NITROGEN EVOLUTION IN SHEEP CHEESE EXTENDED WITH DEFATTED SUNFLOWER MEAL

Baldi E.(1), Lencioni L.(2), Fiorentini R.(3), Galoppini C.(3)

1) Ufficio Repressione Frodi di Pisa - Ministero Agricoltura e Foreste;
2) Istituto di Chimica Agraria dell'Università di Pisa;
3) Istituto di Industrie Agrarie dell'Università di Pisa.

SUMMARY

Three sunflower protein meals produced by different neans: whole hexane-extraction (WHE) of industrial origin, dehulled hexane-extraction (DHM) and dehulled ethanol-extraction (DEM), were tested in a large scale cheese-making process using sheep milk with 1% meal added. This paper reports the evolution of the total soluble nitrogen (TSN) and non-precipitable soluble nitrogen (USN) during cheese ripening, together with the electrophoretic pattern of the meals, wheys, curds and ripened cheeses.

The degree of protein denaturation of the added meal seems to play a role in the proteolysis of cheese, probably because of its influence on the activity of the sunflower's proteolytic enzymes. In fact, the highest of TSN and USN values were observed in the cheese extended with the less denatured meal (DHM).

The addition of sunflower meal also induces the formation during ripening of protein subunits of medium to low molecular weight not observed in the controls.

INTRODUCTION

Defatted sunflower meal is a potential protein source for human consumption because of its nutritional and functional properties.

As part of a broader research project on vegetable protein technology, the possibility of adding defatted sunflower meal to traditional and widely used foods such as dairy products was tested.

In this study sunflower meals were added to cheese during the production phase and the effect on the proteolytic procesess was evaluated in terms of the total and non-precipitable soluble nitrogen levels and of the electrophoretic pattern of protein.

MATERIALS AND METHODS

Dehulled ethanol-extracted (DEM) and hexane-extracted (DHM) meals were prepared in the laboratory from sunflower cv. Stromboli (Baldi et al., 1988). The whole hexane-extracted meal (WHM) was obtained from industrial sources.

The meals were tested in a typical large-scale Italian cheese making process using sheep milk with 1% meal added during the curdling phase. All of the cheeses were ripened for 1 month at 8°C and 90% R.H. and sampled at 0, 3, 5, 8, 12, 16, 21 26 and 31 days of ripening.

The total soluble nitrogen (TSN) and non-precipitable soluble nitrogen (USN) were determined as described by Calzolari et al. (1980).

SDS-electrophoresis was performed using a Biorad Mini Protean IID Cell and a 12% acrylamide gel according to the method of Laemmli (1970). Cheese samples were extracted for 10 minutes in boiling sample buffer and the staining was performed following the silver stain method as modified by Wray et al. (1981)

RESULTS AND DISCUSSION

Figure 1 reports the changes in TSN and USN observed during ripening. In the control cheese their levels showed an evolution over time similar to that reported by Lencioni et al. (1988). In con-

trast particularly high values for the above parameters were found in the DHM-enriched cheese. Only at full ripening did the control cheese shows a TSN content close to that of the DHM-enriched cheese.

The electrophoretic pattern of the proteins in the meals, wheys, curds and ripened cheeses are reported in figures 2 and 3. In particular, figure 2 shows that the WHM obtained from industrial processing had a protein pattern close to that of the dehulled fullfat meal of cv. Stromboli, even if a poorer focalization probably due to the formation of protein derivatives during the preliminary treatment of the seeds, was obtained. The other

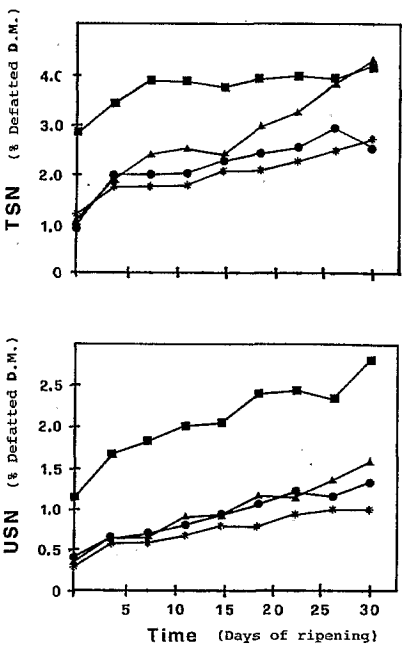

Fig. 1 - Total soluble nitrogen (TSN) and unprecipitable soluble nitrogen (USN) evolution during ripening of control (▲-----▲), DEM-enriched (●-----●), DHM-enriched (■-----■) and WHM-enriched (*-----*) cheeses.

