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“Our commitment to gender equality was consolidated in 2019. The CNIO together with the Works Council elaborated a very ambitious CNIO Equality Plan. This is an exciting time for the Centre and a step forward on the road to gender equality.”

MARIA A. BLASCO
Director
This year, once again, I am proud to convey how the CNIO has moved forward in so many directions, pushed by the extraordinary work of our people. In our goal to achieve scientific leadership and international impact, we succeed in 2019 to place the CNIO on the map as one of the top cancer research centres in Europe and worldwide. In 2019, CNIO researchers authored a total of 230 papers, 33 of which were published in journals with impact factor between 10 and 15, and 24 publications in journals with impact factor greater than 15. This year, according to the Nature Index, considering our scientific contributions in the life sciences and healthcare field, the CNIO ranked second among cancer-focused institutions in Europe. These indicators are a testimony of our scientific impact on basic and translational cancer research.

Science is constantly evolving, and so do we as a Centre, by incorporating new groups working on new research lines that best complement those already existing. Thus, in 2019 we reinforced our basic research arm by recruiting 2 new Research Groups to the Molecular Oncology Programme: the Transformation and Metastasis Group, led by Eva González Suárez, coming from IDIBELL, Barcelona; and the Topology and DNA Breaks Group, led by Felipe Cortés, formerly at CABIMER-CSIC, Sevilla. Both researchers hold prestigious ERC Consolidator Awards. These 2 Groups will contribute to reinforcing the already prominent role of the CNIO in 2 areas considered as critical in cancer research, namely genome integrity and metastasis.

The Structural Biology Programme also incorporated 2 Junior Research Groups: the Computational Cancer Genomics Group, led by Solip Park, formerly at the Centre for Genomic Regulation, Barcelona; and, towards the end of the year, the Computational Oncology Group, led by Geoffrey John Macintyre, coming from the Cancer Research UK Cambridge Institute, UK. These 2 Junior Groups will focus their efforts on the field of systems biology and computational genomics applied to the study of cancer. During the recruitment process we counted on the unparalleled support of Raúl

Maria A. Blasco
Director
steps a pivotal role. In the last two years, our media coverage interested by almost 75%, featuring stories about our CNIO efforts to fight cancer and ageing-related diseases, which also play a pivotal role. In the last two years, our media coverage interested by almost 75%, featuring stories about our CNIO efforts to fight cancer and ageing-related diseases, which also play a pivotal role. In the last two years, our media coverage interested by almost 75%, featuring stories about our CNIO efforts to fight cancer and ageing-related diseases, which also play a pivotal role. In the last two years, our media coverage interested by almost 75%, featuring stories about our CNIO efforts to fight cancer and ageing-related diseases, which also play a pivotal role. In the last two years, our media coverage interested by almost 75%, featuring stories about our CNIO efforts to fight cancer and ageing-related diseases, which also play a pivotal role. In the last two years, our media coverage interested by almost 75%, featuring stories about our CNIO efforts to fight cancer and ageing-related diseases, which also play a pivotal role. In the last two years, our media coverage interested by almost 75%, featuring stories about our CNIO efforts to fight cancer and ageing-related diseases, which also play a pivotal role. In the last two years, our media coverage interested by almost 75%, featuring stories about our CNIO efforts to fight cancer and ageing-related diseases, which also play a pivotal role. In the last two years, our media coverage interested by almost 75%, featuring stories about our CNIO efforts to fight cancer and ageing-related diseases, which also play a pivotal role.
“Discoveries made by CNIO scientists are constantly expanding the frontiers of our knowledge, and 2019 was no exception.”

