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Review Article

Significance of Onocogenes and Tumor Analysis

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Abstract

It deals with the histopathology of the tumors and their gene analysis and also include the briefing of different tumor analysis and genetics of tumors.

Keywords: Tumors; Oncogenes; Tumor; Pan-Cancer; Pancreatic Tumor; Lung Carcinoma

Gene analysis

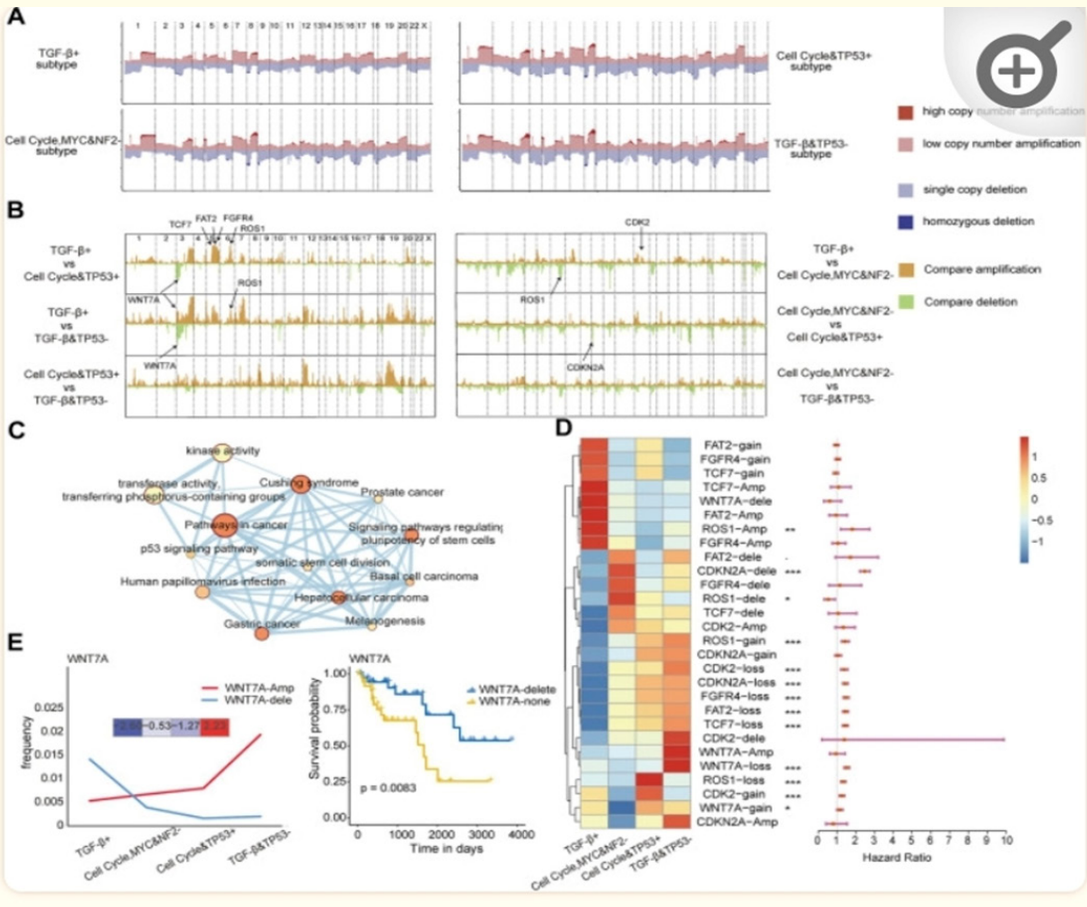

Figure 1

Somatic CNA frequency of individual genes in each subtype plotted along the [1] chromosomes. (B) Comparisons of [2] somatic CNA between subtypes with −log10 FDR plotted along the chromosomes [3] (Fisher's exact test). (C) Interaction of the enriched pathways. The size represents the [4] number of genes, and the color represents the p-value [5]. (D) Differential in copy number variation across the four subtypes of the four copy number variation states of the seven genes and their relationship with the prognosis. (E) Changes in the [6] number of amplified and deletetion samples of WNT7A in the four [7] subtypes; the expressed WNT7A in the four subtypes (left) and the difference in survival between the [8] two categories.

Tumor analysis

Pan-cancer genomic analysis of multiple tumor types

A major challenge of large sequencing data is identifying and distinguish the low frequency of clinical relevant mutated genes from passenger mutations One strategy to overcome this problem is to combine samples across multiple tumours types in the so called "pan-cancer analysis" to increase the statistical power of identifying low-frequency novel and potentially actionable genes [9].

A study by Ciriello., *et al*. more than 3000 samples across 12 tumor types to hierarchically stratify.

Lung cancer

Lung cancer is the most common cause of cancer related mortality. Non-small cell lung carcinoma (NSCLC) constitutes approximately 85% of all lung cancers and the remaining 15% are small cell lung carcinoma (SCLC). Patients with adenocarcinoma histology constitute nearly half of all NSCLC, of which a third have squamous cell carcinoma (SCC) histology [10].

