone Sorbitol) medium (2% peptone, 1% yeast extract, 2% sorbitol). Then methanol was added to 1% final concentration. All bacterial transformants were selected in plates of low-salt LB (Luria-Bertani) medium

containing zeocin (1% tryptone, 0.5% yeast extract, 0.5% sodium chloride, 1.5% agar, 25 mg/mL zeocin). All bacterial cultures were maintained at 37°C.

Construction of eα' gene expression vector. The eα' gene was amplified by PCR on an expression *Pichia pastoris* plasmid DNA template (pPICZαB) containing an insert (tα') comprising the sequence of interest (eα'). The oligonucleotide 5'-GAAAAGATAGATTAAAG**CTGCAG**TGGAGGAAG -3' was designed to generate PstI restriction site at the 5' end of eα' gene. This mutation resulted in an alanine residue insertion in the N-terminal position of eα'. A second oligonucleotide 5'-CCCTTCTTATTCTT**TCTAGA**TCATGGTTCTCTTTGAGACTC -3' was designed to generate XbaI restriction site at the 3' end of eα' gene. Both oligonucleotides were dissolved in mQ sterile water. The PCR reaction mixture consisted of 0.5 mM primers, 0.8 mM dNTPs (Eppendorf, Hamburg, Germany), 30 ng template (pPICZαB /tα'), 2.5 U Taq DNA Polymerase, PCR buffer (final composition: 50 mM KCl, 1.5 mM $MgCl_2$, 20 mM Tris-Cl, pH 8.4 and mQ sterile water to a final volume of 25 mL). PCR amplification was carried out on a Perkin Elmer Geneamp PCR System 2400 thermocycler (Perkin Elmer Corp., Wellesley, MA) using the following conditions: start at 94°C for 10 min; 30 cycles at 94°C for 40 sec, 60°C for 40 sec, 72°C for 20 sec; final extension 72°C for 10 min and maintained at 4°C. The PCR product of 465 bp was enzymatically digested to a full size construct of 423 bp and it was cloned into pPICZαB vector resulting in the pPICZαB-eα' construct and transformed in XL1-Blue *E. coli* cells. Positives clones were selected on semisolid LB media containing tetracycline and zeocin. One of these clones was sequenced by Primm (Milano, Italy) to ensure that no mutation occurred in pPICZαB-eα' construct sequence. Twenty μg pPICZaB-eα' construct and 30 μg expression vector pPICZαB (negative control) were linearized by

digestion with the restriction enzyme SacI and then purified.

Transformation of pPICZaB-eα' in P. pastoris genome. Wild type (wt) yeast cells were transformed by electroporation with 20 μg linearized pPICZαB-eα' construct and 30 μg linearized pPICZαB on an Eppendorf (Hamburg, Germany) electroporator 2510 apparatus set at 1.5 kV. Transformants were first selected by plating on YPD plates containing 100 mg/mL of zeocin. In order to verify the integration of our construct into transformed P. pastoris genome, the Dneasy Plant Mini Kit (QIAGEN, Hilden, Germany) was used to extract genomic DNA. Genomic DNA was used as template to verify the insertion of the construct at the alcohol oxidase promoter (AOX1) site by PCR using 5'AOX1 (5′-GACTGGTTCCAATTGACAAGC-3′) and 3'AOX1 primers (5′-GCAAATGGCATTCTGACATCC-3′) . The PCR reaction mixture consisted of 0.5 mM primers, 0.25 mM dNTPs, 100 ng for genomic template, 2.5 U Taq DNA Polymerase, PCR buffer (final composition as above). PCR reaction was performed using the following conditions: start at 94°C for 10 min; 30 cycles at 94°C for 40 s, 60°C for 40 s, 72°C for 20 s; final extension 72°C for 10 min and maintained at 4°C.

Transformant clone selection. Eighteen Zeo^+ transformants and one transformant containing pPICZαB expression vector (negative control) were grown in 50 mL of YPS medium at 30°C in a shaking (180 rpm) incubator to an OD_{600} = 5. The inducing phase was triggered by adding methanol to 1% final concentration and prolonged for 24 hours. Aliquots of the supernatants were examined for expression of eα' by SDS-PAGE. The clone transformant with the highest eα' expression was selected for fermenter scale production of the recombinant protein.