During 2019, our scientists made great contributions towards a better understanding of how cancer originates and its potential treatments. We have revealed new strategies that could help to treat pancreatic tumours and contributed to clinical efforts in testing the efficacy of immunotherapy in lung cancer. We have proven that mutations affecting how cells sense the presence of nutrients can drive carcinogenesis and provided some initial ideas as to how to treat these tumours. We now also know that the synthesis of certain lipids is particularly essential during the initial steps of breast carcinogenesis and developed new biomarkers based on the lymph that could be taken to clinical practice. We have been able to establish primary uroepithelial organoids, which was a long-sought aim in the bladder cancer research and revealed how mutations in the cohesin subunit SA2 might drive carcinogenesis by regulating gene expression. We have also identified strategies that are particularly toxic for cells with more chromosomes than normal, something very frequent in tumour cells. Besides from cancer, contributions from CNIO scientists often have implications in other areas that are of high relevance for human health. For instance, we have revealed new clues about why different species age at different rates and obtained an atomic view understanding of some key pathogens, such as those that drive tuberculosis. We also have discovered strategies that increase the survival of mice exposed to ionising radiation, by protecting stem cells. Writing this annual overview is always a gratifying moment of reflection for me, as it reminds me of the reasons that made me join CNIO in the first place. I am in great company: Thanks to you all for your hard work and for making it possible. We should all be proud of where we are.
Basic Research

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MOLECULAR ONCOLOGY PROGRAMME

ÓSCAR FERNÁNDEZ-CAPETILLO Programme Director

The Molecular Oncology Programme (MOP) is the largest research programme at the CNIO, hosting 11 Senior and 4 Junior Groups. Scientists at the MOP focus on trying to obtain a mechanistic understanding of how cells in our body work, as well as to identify the molecular alterations at the cellular level that drive carcinogenesis. In addition, they try to generate new ideas and strategies to combat the disease. To do so, MOP Research Groups use a wide range of technologies including molecular and cellular biology, mouse models, genomics and patient material. The Programme encompasses expertise related to some of the most active areas of research in molecular oncology, including DNA and chromosome stability (Maria A. Blasco, Óscar Fernández-Capetillo, Massimo Squatrito and Ana Losada); oncogenes and cell cycle kinases (Mariano Barbacid); DNA replication (Juan Méndez); mitosis (Marcos Malumbres); melanoma (María S. Soengas); molecular pathophysiology of epithelial tumours of the bladder and pancreas (Francisco X. Real); growth factors, metabolism and cell signalling (Nabil Djouder and Alejo Efeyan); and metastasis (Manuel Valiente and Héctor Peinado). During 2019, 2 additional Senior Groups joined the MOP: the Transformation and Metastasis Group, led by Eva González Suárez; and the Topology and DNA Breaks Group, led by Felipe Cortés Ledesma - both supported by an ERC Consolidator grant. My warm welcome to both, and best wishes for a bright future at CNIO.

In terms of scientific publications, this year once again, the Molecular Oncology Programme has continued to be on the frontline of oncology research. The top-level quality of the research conducted by each of these Groups is exemplified through 11 papers published in Nature journals (Nature, Nature Cell Biology, Nature Communications, Nature Genetics, Nature Medicine, Nature Metabolism), 3 papers in Cell Journals (Cancer Cell, Molecular Cell), and 1 paper in Science; additional excellent contributions were made to Annals of Oncology, EMBO Journal, EMBO Molecular Medicine, European Urology, Gut, Science, JNCI, The Journal of Clinical Investigation, The Journal of Clinical Oncology, and The Journal of Experimental Medicine.

Scientists at the MOP are at the forefront of their respective fields of research and, besides from their publications, they contribute to, participate in and/or lead multiple scientific events aimed at both specialists and the general public.

“Many of our scientists are making an effort to translate their discoveries into therapies. We are not there yet, but I am firmly convinced that we are advancing on solid grounds. Let 2020 be our year.”
We study the mechanisms by which tumour cells are immortal and normal cells are mortal. Immortality is one of the most universal characteristics of cancer cells. The enzyme telomerase is present in more than 95% of all types of human cancers and absent in normal cells in the body. Telomeres are nucleoprotein complexes located at the ends of chromosomes, essential for chromosome protection and genomic stability. Progressive shortening of telomeres associated with organism ageing leads to ageing. When telomeres are altered, adult stem cells have a maimed regenerative capacity.

Our research focuses on:

→ Generating mouse models to validate telomeres and telomerase as therapeutic targets for cancer and age-related diseases.

→ The interplay between telomeres and DNA repair pathways.

→ The role and regulation of non-coding telomeric RNAs or TERRA.

→ Testing telomerase gene therapy in ‘telomere syndromes’ and age-related diseases.

→ The role of telomerase and telomeres in adult stem cell biology and in nuclear reprogramming of differentiated cells to iPS cells.