Colorectal cancer

Colorectal cancer (CRC) is the third most common and second lethal malignancy in men and women in the United States Fearon and Vogelstein described a multi-progression model of adenoma to carcinoma as a consequence of tumor suppressor gene unactivation (e.g., APC, TP53, and SMAD4) and oncogene activated (e.g., KRAS, BRAF and PIK3CA)during early 1990s emphasizing the role of genomic alterations in the malignant transformation process. CRC has a heterogeneous mutational.

Melanoma

The MAPK pathway is frequently dysregulation of malignant melanoma, due to mutations of BRAF and RAS genes or other genetic or epigenetic events. A recent study of 183 melanomas (140 cutaneous, 35 acral, 8 mucosal) found the MAPK pathway to be enriched 1.34 fold [150]. Alterations in the MAPK pathway were found in 179 of the 183 tumors. Only 11% (15/140) of cutaneous melanomas were wt BRAF/RAS/NF1, whereas 51% (22/43) of non-cutaneous melanomas.

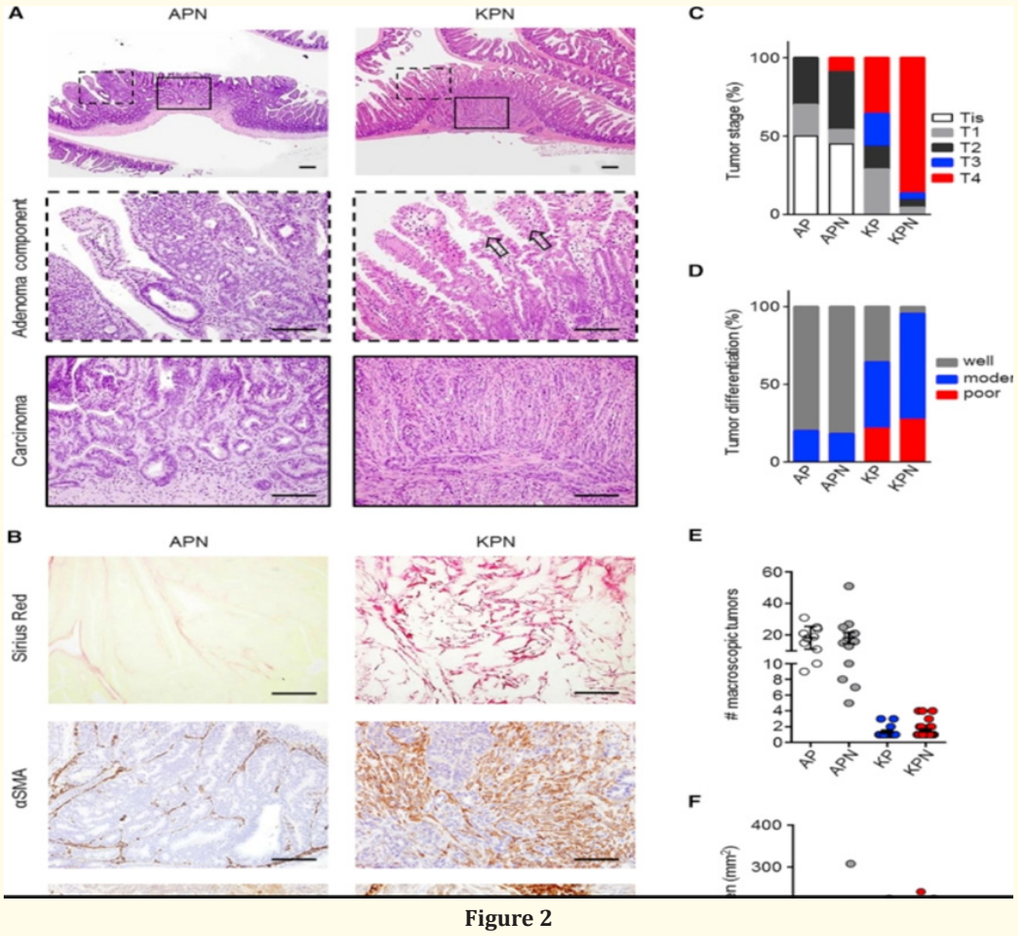

Figure 2

NOTCH1 Drives Intestinal Metastasis in an Autochthonous Model (A) Schematic description of genetic crossing strategies. Cre, cre-recombinase; ER, estrogen receptor; loxP, Cre-Lox recombination site; IRES, internal ribosome entry site. (B) Kaplan-Meier survival curves of intestinal tumor free survival; PN, n = 21; AP, n = 10; APN, n = 12; KP, n = 15; KPN, n = 31. (C) Incidence of metastases (%) per genotype; PN, n = 21; AP, n = 10; APN, n = 12; KP, n = 14; KPN, n = 29. DIA, diaphragm; LN, lymph-node; Peri, peritoneal carcinomatosis. (D and E) Number (D) and burden (E) of macroscopic metastases of KPN mice. Error bars represent mean ± SEM. (F) Left image: representative image of macroscopic liver metastatic burden of KPN mice.

Discussion

In this we discussed about the genetic Analysis and tumor analysis and formed the relationship between them that on dysregulation of oncogenes can lead to formation of tumors or any kind of cancer.

Conclusion

Significance of tumors analysis and genetic analysis of oncogenes are that we can monitor the early cases of cancer through oncogenes (before first stage or pre first stage).

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