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Mixed proteome analysis to elucidate complex symbiotic interactions

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Proteome analysis using LC-MS/MS is an important approach for a comprehensive characterization of complex biological systems. Steady improvement in MS has transformed the depth of proteome analysis. However, the separative power of the techniques currently available is still insufficient to analyze complex proteome samples. To overcome this weak point, we have developed a monolithic super-long silica column with Dr. Minakuchi (Kyoto Monotech, <http://www.k-monotech.co.jp/>). The column showed very high separative performance and LC-MS/MS system equipped with a monolithic column can identify many proteins in living cells in one-shot. Using this system, we developed a method of “mixed and quantitative proteome analysis” in which proteome samples from several different organisms were simultaneously analyzed without the need to isolate the individual living cells. Omitting the individual cell isolation steps is important because these steps are known to alter the states of protein networks by causing various artifacts from unnecessary stresses. Our methods provide novel insights into the relationship between organisms with complex interactions and should lead to a better understanding of mechanisms of infectious diseases and symbiosis.

Biography

Wataru Aoki obtained his PhD degree in Biology from Kyoto University in 2013. He worked in Osaka University as Research Fellow of the Japan Society for the Promotion of Science. He is now working in Kyoto University as an Assistant Professor. His current research interests include development of technologies for next generation proteomics.

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