Expression of eα': fermenter scale. For massive production, the selected clone was grown in 14 L fermenter (Chemap, Switzerland), according

to Invitrogen's "*Pichia* Fermentation Process Guidelines" (Version B, 053002). Inoculum culture is prepared on YNB medium (KH_2PO_4 2.0 g; $(NH_4)_2SO_4$ 10.0 g; $MgSO_4$ $7H_2O$ 1.0 g; NaCl 0.2 g; $CaCl_2$ 0.2 g; Glycerol 100% 10.0 g; KOH to pH 5.2; Distilled water to 1.0 L) in unbaffled shake flasks. After incubation for approx. 24 hours at 30°C at 250 rpm, 1.0 L of seed culture is used to inoculate the fermenter, prepared with 8.5 L of Basal Salt Medium (H_3PO_4 85% 227 mL; $CaSO_4$ $2H_2O$ 7.9 g; K_2SO_4 155 g; $MgSO_4$ $7H_2O$ 127 g; KOH 35 g; Glycerol 100% 340 g; Distilled water to 8.5 L; pH adjusted to 5.0 with NH_4OH after sterilization). Both cited culture media are supplemented with biotin and inositol (1 mg/L each). Basal Salt Medium is also supplemented with modified PTM_1 Trace Salt Solution (H_2SO_4 96% 2.5 mL; $CoC_2O_4 \cdot 2H_2O$ 243 mg; $CuSO_4 \cdot 5H_2O$ 3.0 g; KI 44.5 mg; $MnSO_4 \cdot H_2O$ 1.5 g; $Na_2MoO_4 \cdot 2H_2O$ 100 mg; H_3BO_3 10 mg; $FeSO_4 \cdot 7H_2O$ 32.5 g; $ZnCl_2$ 10 g; Distilled water to 500 mL).

Growth of the microorganism and expression of heterologous protein are obtained via a three steps process. A first batch growth phase (glycerol as C-source) of approx. 24 hours is followed by a fed-batch phase (glycerol as limiting C-source) of approx. 4 hours. During these first two phases, pH is maintained at 5.0 by adding NH_4OH 20 %. Once all the glycerol is consumed, a methanol feed is initiated to trigger the eα' protein expression and pH is shifted to 6.0 by adding NH_4OH 20 %. Methanol fed-batch phase lasts for approx. 24 hours. During these two fed-batch phases the Dissolved Oxygen (DO%) in maintained stable at 30% by fine electronic regulation of agitator speed (rpm), while aeration rate (vvm) is progressively increased manually. Every few hours, the C-source limiting condition is checked by following the DO% level: its value should show a sharp increase after a sudden stop of methanol feed and, vice versa, a rapid decrease after resumption of it. Every few hours, samples are taken in aseptic conditions from the fermenter for the

following analyses: Optical Density (lambda 600 nm), cell biomass % (wet weight), sterility, microscopic observation, SDS-PAGE.

Purification of eα': downstream processing of fermentation broth. About 9.2 L of culture is spilled from the fermenter and cooled on ice. All the subsequent operations are carried out at +4°C. The whole culture is separated by centrifugation (Centrikon T-124, Kontron Instruments) at 3,000 ×g for 30 min; biomass (pellet) is discarded; about 7.5 L of supernatant is clarified by depth filtration on Zetaplus 30SP (Cuno) and subsequently microfiltered on 0.22 μm filter (Millipak 100, Millipore). The clear filtrate is concentrated via ultrafiltration on polyethersulfone membrane, MWCO 10 kDa (Omega filter, Pall). The concentrate, about 300 mL, is diafiltered versus 3.0 L of Tris-HCl 10 mM pH 7.2 and finally lyophilized. With this procedure were obtained 34.5 g of lyophilized powder, showing rather low degree of contaminant proteins on SDS-PAGE and having a total protein content of about 25 % p/p (Bradford Protein Assay, Bovine Serum Albumin as calibration standard).

Purification of eα': chromatographic purification.

For higher performance gel electrophoresis, NuPAGE® Pre-Cast Gel System (Invitrogen) was used according to supplier's procedures. Two grams of lyophilized powder were dissolved in 150 mL 50 mM Tris-HCl, pH 7.50 and loaded on a DEAE-cellulose column (6 × 10 cm, Whatman, Maidstone, UK) equilibrated with the same buffer. The elution of retained proteins was carried out with the same buffer containing 150 and 250 mM NaCl respectively. The fraction eluted with 0.25 M NaCl (300 mL) displayed the greatest content of eα'. The solution was concentrated to 100 mL by freeze-drying and then dialyzed with a 6000-8000 Da membrane at 4°C for 24 hours with milliQ ultrafiltered water and then lyophilized. About 370 mg of protein were obtained.

In order to verify the protein homogeneity, about 1 mg of protein was

loaded on a Symmetry C4 (4.6 × 250 mm) reverse phase column. Buffer A (ultrafiltered water and Trifluoroacetic Acid 0.1%) and buffer B (Acetonitrile 100% + Trifluoroacetic Acid 0.1%) were used.