“Our studies showed that combination therapy with TRF1 inhibitors might become an effective strategy to inhibit cancer growth and combat drug resistance in glioblastoma and other tumours.”
RESEARCH HIGHLIGHTS

New effective drug combinations for glioblastoma in mice

Since the maintenance of telomeres, the eukaryotic chromosome ends, is essential to sustain cancer cell growth, they are considered a universal anti-cancer target. Telomeres are protected by the shelterin complex; targeting the shelterin complex may be an effective anti-cancer strategy. Glioblastoma is the most aggressive brain tumour, with very poor prognosis. Patients with glioblastoma usually develop resistance to treatments. We had previously shown that genetic and chemical inhibition of the shelterin protein TRF1 impairs tumour growth in mice. In this study, we report the combination of two FDA-approved drugs and drugs in clinical trials. We found that inhibition of several kinases of the Ras cancer pathway, including ERK and MEK, deactivates TRF1 (FIGURE 1).

This highlights the potential of combination therapies based on TRF1 inhibition as a promising therapeutic strategy to overcome drug resistance and effectively block glioblastoma growth.

Regulation of the transcriptional landscape of pluripotent cells

Pluripotent cells can give rise to all the cells of the body. Harnessing pluripotency may therefore open the door to regenerative medicine and organ culture for transplants. The genetic and epigenetic mechanisms that regulate pluripotency remain unknown. We have now uncovered one of the epigenetic signals controlling pluripotency that explains the observed powerful connection between pluripotency and telomeres. We found that the shelterin protein TRF1 regulates the genome-wide binding of polycomb and polycomb H3K27me3 repressive marks to pluripotency genes, thereby exerting epigenetic changes that contribute to the maintenance of mouse embryonic stem cells (ES) in a naive state. TRF1 mediates these effects by regulating PRC2, the polycomb RNAi. We propose a model in which TRF1-dependent changes in PRC2 levels modulate polycomb recruitment to pluripotency and differentiation genes, explaining why TRF1 is essential for the induction and maintenance of pluripotency (FIGURE 2).

Telomere rate of shortening predicts species life span

The shortening of telomeres below a critical length can trigger ageing and shorter life spans in mice and humans by induction of a persistent DNA damage response at the telomeres and loss of cellular senescence. We set to determine whether telomere shortening can be a single parameter to predict species longevities. To this end, we measured in parallel the telomere length of a broad variety of species (birds and mammals) of very different life spans and body sizes, including mouse, goat, Audouin’s gull, reindeer, griffon vulture, bottlenose dolphin, American flamingo, and Sumatran elephant. We found that the telomere shortening rate, and not the initial telomere length alone, is a powerful predictor of species life span. Critical telomere shortening and the consequent onset of telomeric DNA damage and cellular senescence are a general determinant of species life span.

Less metabolic ageing and longer life spans in mice with hyper-long telomeres

Short telomeres in mice and humans trigger age-related pathologies and shorter life spans. We measured mouse ES cells with longer telomeres than normal (hyper-long telomeres) in the absence of genetic manipulations, which contributed to all mouse tissues. We have now obtained mice in which 100% of their cells derive from hyper-long telomere ES cells and observed that they have longer telomeres and less DNA damage with ageing. Hyper-long telomere mice are lean, show low cholesterol and LDL, improved glucose and insulin tolerance, and have less cancer and increased longevity. Thus, longer telomeres than normal in a given species are not deleterious, showing instead beneficial effects such as increased longevity, delayed metabolic ageing and less cancer.

AWARDS AND RECOGNITION

- Member of the Advisory Board of the Spanish Ministry of Health and Social Services, Madrid, Spain.
- Vice-President of SOPMa (“Semin-Onto-Cells” Centre and “Maria de Hiedra” Units of Excellence Alliance), Spain.
- Member of the Board of Trustees of the Museo Nacional del Prado, Madrid, Spain.
OVERVIEW

KRAS oncogenes have been identified in one fifth of all human cancers. Yet, no selective inhibitors have been approved so far. Moreover, attempts to block KRAS oncogenic activity with selective inhibitors of KRAS signalling pathways have failed so far due to unacceptable toxicities. In our laboratory, we have continued our quest to validate therapeutic targets for KRAS driven lung and pancreatic tumours using a new generation of genetically engineered mouse tumour models that allow us to evaluate their anti-tumour properties as well as their potential toxic effects in tumour-bearing mice. These studies have allowed the identification of RAF1 as the only target within the MAPK signalling pathway capable of inducing significant tumour regressions in advanced KRAS/TRP53 mutant tumours without inducing major toxicities. We are now focusing our research interests on: (i) devising therapeutic strategies to selectively targeting RAF1 and (ii) identifying additional targets that may cooperate with RAF1 inhibition, with the ultimate goal of translating these results to the clinic.

