Summary

The upper gastrointestinal tract is the origin of a heterogeneous group of tumors comprising squamous cell carcinoma of the esophagus, adenocarcinoma of the esophagus (Barrett carcinoma), and gastric adenocarcinoma mainly. Among these three tumor entities there are differences in the pattern of genes affected during carcinogenesis. This review aims to describe the most important molecular genetic findings focusing on specific oncogenes (e. g. c-erbB2) or tumor suppressor genes (e. g. p53), as well as on genes involved in cell cycle regulation (e. g. cyclin D1, p16, retinoblastoma ), cell adhesion (E-cadherin ), and proteolysis.
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