Rheology and Fibre Formation in Extruded Meat Analogues

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ABSTRACT

Plant proteins such as soy, pea and wheat gluten are known to form a fibrous structures resembling chicken meat when extruded at elevated temperature with subsequent active cooling. The current hypothesis on the mechanisms responsible for the fibre formation contribute to understanding but are not sufficient to describe the full picture and cannot be used to predict fibre formation ability of protein melts thus hampering the use of more sustainable protein sources. Overall, the hypotheses range from "physical", describing mechanisms in terms of fluid dynamics, heat transfer and phase separation, to "chemical" emphasizing the chemical interactions between protein chains or polymer crystallites.

The aim of the present study to use rheological data of protein melts combined with simulation to elucidate the fibre formation mechanisms and this paper will show an example.

INTRODUCTION

The food chain contributes 25% of the total greenhouse gas emissions, with meat production alone contributing 14.5% [1]. Food production utilizes many natural resources and 75% of the arable land in Europe and North America is used for meat production. Global meat consumption doubled between 1961 and 2009. The global population is growing, and meat consumption is predicted to further increase until at least 2050 [2]. The increase in meat consumption is alarming also from a nutritional perspective, as excessive consumption has been linked to health problems, such as coronary heart disease and certain cancers.

Sales of plant-based meat-analogues has skyrocketed the last five years even if the production methods were known already in the early 90ies[3]. Fibrous analogues are today commercially produced from soy, pea protein and wheat gluten protein, utilizing an extruder to form a protein melt at high moisture content, high temperature and high pressure with subsequent active cooling on exit[4-6]. The product is commonly referred to as High-Moisture Meat Analogues, HMMA. It is known how to produce the fibres in HMMA but not exactly why they are formed. Consequently, it is currently difficult to utilize the full potential of these techniques.

MATERIAL AND METHODS

Sample preparation

Pea protein isolate with 85% protein content, (Roquette Pisane, Lestrem, France) was mixed with 15% pea fibre (Cosucra Swelite Warcoing, Hainaut, Belgium) and fed into an extruder (Brabender TwinLab-F 20/40, Duisburg, Germany) where water was added to 62% of the total weight. The powder-water mixture was heated and sheared in the extruder to 100°C to form a melt and extruded into a 13 mm cylinder which was air cooled instead of going into the cooling die, se **Fig. 1**. The same mixture is known to form a fibrous structure when heated to 150°C with subsequent cooling to 80° in the cooling die.

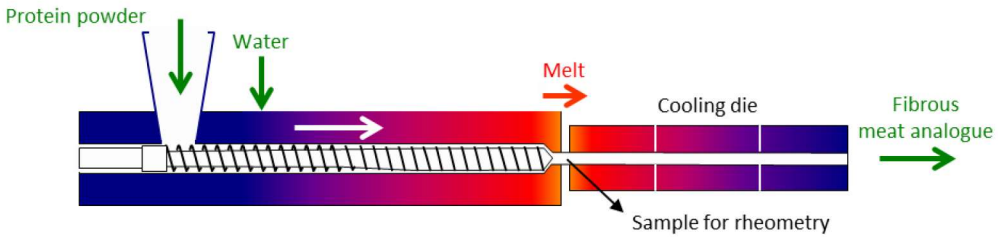

FIGURE 1: Principle of extrusion and sample preparation.

Rheometry

An HR 30 rheometer (TA Instruments, New Castle, DE, USA) was used for Small Amplitude Oscillatory Shear (SAOS) analysis, equipped with a 25 mm-diameter parallel plate system. Both plates were temperature controlled and the measuring system was enclosed in a solvent-trap enclosure. Slices 13 mm in diameter and 2 mm thick were cut using a vacuum holder[7] and placed in the measuring gap. The gap was actively adopting to changes in samples volume with temperature. Mechanical spectra at 0.1-30 Hz were recorded during heating at 10°C intervals to give complex viscosity as a function of angular frequency.

Shear viscosity was determined at 120°C and 140°C using a capillary viscometer (Göttfert RG 20, Buchen, Germany). Two round capillary dies with different aspect ratios (active length/diameter) of 20/1 and 20/2 were used.

Simulation

Cooling of a protein melt from 160°C to 60°C in a cooling die with square cross-section was simulated using Comsol Multiphysics (Comsol AB, Stockholm, Sweden). The simulation included flow, heat transfer and phase separation as an extension of a previous study by Murillo and co-workers[8].

RESULTS AND DISCUSSION

Simulation of what happens with a protein melt during cooling including several different mechanisms requires input of material properties of the melt and the conditions of the extruder process. In the simulation described here we include heat transfer (thermal conductivity, specific heat capacity), a power-law fluid, phase separation (Cahn-Hilliard equations) and the melt entry temperature and temperatures of the die wall.

The simulation requires rheological data of at least shear viscosity as a function of shear rate and temperature which is quite a challenge, especially for the high temperatures and pressure present in the extruder. Current rheometers are not equipped to cater for high-viscosity, high-moisture samples at typical conditions of 150°C and 5 bar pressure. This would require high-

pressure measuring cells equipped with parallel plate measuring geometries and these are difficult to come by. There are results published using viscometers designed initially for rubber testing as these are more enclosed and can retain moisture[9].

