Enzymatic hydrolysis of sunflower proteins: preliminary results

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Introduction

In the past few decades plant proteins have found increasing uses in human diet [1-3]. Experimental results have shown that sunflower proteins have interesting prospects for use in the food industry [4-6]. One way of improving and expanding the functional properties of proteins is to subject them to controlled enzymatic hydrolysis. However, in some cases this technique is limited by the bitter taste imparted by peptides with large amounts of hydrophobic aminoacids [7]. Controlled proteolysis of sunflower defatted meals (SDM), especially if originating from industrial plants that dehull the seeds, would permit a considerable improvement of the protein component and a more versatile dietary use. Such hydrolysis can be obtained with commercial enzymes of microbial origin as well as endogenous enzymes [8]. In the latter case SDM must come from cold-type extractions plants (e.g. Dyrex System) or those that make use of supercritical fluids, a technique still in the experimental stage. Our aim was to study the main parameters involved in the enzymatic proteolysis of industrial SDM to optimize a procedure for producing protein hydrolyzates with improved functional characteristics.

Methods and Results

Hydrolysis parameters. Industrial SDM was subjected to controlled proteolysis in the presence of Alcalase. The degree of hydrolysis (DH), expressed as the percent of hydrolyzed peptide bonds compared to the total [9] was determined for different protein—substrate concentrations, pHs (7-11), temperatures (30-70 °C) and times (0-6 h). The trend of the degree of hydrolysis as a function of protein—substrate concentration showed nearly perfect linearity of proteolysis with increasing protein concentrations and appeared to be a first-order reaction. One can infer that by using protein concentrates or isolates higher DH could be reached, with shorter hydrolysis times, smaller enzyme quantities and lower temperatures. The most efficient temperature was 60 °C. At higher temperatures the enzyme remains active, but the DH does not improve. With regard to pH, the DH doubled from 10 to 20 by increasing the pH from 8 to 10.

Electrophoresis. In agreement with the finding for DH as a function of hydrolysis time, the electrophoretic patterns confirmed that Alcalase has its strongest proteolytic effect during the first 30 minutes. In fact, as can be seen in fig. 1, after this time the bands of the proteins with the highest molecular weights disappear without the formation of smaller peptides. As proteolysis proceeds, one notes a decrease in the concentration of the proteins present after the first 30 minutes only.

Functional properties. Fig. 2 shows the isoelectric solubility at pH 4 of proteins treated with 7.5, 25, 50, 75 and 100 mg of Alcalase per gram of protein (N x 6.25). The poor solubility of the proteins in SDM is evident (it is presumed that they are mostly denatured by the high operating temperatures of the defatting process). With just 7.5 mg of Alcalase at 50 °C for 2 h solubility increases from 17.5% in the control (DH 0) to 45%. Increasing the enzyme con-

centration results in an almost linear increase in DH and a corresponding increase in isoelectric solubility, which reaches 82.5% with an enzyme/substrate ratio of 100 mg/g. As to the whipping properties of hydrozylates, samples at 5-25 DH were prepared varying the enzyme/protein ratio and the treatment time and were tested according to Adler-Nissen and Olsen [10]. While no correlation was found between whipping expansion and DH, the samples with higher DH showed a higher foam stability, up to 10 times the control for the most hydrolyzed samples. The hydrozylates are brown and transparent. As only those with the higher DH have a toasted, slightly bitter taste, these hydrozylates have potential use in fruit drinks.

References

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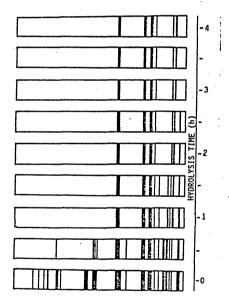


Fig. 1. Electrophoresis of SDM proteins hydrolyzed with Alcalase (enzyme/substrate = 75 mg/g) at pH 9.5 and 50 °C.

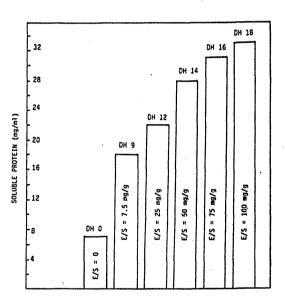


Fig. 2. Isoelectric solubility of SDM proteins as a function of the DH and enzyme/substrate ratio (E/S). The total initial protein concentration was 40 mg/ml.