Restricted Bovine Serum Albumin Diffusion through the Protein Network of Pasta

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Food digestion may be influenced by the diffusion processes that govern the accessibility of substrates to enzymes, both within the intestinal lumen and within the food structure itself. The purpose of this study was to determine the diffusion coefficient (*D*) of bovine serum albumin (BSA), which simulates α-amylase diffusional behavior, in the pasta protein network. A diffusion cell consisting of two well-stirred compartments separated by a lasagne matrix was designed and used. Starch was enzymatically removed from the lasagne, and ^{14}C-BSA was allowed to diffuse through the protein matrix for 26 h. The *D* obtained was ∼2-fold lower than the self-diffusion coefficient of BSA in free solvent. Protein network tortuosity, which increases path length diffusion, was probably the main factor involved in this restricted diffusion process. The presence of emulsified lipid, which is partly representative of the digestive environment, did not limit BSA diffusion toward and within the pasta protein network.

Keywords: *Pasta protein network; diffusion; digestion*

INTRODUCTION

It is generally considered that foodstuffs, after their passage through the stomach, are emptied in the form of chyme and not as particles with an intact physical structure. However, from the mouth to the large intestine, some foodstuffs or fiber may retain a complex solid structure (Noah et al., 1998; Hoebler et al., 1997). Enzyme diffusion processes in food structure (in the upper digestive tract) or fiber (at the colonic level) appear to be a key factor determining the rate at which macromolecules are degraded into nutrients. Although the diffusivity of solute through model foods has been exhaustively studied for biotechnological purposes, for example, the diffusion of NaCl through cheese (Zorrilla and Rubiolo, 1994) and agar gel (Djelveh et al., 1989) or of bovine serum albumin (BSA) (which simulates α-amylase) through starch gels (Leloup et al., 1990), no studies to date have investigated the influence of complex food structure on enzyme diffusion in the digestive process.

Enzyme penetration/diffusion into food is determined mainly by physicochemical factors such as the tortuosity, porosity, and crystallinity of food components. Among these factors, porosity has been most studied, especially in the case of fiber. It has been shown in vitro that the hydrolysis of cellulosic material is strongly related to the available pores for diffusion of cellulase (Wong et al., 1988; Tanaka et al., 1988). It is also now well-established that the increase of fiber porosity by technological processes or in vitro digestion increases the initial rate of in vitro fermentation by bacterial enzymes (Guillon et al., 1992; Auffret et al., 1993; Fardet et al., 1997). In the case of complex foodstuffs, very few studies have tried to relate the porosity of food structure to its digestion, although one technological study has shown that the fine structure of the processed rice food matrix (normally cooked, autoclaved, and retrograded), especially the pore size distribution, was correlated with in vitro starch digestibility (Ito et al., 1988).

Porosity depends mainly on food texture, as determined by technological processes. For example, the different textures of bread and pasta affect the rate of starch degradation in vitro and in vivo: Because of the loose texture of bread, starch is rapidly degraded, whereas the compact texture of pasta restricts the access of α-amylase to starch (Granfeldt and Björck, 1991; Karinthi, 1995). In pasta, the low degree of starch swelling, and especially the presence of a fine and insoluble protein network, may slow starch degradation (Colonna et al., 1990). The mechanisms by which this protein network impairs α-amylase action are not well-elucidated. Light and electron microscopy have shown that this network is highly porous and tortuous, with holes in the range of 0.5−40 μm (Fardet et al., 1998). The network surrounds the starch granules, but some connections in the walls of the protein network itself (∼0.5−3 μm) allow access of all the potential degradable starch fractions to α-amylase. Thus, the porosity of the protein matrix is not a limiting factor for starch hydrolysis (Fardet et al., 1998).

The main purpose of this study was to test the hypothesis that the geometry of the protein network (i.e., tortuosity) plays a major role in the slow degradation of starch by restricting the diffusion rate of α-amylase. The diffusion of radiolabeled methylated BSA

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10.1021/jf980371n CCC: $15.00
Published on Web 10/24/1998