“We have achieved, for the first time, the complete regression of a significant percentage of advanced K-Ras/Trp53 mutant pancreatic ductal adenocarcinomas by inducing the systemic ablation of combined RAF1 and EGFR expression.”
Complete regression of advanced pancreatic ductal adenocarcinomas upon combined inhibition of EGFR and RAF1 expression

We have developed a new GEM strain that separates temporally and spatially tumour development from target ablation/inhibition. This strain, K-RasG12V;Elas-creERT2, designated as KPeFC, incorporates 2 distinct recombinases, FlpO and CreERT2. FlpO is responsible for tumour induction, whereas expression of the tamoxifen (TMX)-inducible CreERT2 recombinase is driven by the human Ubiquitin C promoter (hUBC). Thus, exposure of KPeFC mice to a TMX-containing diet allows the systemic recombination of any conditional floxed allele added to this strain. We used this strain to interrogate the therapeutic properties of ablating RAF1 and EGFR based on previous observations using initiation models. Tumour-bearing KPeFC/EGFR<sup>lox/lox</sup>c-RAF<sup>lox/lox</sup> mice were exposed to a TMX-containing diet. Eight of 12 KPeFC/EGFR<sup>lox/lox</sup>c-RAF<sup>lox/lox</sup> mice displayed a rapid decrease in tumour volume upon TMX exposure. Six of these mice became tumour-free by micro-ultrasound analysis after 6 weeks of TMX exposure. Four mice were sacrificed after 6 weeks of TMX exposure, whereas the remaining animals were allowed to survive for 10 additional weeks. No tumour reappearance was observed during this time period. Moreover, detailed histological examination of their pancreata revealed normal tissue architecture, indicating that these tumours had completely regressed. Many therapies fail in the clinic due to unacceptable toxic effects. However, systemic deletion of EGFR and RAF1 expression completely interfered with the proliferative capacity of those cells derived from 9 out of the 10 PDX tumour models. Four of the PDX-derived tumour models that fully responded to EGFR or c-RAF knockdown were injected into immunocompromised mice. Again, only the combined knockdown of EGFR and c-RAF effectively inhibited growth of these human PDAC tumour cells in vivo. These observations suggest that combined inhibition of EGFR and c-RAF expression may have significant therapeutic activity in human PDAC tumours.

In the absence of EGFR or RAF1 expression. Transcriptional analyses did not reveal significant differences with tumours harboured by KPeFC<sup>lox/lox</sup> mice. The TMX diet did not respond to the TMX diet. Histopathological analyses did not reveal significant differences with tumours present in control animals. Surprisingly, these tumours retained active MAPK and PI3K/AKT signalling pathways even in the absence of EGFR or RAF1 expression. Transcriptional analysis of tumour cells derived from tumours that did not respond to EGFR and RAF1 ablation revealed very distinct transcriptional profiles with more than 2,000 differentially expressed genes when compared with those tumours that regressed upon RAF1 and EGFR ablation.

Gene Set Enrichment Analysis (GSEA) identified several pathways enriched in the resistant tumour cells, including those corresponding to ‘EGF targets’, ‘EMT’ and ‘MYC targets’. Other enriched pathways included the ‘PI3K/AKT/mTOR’ and ‘IL6/JAK/STAT3’ signalling pathways. Comparison of data obtained by RNAseq analysis with a transcriptional classification of human PDACs (Bailey et al., 2016) revealed that NC cells displayed a transcriptional profile most similar to the ‘squamous subtype’.

