

Nanostructure of hydrated wheat protein gliadin as revealed by SAXS

Nobuhiro Sato^{1,*}, Aoi Matsumiya², Yuki Higashino², Satoshi Funaki², Yuki Kitao², Yojiro Oba¹, Rintaro Inoue¹, Masaaki Sugiyama¹, and Reiko Urade²

¹ Research Reactor Institute, Kyoto University, Kumatori, Osaka 590-0494, Japan

² Graduate School of Agriculture, Kyoto University, Uji, Kyoto 611-0011, Japan

1 Introduction

The physical properties of wheat dough are much affected by those of its component, gluten. Gluten is mainly composed of two proteins: glutenin and gliadin. The former is responsible for elasticity; the latter is for viscosity. Glutenin forms high-molecular-weight network structure connected with intermolecular disulphide bonds. In contrast, gliadin is a monomeric protein with intramolecular disulphide bonds. Gliadin had been known to be insoluble in water and had usually been extracted from dough with aqueous ethanol or dilute acids. However, Ukai et al. found that gliadin can be extracted from NaCl-containing dough with distilled water [1]. It is expected that the behavior of gliadin extracted in water resembles more closely that of gliadin in real dough. Although gliadin is soluble in water at low concentrations, it is no longer soluble and forms hydrated solids at high concentrations. Nanostructure of such condensed matters can effectively be disclosed by small-angle X-ray scattering (SAXS). In this study, we investigated the nanostructure of gliadin assembly in distilled water over a wide concentration range by SAXS.

2 Experiment

Dough was prepared by mixing and kneading wheat flour (Super King™, Nisshin Flour Milling, Inc.) with 0.5 M NaClaq. It was repeatedly kneaded in distilled water and the third and sixth washing solutions were collected and centrifuged. Then, NaCl was added to the supernatant to precipitate gliadins.

The SAXS measurements were carried out on the BL-10C beam line of the Photon Factory. Solutions were put in a 1-mm thick aluminum cell with 20- μm thick quartz windows, while hydrated solids were put in a 1-mm thick PTFE sandwich cell with windows of 7.5- μm thick Kapton® films (TORAY-DuPont). The X-ray wavelength was 0.1488 nm, the sample-to-detector distance was around 2 m, and the observed q -range was 0.06–2.5 nm⁻¹. The scattered beam was detected with R-Axis VII (RIGAKU) or PILATUS 2M (DECTRIS). The typical X-ray exposure time was 300 s.

3 Results and Discussion

Gliadin is soluble in water below 10 wt%. Figure 1 left shows SAXS profiles of gliadin aqueous solutions. At a very dilute concentration (0.1 wt%), the scattering curve can be analyzed by three-component Guinier relationship. The lowest R_g value obtained by the Guinier analysis is found to be 5.68 nm, which corresponds to a monomeric

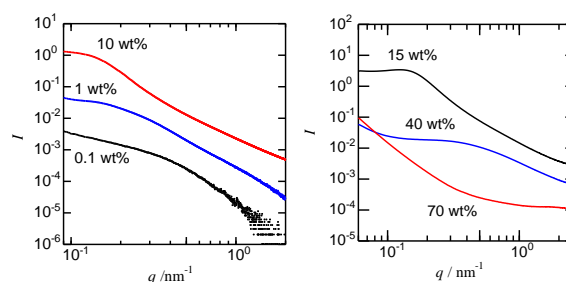


Fig. 1 SAXS profiles of gliadin aqueous solutions (left) and gliadin hydrated solids (right). In the right figure, profiles are vertically shifted for clarity.

gliadin molecule. It is also suggested that the other larger components correspond to dimers and oligomers. A small shoulder appears at $q = 0.21 \text{ nm}^{-1}$ at 1 wt%, and shifts to 0.13 nm^{-1} at 10 wt%. This shoulder is indicative of interparticle interference between aggregated gliadin domains. The domain separation distance calculated with the Bragg's equation is found to be 30 and 48 nm for 1 and 10 wt%, respectively.

Figure 1 right displays SAXS profiles of hydrated solids. The SAXS profile for 15 wt% solids is quite similar to that of the 10 wt% solution. In spite of different physical states, the SAXS profiles are similar to each other, indicating that the nanostructure of these two samples are quite alike. At 40 wt%, the shoulder at 0.13 nm^{-1} diminishes and new broad shoulder appears at 0.45 nm^{-1} (= 14 nm in real space). This shoulder indicates density fluctuation inside the aggregated gliadin domains. Finally, this shoulder diminishes at 70 wt%, and the upturn at the low- q region becomes prominent due to the formation of large aggregates. The poor water content leads to poor free space inside the domains and reduces the density fluctuation.

As described above, it is demonstrated that with increasing concentrations SAXS profiles change continuously, but the assembly states are largely different according to the interparticle interference and density fluctuation.

References

- [1] T. Ukai, Y. Matsumura, R. Urade, *J. Agric. Food Chem.*, **56**, 1122 (2008).

* sato-n@rri.kyoto-u.ac.jp