## Development of Time-Resolved Vacuum-Ultraviolet Circular Dichroism Spectroscopy and its Application to the Interaction Analysis betweenβ-Lactoglobulin and Lipid Membrane

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Structure of protein changes depending on the solvent environments including the presence or absence of membrane, leading various physicochemical phenomena. In this study, vacuum-ultraviolet circular dichroism (VUVCD) spectroscopy combined with time-resolved measurement was used for the analysis of conformational changes of protein induced by membrane interactions. In the time-resolved measurement, we have made a microfluidic cell that can efficiently mix protein solution and lipid membrane solution at a low flow velocity [1-2], and installed it in the VUVCD system equipped with a Schwarzschild focusing system that can miniaturize the synchrotron radiation light below 100 micrometers.

 $\beta$ -Lactoglobulin ( $\beta$ LG) was used as a model protein being capable of interacting with membrane such as lysophosphatidylglycerol lipids (LysoDMPG). Time-resolved VUVCD spectra were measured from 260-180 nm in the range of time resolution from 1 to 15sec at the lipid/protein concentration ratio = 50. After a liner dichroism has no effect on the CD spectrum at the low flow situation, the time-resolved spectra of  $\beta$ LG were analyzed. The result shows that the secondary structure of  $\beta$ LG changes from  $\beta$ -strand to  $\alpha$ -helix structures as the time after the mixing passes, indicating that  $\beta$ LG forms a membrane-bound structure within a few seconds. The time-dependent VUVCD spectra were analyzed by singular value decomposition method, and it was found that the structural change was composed of two states.



FIGURE 1. Time-resolved VUVCD spectra of  $\beta$ LG for interaction with LysoDMPG in the range of 260-180 nm at the lipid/protein concentration ratio = 50

## References

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