Electrophoretic techniques. SDS-PAGE under reducing conditions (2% β-mercaptoethanol) was carried out on 12% polyacrylamide gels, according to ref. 11, using a mini-Protean II cell (Bio-Rad). The gels were stained with Coomassie Blue.

Cell cultures. The established human hepatoma cell line (HepG2) was obtained from American Type Culture Collection (Rockville, MD). Eagle's minimum essential medium (MEM), fetal calf serum, trypsin-EDTA (1x), penicillin (10^5 U/L), streptomycin (100 g/L), tricine buffer (1 mmol/L, pH 7.4) and non-essential amino acid solutions (100x) were from GIBCO (Madison, WI). Petri dishes were from COSTAR (Cambridge, MA). Filters were from Millipore (Bedford, MA). The Protein Coomassie Plus Protein Assay kit was purchased from Pierce (Rockford, IL, USA). ^{125}Iodine, carrier free, in 100 mmol/L NaOH, was from Perkin Elmer Life Sciences (Boston, MA). Sephadex G25 columns (PD10) were from Pharmacia Biotech (Uppsala, Sweden). LDH and MTT kit were from Sigma Diagnostics (Milano-Italy). All other chemicals were of analytical grade from Merck (Darmstadt, Germany). Cells were grown in monolayers in 90 mm-diameter Petri dishes, and maintained at 37°C in a humidified atmosphere of 95% air, 5% CO_2 in MEM supplemented with 10% fetal calf serum (FCS), non essential amino acid solution (1%, v/v), penicillin (10^5 U/L), streptomycin (0.1 g/L), tricine buffer (20 mmol/L, pH 7.4), $NaHCO_3$ (24 mmol/L) and sodium pyruvate (0.11 g/L). For experiments designed to evaluate the LDL receptor modulation, cells were seeded in 35 mm plastic dishes (3-5 x 10^5 cells) and used just before reaching confluence. In all cell culture experiments, the medium was changed every 2-3 days. In order to assess cell viability, culture media from cells exposed to eα'

at different concentrations were tested by methyltetrazolium salts (MTT) assay, essentially as described in ref. 9. Cell enzyme leakage was determined by measuring lactate dehydrogenase (LDH) activity, using a kinetic (LDH/LD) diagnostic kit (Sigma Diagnostics). LDL ($1.019 \leq d \leq 1.063$ g/L) were isolated by sequential preparative ultracentrifugation [12] from the plasma of clinically healthy normolipidemic volunteers. Lipoproteins were labeled according to the method of McFarlane as modified by Bilheimer et al. [13], and previously described [3]. ^{125}I-LDL were sterilized by filtration (Millipore filters, 0.45 μm pore size) and stored at 4°C until use. Human lipoprotein deficient serum (LPDS) was prepared as previously described [9].

Uptake and degradation of ^{125}I-LDL. Monolayers of cells were preincubated at 37°C for 24 h in MEM supplemented with 5g/100g LPDS to up-regulate the LDL-receptors [2], in the presence/absence of eα' at different concentrations listed in Table or 3.5 μmol/L α' purified subunit or 1.0 μmol/L simvastatin. A fixed concentration (7.5 mg/L) of ^{125}I-LDL was then added to the medium and the incubation continued for a further 5 h at 37°C. Specific uptake (binding + internalization) and degradation of ^{125}I-LDL were evaluated as previously reported [2].

Statistical analyses. Differences in cell uptake and degradation of LDL after cell incubation with eα' at different concentrations were determined by ANOVA followed by Dunnett's test. Values are expressed as means ± SD; *P* values < 0.05 were considered as statistically significant.

Results

Expression of eα' in Pichia pastoris. The structure of the plasmid used to transform *Pichia pastoris* cells is shown in **Figure 1**. The sequence of the insert and its alignment with the α' subunit are shown in **Figure 2**. As mentioned in the Materials and Methods, the only difference between the recombinant and wild type polypeptides consisted in the N-terminal first

amino acid residue which, for technical reasons, was an alanine in the recombinant chain. The clone showing the greatest production of recombinant polypeptide, as judged by SDS-PAGE analysis of the culture medium (not shown), was selected for massive production. **Figure 3-A** shows the electrophoretic analysis of the supernatant of the yeast culture before (lane n.1) and after induction with methanol for 1 – 8 – 19 and 25 hours (lane n.2, n.3, n.4, n.5). At it is shown, an evident band at an apparent molecular weight of about 20 kDa arises as a consequence of the induction.