Finally, we determined whether combined inhibition of EGFR and c-RAF signalling could provide therapeutic benefit to PDAC patients. To this end, we knocked down their expression in cells derived from 10 PDX tumour models harbouring K-RAS and TRP53 mutations. Individual knockdown of EGFR or c-RAF expression reduced their proliferative properties to various extents. More importantly, combined knockdown of EGFR and c-RAF expression completely interfered with the proliferative capacity of those cells derived from 9 out of the 10 PDX tumour models. Four of the PDX-derived tumour cells that fully responded to EGFR or c-RAF knockdown were injected into immunocompromised mice. Again, only the combined knockdown of EGFR and c-RAF effectively inhibited growth of these human PDAC tumour cells in vivo. These observations suggest that combined inhibition of EGFR and c-RAF expression may have significant therapeutic activity in human PDAC tumours.
OVERVIEW

The Cell Division and Cancer Group is interested in deciphering the mechanisms by which cell division and cell proliferation are regulated in a variety of mammalian cell types. Our scientific interests are: i) to understand the basic control mechanisms that regulate the cell division cycle; ii) to characterise the physiological and therapeutic consequences of cell cycle deregulation; iii) understanding self-renewal and pluripotency in stem cell biology and tumour development; and iv) finding and validating new targets for cancer therapy. As a final goal, we aim to generate information that will be useful for understanding basic mechanisms of cell function and to improve therapeutic strategies against cancer cell proliferation.

“We have investigated the implication of cell cycle kinases such as CDK4/6 and MASTL in cell proliferation and metabolism, and their relevance as therapeutic targets in breast and pancreatic cancer.”
CDK4/6 inhibitors have recently been approved for the treatment of advanced breast cancers, and inhibiting CDK4/6 activity is considered an attractive therapeutic intervention for multiple malignancies. However, it is generally assumed that these inhibitors should not be used in combination with classical chemotherapy as seeing as CDK4/6 inhibition arrests cells in G1, thereby protecting tumour cells from the cytotoxic effect of classical chemotherapy acting either in S-phase or mitosis in proliferating cells. This is a major problem for cancer patients, as the standard of care for most patients with advanced disease is ‘classical’ chemotherapy (DNA damaging agents, topoisomerase inhibitors, taxanes etc.).

Using pancreatic adenocarcinoma (PDAC) as a model, in collaboration with M. Hidalgo (CNIO and Cornell University, NY, USA) and D. Shields (Pfizer, USA), we generated data suggesting that, both in vitro and in vivo, applying CDK4/6 inhibitors right after taxanes strongly cooperates to prevent tumour cell proliferation. We have also demonstrated that the mechanism behind these observations is the requirement for CDK4/6 activity in homologous recombination, which is required for recovery from the chromosomal damage imposed by taxanes. This mechanism immediately suggests that CDK4/6 inhibitors could be efficiently used after a variety of classical chemotherapies, including nucleotide analogues, topoisomerase poisons and other DNA damaging agents, microtubule poisons, targeted anti-mitotic therapies, etc., as well as radiation. These results may have a major impact on the application of cell cycle inhibitors in the clinic in a variety of tumour types, and we are currently evaluating possible scenarios to move this strategy into clinical trials in cancer patients.

**RESEARCH HIGHLIGHTS**

**New applications of inhibiting CDK4/6 kinases in cancer therapy**

CDK4/6 inhibitors have recently been approved for the treatment of advanced breast cancers, and inhibiting CDK4/6 activity is considered an attractive therapeutic intervention for multiple malignancies. However, it is generally assumed that these inhibitors should not be used in combination with classical chemotherapy as seeing as CDK4/6 inhibition arrests cells in G1, thereby protecting tumour cells from the cytotoxic effect of classical chemotherapy acting either in S-phase or mitosis in proliferating cells. This is a major problem for cancer patients, as the standard of care for most patients with advanced disease is ‘classical’ chemotherapy (DNA damaging agents, topoisomerase inhibitors, taxanes etc.).

