

Dissertation Abstract

Report no.	(Course-based) No.1026	Name	郭 浩根
Dissertation title	Characterization of Histone Variants and their Post-Translational Modifications by Proteomic Analysis (ヒストンバリエントと翻訳後修飾のプロテオミクスによる解析)		
<p>Abstract</p> <p>Various post-translational modifications (PTMs) are decorated in histone variants and histones and their PTMs intricately exist in chromatin. Histone variants consist of similar sequence and several patterns of PTMs co-exist in histones. They are related to biological activities such as transcriptional functions and chromatin remodeling. Hence, they are of interest to epigenetics and proteomics because of their unique structural and functional features and characterization research of histone variants and their PTMs is required for determining their site and sequence. Here, we reported the characterization of histone variants and their PTMs from the mouse testis by mass spectrometry (MS)-based top-down analysis. Histone variants and their PTMs were separated by high performance liquid chromatography on the reversed-phase column with ion-pairing reagent and then they were measured by MS. Testis-specific histones were successfully separated and characterized in this research and we found high-expressed somatic histones in the epididymis compared to the histones in the testis. Our data showed that PTMs were detected in histones variants from the mouse testis. Especially, K9 methylations on N-terminals of histone H3 variants were observed using MS. MS-based characterization research on histone variants and their PTMs is important to understand their specific patterns and sites. In this research, the results show the comprehensive approach for the characterization of histone variants and their PTMs by the MS-based top-down approaches. These strategies will provide information for the next proteomic and epigenetic studies and be applied for identifying other samples to find novel or specific patterns on proteins.</p>			