

Differential Interaction of HPV16 E7 Oncoprotein in Cervical Cancer Cells

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Molecular pathology of cervical cancers associated with human papillomavirus infection is presently unclear. In an effort to clarify this issue, we utilized proteomics, surface plasmon resonance (SPR) technology and immunoprecipitation. Also, the Gene Ontology (GO) analysis was used to systematically characterize the global expression profiles at cellular process levels. Six HPV-infected human cervical cancer cell lines were used. We identified 18 proteins showing a more than 2 fold difference in their expression. The protein expression profiles were classified into mutually dependent 115 function sets, resulting in 217 cellular processes according to the GO. The GO analysis suggested that cervical cancer cells underwent repression of cancer-specific cell adhesive properties. Also, genes belonging to DNA metabolism such as DNA repair and replication were strongly down-regulated, whereas significant increases were shown in protein degradation and in protein synthesis. In order to get insights into binding kinetics between HPV 16 E7 protein and the differentially expressed proteins with high specificity and sensitivity, we produced a recombinant E7 protein and analyzed its binding partners. The SPR and immunoprecipitation were showed cell-specific interactions between E7 and its target proteins. By omics approach, potentially significant pathogenetic cellular processes were identified and showed the evidence that indicates similarities and differences between the molecular

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Key words : Cervical neoplasia, Proteomics, Immunoprecipitation, Surface plasmon resonance