**MASTL: a cell cycle kinase with new roles in the control of metabolism**

Work in the last few years has established a new cell cycle regulatory module involving the protein kinase MASTL, also known as Greatwall in flies or Xenopus, in the control of PP2A phosphatase activity. This regulation has been shown to be critical for maintaining CDK1-mediated phosphorylation of mitotic substrates, and MASTL is now considered an essential cell cycle kinase of relevance in cancer therapy. Our recent data suggest an unexpected connection between MASTL and the feedback loop that controls AKT activity in response to maintained mTOR/S6K signalling. This feedback loop is an essential component of mTOR signalling to prevent excessive AKT activity upon continuous nutrient signalling and has major implications in multiple AKT-mTOR-downstream processes. MASTL ablation impairs the proper regulation of this feedback loop, resulting in hyperactivation of AKT. This work not only adds a new parallel pathway that restricts phosphatase activity upon mTOR/S6K signalling, but also provides a molecular mechanism for our in vivo data showing increased glucose tolerance in MASTL-deficient mice. The possibility of modulating MASTL-PP2A activity in some metabolic disorders like diabetes or obesity will be studied in the lab during the upcoming months.

**Understanding pluripotency and improving the use of pluripotent cells in regenerative medicine**

How pluripotent cells control their self-renewal and differentiation potential is a major topic of research in our lab. Our recent work suggests that a microRNA expressed in early development, miR-203, can be used to induce naive pluripotency in both murine and human iPSCs and ESCs, thereby enhancing the potential of these cells in vitro and in vivo. Mechanistically, this effect is mediated through the repression of de novo DNA methyltransferases Dnmt3a and Dnmt3b and genome-wide demethylation of DNA in pluripotent cells, thereby favouring the generation of differentiated cells of interest in regenerative medicine.

**PUBLICATIONS**


**PATENT**

In the Genomic Instability Group, our aim is to obtain a mechanistic understanding of cancer and other age-related diseases, and then use this information to develop new therapies. To this end, we combine molecular and cellular biology approaches with chemical and genetic screens. In addition, we also develop mouse models of disease, which we can later use as platforms for testing new treatments. Using these tools, in recent years, we have made exciting discoveries in several areas such as mechanisms of resistance to cancer therapies, targeting nucleolar stress in cancer, drug development and neurodegeneration. Ultimately, our objective is to find new or better treatments for human disease.

“In 2019, we have further invested in the technologies to conduct forward genetic screens in mammalian cells and revealed a new mechanism of action for USP7 inhibitors that are being developed as anticancer agents.”
Targeting cells with higher ploidy

Haploid organisms, such as yeast, have for the majority of the 20th century been the model of choice to conduct forward genetic screenings, the reason being that mutations in a allele frequently suffice to reveal a phenotype. Because many biological questions are intrinsic to mammals, attempts to isolate and grow haploid mammalian cells in culture initiated in the 1960s, and were finally developed in the last decade. However, despite their usefulness, haploidy remains an unstable state in mammalian somatic cells as these cultures rapidly become enriched in diploids. A few years ago, we revealed that the so-called ‘diploidization’ was rather a selective loss of haploid cells due to the activation of a p53-dependent response. Based on this property, we have now performed a chemical screen in human haploid cells aiming to identify compounds that facilitate the maintenance of haploid cells in culture. Our search identified that 10-Deacetyl-baccatin-III, a precursor in the synthesis of taxol, could do so. Remarkably, this compound not only selects for haploidy, but also presents a general capacity to select for diploid cells in mixed cultures of diploid and tetraploid cells (FIGURE 1).

Altogether, this study has identified a compound that solves the problem of ‘diploidization’ of haploid mammalian cell lines and has revealed a general strategy to select for cells with lower ploidy in mixed cultures of mammalian cells.

USP7 counteracts the activation of the mitotic programme

Chemical inhibitors of the deubiquitase USP7 are currently being developed as anticancer agents due to their capacity to upregulate the tumour suppressor P53. However, besides from this activity, USP7 inhibitors also generate DNA damage in a p53-independent manner, and the actual molecular mechanism underlying its genotoxicity remains unknown. We previously reported that USP7 has an essential role to ensure replication progression, and thus USP7 inhibitors prevent the completion of this process. Our more recent results illustrate that this effect occurs concomitantly with a premature activation of mitotic kinases, such as CDK1, throughout the cell cycle, which impairs chromosome condensation and is toxic for mammalian cells (FIGURE 2). This year, we have delved into the molecular mechanisms triggering this premature process and found that USP7 deubiquitase works through the interaction with the phosphatase PP2A, which, in turn, is one of the proteins involved in the control of the mitotic activation programme. Supporting our model, the toxicity of USP7 inhibitors is alleviated by lowering CDK1 kinase activity or activating PP2A phosphatase. Our results provide new information regarding the regulation of the mitotic activation programme and are the first example of triggering premature mitosis through the perturbation of ubiquitin signalling. Additionally, these studies reveal that the anticancer properties of USP7 inhibitors are actually related to the premature activation of the mitotic machinery in cells that have not yet fully replicated their genome.
OVERVIEW

