OVERVIEW

The scope of the research carried out by our Group ranges from the identification of etiological agents and mechanisms, to the translation of the findings into the clinical and Public Health domains, focusing on bladder, pancreatic, and breast cancers.

We employ a wide variety of biomarkers to better characterise exposures, genetic susceptibility patterns, and cancer outcomes. Omics data provide a unique opportunity in this regard and the Group explores its integration in epidemiologic studies.

The strategic goals of the Group are to:

- Identify non-genetic and genetic factors, as well as their interactions, associated with cancer development and progression and with its molecular/omics subphenotypes.
- Develop and apply statistical/informatics tools to model the risk and course of patients with cancer by integrating epidemiological and clinical data with omics information.
- Assess clinical and public health strategies for cancer control using current genomic tests and data.

“The Integration of omics and non-omics data in the same risk models poses several challenges and demands appropriate analytical strategies. We are contributing to this field towards the personalised prevention of cancer.”
RESEARCH HIGHLIGHTS

Research findings

In 2019, the Group focused its research on pancreatic and bladder cancers. Regarding pancreatic cancer (PC), we progressed in the characterisation of pancreatic cancer risk factors by investigating the common genetic background of PC and other solid tumour types. We also furthered our understanding of the molecular mechanisms underlying PC development and simultaneously advanced our knowledge of the mechanisms underlying PC development and simultaneously investigated AIDs. Several inflammatory-related morbidities shared a common genetic component with PC, pointing to a potential link between them. Gene-disease associations were furthered in the PanGenEU case-control study population of 1,705 PC cases and 1,084 controls. This analysis confirmed that having any of the 9 autoimmune diseases studied was significantly associated with a reduced risk of PC, which further decreased in subjects having ≥2 AIDs. Several inflammatory-related morbidities shared a common genetic component with PC based on public databases. These molecular links could shed light onto the molecular mechanisms underlying PC development and simultaneously generate novel hypotheses (FIGURE 1). Furthermore, we pursue the characterisation of the genetic susceptibility and somatic alteration landscape of PC by participating in international large-scale investigations. Regarding bladder cancer (BC), the Group participated in several clinical trials on immunotherapy and vitamin D in BC. We continue to sustain the Spanish Familial PC Registry (PanGenFAM) and the European Registry of PC (PanFeiet). We also lead the Research Work Stream of the Pancreatic Cancer Europe (EPC) multitakeholder platform. By joining efforts and participating in the European Alliance of Personized Medicine Annual Meeting, we also made advances in increasing awareness of PC among health policy makers and in discussing the urgent need to invest in PC research.

Methodological contributions

The Group continues to explore analytic strategies and tools to integrate both omics and non-omics (OnO) data. In this regard, we reported that the efforts to integrate OnO data are scarce, having been done mainly in the epidemiologic field. We identified and listed the challenges in OnO data integration and proposed integrative analytical strategies towards its integration (FIGURE 2).

Translational activities

The Group actively provides methodological support to several clinical trials on immunotherapy and vitamin D in BC. We continue to integrate both omics and non-omics (OnO) data. In this field, we continue to sustain the Spanish Familial PC Registry (PanGenFAM) and the European Registry of PC (PanFeiet). We also lead the Research Work Stream of the Pancreatic Cancer Europe (EPC) multitakeholder platform. By joining efforts and participating in the European Alliance of Personized Medicine Annual Meeting, we also made advances in increasing awareness of PC among health policy makers and in discussing the urgent need to invest in PC research.

Figure 1 Gene network of medical conditions associated with pancreatic cancer through common genes. (A) Networks of diseases that share genes with pancreatic cancer and all corresponding connections. (B) Network of diseases that share genes with pancreatic cancer, only connections with pancreatic cancer are shown. Edge width represents the Jaccard index for each disease pair; Jaccard indices were multiplied by 100 in order to allow better visualisation. Node size represents the number of genes obtained through DisGeNET for each medical condition.

Figure 2 Challenges found in the integration of omics and non-omics (OnO) data and analytical designs for building hybrid models containing OnO data.