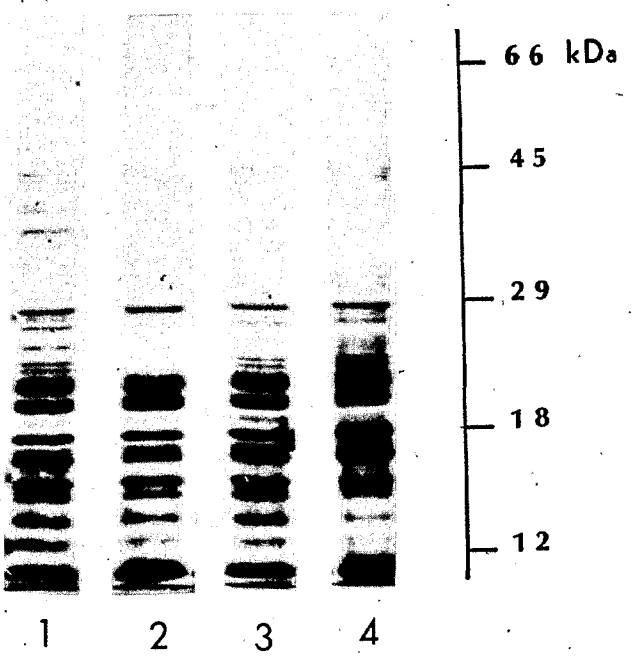

Fig. 2 - SDS electrophoresis of sunflower meals: 1) dehulled full-lfat meal, 2) dehulled ethanol-extracted meal (DEM), 3) dehulled hexane-extracted meal (DHM), 4) whole hexane-extracted meal (WHM).

two meals tested showed a similar electrophoretic pattern, although the two subunits at 23-25 kDa were not seen in DEM.

In the wheys and ripened cheeses obtained from extended trials (fig. 3a) some protein bands which were absent both in the whey and cheese controls were focalized. Strong differences were found when the protein patterns of the extended curds and ripened cheeses were compared to that of the control (fig. 3b).

Considering the electrophoretic pattern of the curds and cheeses, together with the high proteolytic levels in the DHM samples (the less denatured meals) just 6 hours after curdling, it can be hypothesized that hydrolysis in cheese is enhanced by sunflower proteolytic enzymes.

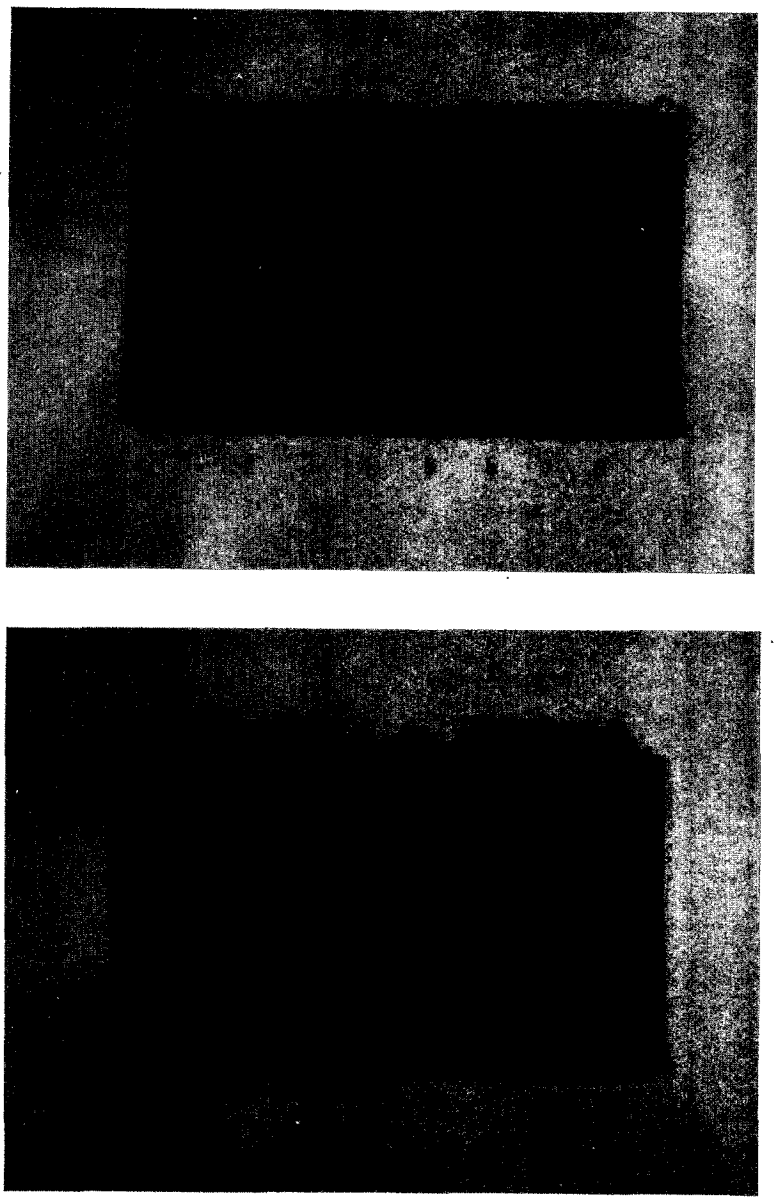

Fig. 3 - SDS electrophoresis of: a) wheys and ripened cheeses of control (1,5) and DHM (2,6), WHM (3,7), DEM (4,8) enriched products; b) curds and ripened cheeses of control (9,10) and DHM (11,12), WHM (13,14), DEM (15,16) enriched products.

The extended products obtained by the addition of dehulled meals were fairly similar in appesrence to the control, while the WHM enriched cheese was darker in colour and somewhat fibrous in texture.

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