Assuming the melts obey Cox-Merz rule small amplitude oscillatory shear (SAOS) experiments can be used to determine viscosity as a function of shear rate for moderate temperatures. Even if a solvent-trap enclosure is used or the samples are covered with oil, moisture will evaporate when temperature is approaching 100°C. SAOS was therefore used for moderate temperature and capillary viscometry for temperature above 100°C. The combined results are shown in **Fig. 2** for a shear rate of 10 s^{-1}, and you can see that the viscosity starts to increase already at 80°C due to moisture evaporation. The temperature dependence follows an Arrhenius type relation, and all data were fed into the simulation.

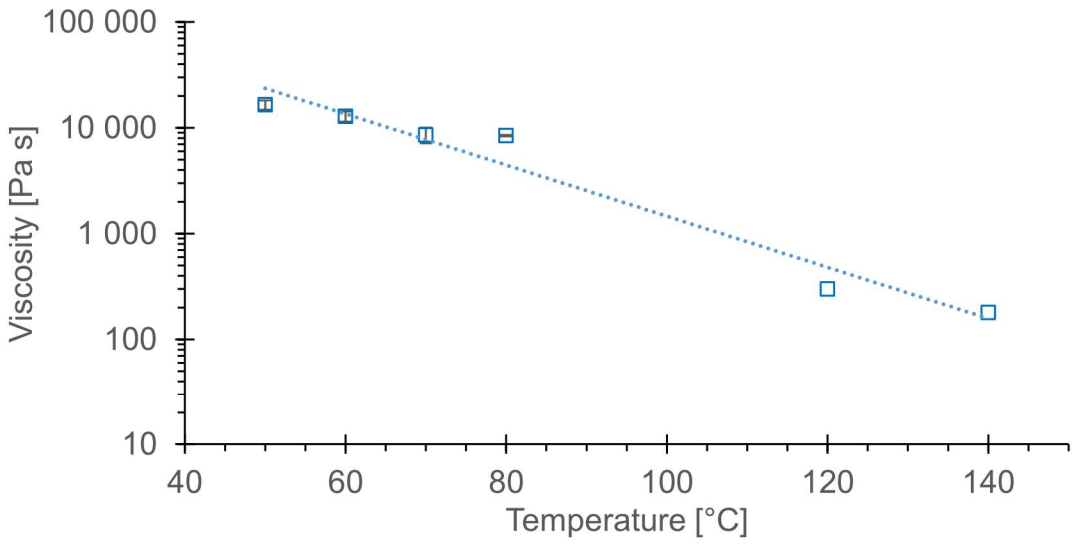

FIGURE 2: Temperature dependence of protein melt viscosity.

Fig. 3a shows the effect of temperature-induced phase separation at steady state in the cooling die which has a rectangular cross-section. When temperature falls below a critical temperature phase separation is initiated. The phase separation is spinodal and results in protein-rich and protein-poor regions. The spinodal decomposition is affected by diffusion and the progresses with time and aligns in the direction of flow. In the middle core region, it can be noted that fibres are not formed due to insufficient cooling, resulting in a partial core-slip, which needs to be remedied by an appropriate length of the die to achieve proper thermal penetration.

The phase separation gives rise to a flaky, fibrous structure and the size of the phase separated regions depends on the resolution of the grid used for the simulation. **Fig. 3a** demonstrates the effect of phase separation rather than mimicking a real structure as more real conditions would require a too high resolution of the grid to be handled by the computational resources available.

The simulated structure nevertheless has similarities to the real structure in **Fig. 3b** but the real structure shows fibres on a much larger size range. The simulation neither catches all directions of fibres present in the product and further mechanisms need to be incorporated in the simulation to fully describe the product structure.

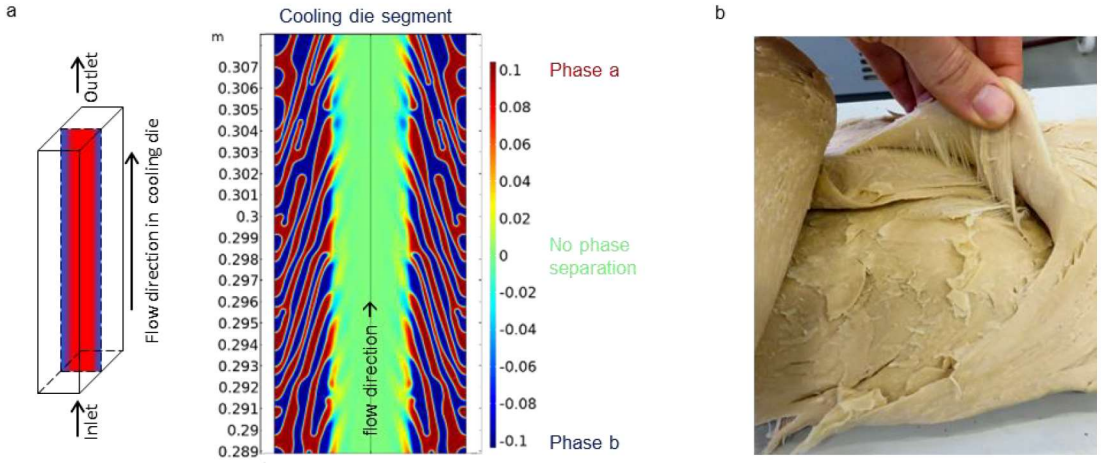

FIGURE 3: a) Simulation of phase separation in a protein melt, and b) structure of the extruded, fibrous plant-protein product.

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