Cancer Classification

1. By Tissue or Cell of Origin (Histogenetic Classification)

This is the most widely used system in clinical oncology.

 Epithelial Origin — Carcinomas Account for ~90% of human cancers

Derived from epithelial cells (lining tissues)

Subtypes:

Adenocarcinoma – arises from glandular tissue (e.g., lung, breast, colon, prostate)

Squamous cell carcinoma – from squamous epithelium (e.g., skin, esophagus, cervix)

 Mesenchymal Origin — Sarcomas Arise from connective tissue (bone, muscle, fat, cartilage)

Examples:

Osteosarcoma

Liposarcoma

Leiomyosarcoma

 Hematologic Origin — Leukemias and Lymphomas Originating from blood-forming tissues or lymphatic system

Subtypes:

Leukemia – e.g., acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL)

Lymphoma – e.g., Hodgkin lymphoma, non-Hodgkin lymphoma

Myeloma – plasma cell malignancy (e.g., multiple myeloma)

 Neuroectodermal Origin Tumors from the nervous system or melanocytes

Examples:

Gliomas (e.g., glioblastoma, astrocytoma)

Medulloblastoma

Melanoma

2. By Primary Site (Topographic Classification)

Defined by the organ or body system where the cancer originated:

Lung cancer

Breast cancer

Brain cancer

Colorectal cancer

Prostate cancer

Pancreatic cancer

Ovarian cancer

3. By Behavior

Benign: Non-invasive, non-metastatic

Malignant: Invasive, with potential to metastasize

4. By Molecular or Genetic Profile

Increasingly used in precision oncology:

HER2-positive breast cancer

EGFR-mutated non-small cell lung cancer (NSCLC)

IDH1-mutant glioma

MSI-high colorectal cancer

Lip cancer

Oral cancer

Pharyngeal Cancer

Although cancer classification has improved, there has been no general approach for identifying new cancer classes (class discovery) or for assigning tumors to known classes (class prediction). Here, a generic approach to cancer classification based on gene expression monitoring by DNA microarrays is described and applied to human acute leukemias as a test case. A class discovery procedure

automatically discovered the distinction between acute myeloid leukemia (AML) and acute lymphoblastic leukemia (ALL) without previous knowledge of these classes. An automatically derived class predictor was able to determine the class of new leukemia cases. The results demonstrate the feasibility of cancer classification based solely on gene expression monitoring and suggest a general strategy for discovering and predicting cancer classes for other types of cancer, independent of previous biological knowledge [1].

Leukemia and prostate cancer are the most common systemic cancers associated with subdural hematoma SDH, and gliomas may predispose to SDH more often than previously recognized. Coagulopathy is common and associated with the worst outcome, but many patients experience good functional outcome and survival [2].

Circulating microRNAs (MicroRNAs) hold great promise as novel clinically blood-based biomarkers for cancer diagnosis and prognosis.

Gastrointestinal cancer

1)
Golub TR, Slonim DK, Tamayo P, Huard C, Gaasenbeek M, Mesirov JP, Coller H, Loh ML, Downing JR, Caligiuri MA, Bloomfield CD, Lander ES. Molecular classification of cancer: class discovery and class prediction by gene expression monitoring. Science. 1999 Oct 15;286(5439):531-7. PubMed PMID: 10521349.
2)
Reichman J, Singer S, Navi B, Reiner A, Panageas K, Gutin PH, Deangelis LM. Subdural hematoma in patients with cancer. Neurosurgery. 2012 Jul;71(1):74-9. doi: 10.1227/NEU.0b013e3182517938. PubMed PMID: 22705720.