**S60-2** Functional analysis epigenetics regulatory factors induced during hepatocarcinogenesis Oshigehiro OSADA<sup>1</sup>, Urara GOMITA<sup>1</sup>, Chiaki YOSHIMI<sup>1</sup>, Masayoshi IMAGAWA<sup>1</sup> <sup>1</sup>Grad, Sch. of Pharm, Sci., Nagoya City Univ.

Malignant transformation and cancer development are induced by a combination of epigenetic and genetic aberrations resulting in dysregulated gene expression and function. Transcription regulation is one of the most important steps in the controlling the amount of protein. Though many histone modification enzymes and components of chromatin are involved in regulation of gene expression, there is a luck of conclusive information on the roles of epigenetics regulatory factors in carcinogenesis.

In order to gain insights into epigenetic aberrations in carcinogenesis, we identified several histone modification enzymes and components of chromatin, which are up-regulated during chemically induced hepatocarcinogenesis. During this process, glutathione transferase placental form (GST-P) is markedly and specifically increased and GST-P has been used as a reliable tumor marker for chemical hepatocarcinogenesis. I will discuss our recent progress on the effect of overexpression of histone modification enzymes and components of chromatin, which are induced during hepatocarcinogenesis, on tumor marker gene expression and malignant transformation.