Purification of eα'. The purification of eα' was achieved by chromatographic methods. Samples from each step were collected and analyzed by SDS-PAGE. The effect of the purification steps on the homogeneity of the identified polypeptide is shown in **Fig. 3-B**. A very low degree of contamination by yeast protein was already achieved in the culture medium, but the further chromatographic steps removed main contaminant proteins and allowed the recovery of the recombinant polypeptide in an almost homogenous form. N-terminal sequence analysis of this band confirmed that this 20 kDa polypeptide corresponded to the eα' chain. The purity of this sample was judged to be suitable for the cell assays.

Biological activity of eα'. The addition of the purified α' subunit, as a positive control, and its truncated α' form to HepG2 cells produced a significant rise in LDL receptor-mediated uptake and degradation compared to the untreated cells , as reported in the following Table.

Table. Effect of α' and its truncated form (eα') on the LDL uptake and degradation by HepG2 cells[1,2]

Sample type	Concentration[3]	Uptake		Degradation	
	μmol/L	*ng ^{125}I-LDL/ mg cell protein*	*%*	*ng ^{125}I-LDL/ mg cell protein*	*%*
LPDS[4]	–	94 ± 5.1	100	80 ± 4.3	100
7S α' subunit	3.5	154 ± 9.1*	164	128 ± 4.8*	160
eα'	0.5	113 ± 7.1*	120	100 ± 10*	125
	1.0	138 ± 9.2*	146	118 ± 9.3*	148
	2.0	169 ± 6.7**	179	157 ± 8.7**	196
Simvastatin	1.0	188 ± 10**	200	143 ± 7.9**	179

[1]The data are means ± SD of 3 independent experiments, each performed in quadruplicate. *P< 0.05 *vs* LPDS and **P<0.001 *vs* LPDS.

[2]Confluent monolayers of HepG2 cells were preincubated for 24 h at 37°C in minimum essential medium with 5% LPDS, in the presence or absence of different concentrations of recombinant polypeptide (eα') or purified α' subunit (7S α') or simvastatin. After the addition of ^{125}I-LDL (7.5 mg/L of medium), cells were incubated for an additional 5 h.

[4]LPDS, lipoprotein-deficient serum.

The results showed that the LDL modulation was dose-dependent with eα' and that the highest concentration was similar to that of the positive control, simvastatin. At no concentration of eα' was there any evidence of cellular toxicity, as determined by the MTT and LDH assays (not shown).

It has been therefore found according to the invention that the amino acid sequence capable of inducing the biological response lies in the N-terminal extension domain of α' chain. Moreover, we found that the N-terminal hydrophilic fragment exerts its effects at concentrations in the order of magnitude as those of simvastatin, a potent hypolipidemic drug. This effect might at least partially be due to the *in vitro* interaction between the above

fragment and thioredoxin, a small multifunctional protein with a redox-active disulfide-dithiol in the conserved active site sequence Cys-Gly-Pro-Cys, as reported by the present inventors [3]. This finding might explain the longer lag phase of LDL oxidation induced by cupric oxide observed in rabbits fed cholesterol-rich diet containing soybean protein *versus* that found in rabbits fed the same diet but containing casein as protein source [22].

The data obtained are particularly interesting because they show for the first time that the N-terminal hydrophilic fragment of soybean 7S globulin α'chain is active in *in vitro* model at concentrations less than 10 μM, that are similar that those reported for simvastatin. Moreover, the use of a recombinant protein rules out any involvement of other protein and non-protein soybean components, including isoflavones, for which a lack of clear benefits and potential toxicity have been reported[23].

The invention provides functional foods and compositions with beneficial effects on various diseases, including hyperlipidemia and cardiovascular disease, to be used alone or in combination with drugs in lipid-lowering therapies, i.e. statins such simvastatin, pravastatin, fluvastatin, atorvastatin, lovastatin.

The compositions of the invention are prepared using conventional excipients and methods. The dosage of the recombinant polypeptide of the invention will depend on several factors, such as patient's weight, age and sex and will be easily determined by the practitioner on the basis of pharmaco-dynamics, pharmacokinetics and toxicological characteristics of the polypeptide. In general, however, said dosage will range from about 50 to about 500 mg, once to three time a day.

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CLAIMS

1. N-terminal hydrophilic fragment Soybean 7S Globulin α' Subunit having SEQ ID1.

2. A process for the preparation of the N-terminal hydrophilic fragment of Soybean 7S Globulin of claim 1, comprising cloning, expression in *Pichia pastoris* and purification of the recombinant polypeptide.

3. Compositions comprising as the active ingredient the N-terminal hydrophilic fragment of the soybean 7S globulin of claim 1 in admixture with a suitable carrier.