

Hierarchical clustering analysis to detect associations between clinical and pathological features of gastric tumors and hypermethylation of suppressor genes

Identificación de asociaciones clínico-patológicas e hipermetilación de genes supresores de tumor

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Background: Methylation is an inactivation mechanism for tumor suppressor genes, that can have important clinical implications. **Aim:** To analyze the methylation status of 11 tumor suppressor genes in pathological samples of diffuse gastric cancer. **Material and methods:** Eighty three patients with diffuse gastric cancer with information about survival and infection with Epstein Barr virus, were studied. DNA was extracted from pathological slides and the methylation status of genes p14, p15, p16, APC, p73, FHIT, E-caderin, SEMA3B, BRCA-1, MINT-2 y MGMT, was studied using sodium bisulphite modification and polymerase chain reaction. Results were grouped according to the methylation index or Hierarchical clustering (TIGR MultiExperiment Viewer). **Results:** Three genes had a high frequency of methylation (FHIT, BRCA1, APC), four had an intermediate frequency (p15, MGMT, p14, MINT2) and four had a low frequency (p16, p73, E-cadherin, SEMA3B). The methylation index had no association with clinica