DNA topoisomerases have a dual relationship with the genome. They are essential to solving the topological problems inherent to all DNA transactions, but their intrinsic mechanism of action can result in the formation of DNA breaks, either accidentally during normal cellular metabolism or upon chemotherapy treatment with the so-called topoisomerase poisons. Imbalances in DNA topoisomerase activity can therefore compromise cell survival and genome integrity, entailing serious consequences for human health, such as developmental and degenerative problems and, very importantly, neoplastic transformation processes and their subsequent response to treatment.

We are interested in understanding: (i) how DNA topoisomerase activity is regulated to integrate different aspects of genome dynamics; (ii) how an imbalance in these processes can lead to the appearance of pathological DNA breaks; and (iii) how cells specifically respond to these lesions to maintain genome stability.

“We have proven a causal link between spontaneous DNA breaks induced by topoisomerase II and cancer development, especially in cancer predisposition human genetic syndromes such as Ataxia Telangiectasia.”
Work of the Group at the CNIO in these last few months since starting in September 2019 has focused on finishing data analysis to establish a link between a deficient response to topoisomerase II (TOP2)-induced DNA double strand breaks (DSBs) and spontaneous cancer predisposition. Specifically, we have worked with animal models of Ataxia Telangiectasia (AT), a human genetic syndrome that results from loss-of-function mutations in ATM.

The ATM kinase is a master regulator of the DNA damage response to DSBs and is a well-established tumour suppressor. Loss-of-function mutations in the gene are not only found frequently in many types of cancer, but also constitute the underlying cause of the neurodegenerative and cancer-prone genetic syndrome Ataxia Telangiectasia. AT patients are particularly predisposed to develop lymphoid cancers, which are thought to arise from inefficient signalling and inaccurate repair of RAG-induced DSBs during V(D)J recombination, and which the Atm-/- mouse models recapitulate in the form of very aggressive T-cell malignancies.

We have unexpectedly found that specifically disturbing the repair of TOP2-induced DSBs by genetically removing the highly specialised repair enzyme TDP2 strongly increases the incidence of thymic tumours in Atm-/- mice, but without changing their molecular characteristics or underlying genomic rearrangements, including a significant association with Tcr loci. Furthermore, we found that TOP2 strongly colocalises with RAG, both in a genome-wide scale and specifically at sites undergoing V(D)J recombination, in a manner that is consistent with its involvement in solving topological problems associated to 3D genome organisation, and that results in increased chromosomal fragility of these regions. Thus, our findings demonstrate a strong causal relationship between spontaneous TOP2-induced DSBs and cancer development, confirming these lesions as major drivers of ATM-deficient lymphoid malignancies, and potentially other conditions and cancer types.
Our research focuses on a protein complex named cohesin that embraces DNA to mediate sister chromatid cohesion, a process essential for chromosome segregation and faithful DNA repair by homologous recombination. Cohesin also plays a major role in the spatial organisation of the genome by promoting long-range DNA looping, which in turn contributes to transcriptional regulation. Mutations in cohesin have been found in several tumour types, most prominently in bladder cancer, Ewing sarcoma and acute myeloid leukaemia. Germ line mutations in cohesin and its regulatory factors are also at the origin of human developmental syndromes collectively known as cohesinopathies.

Our goal is to understand how cohesin works, how it is regulated and how its dysfunction contributes to cancer and other human diseases. In particular, we are intrigued by the existence of different versions of the cohesin complex. We use human cells and mouse models carrying knock out alleles of genes encoding variant cohesin subunits to investigate their functional specificity.

“We have found that cohesin complexes carrying SA1 or SA2 make distinct contributions to the spatial organisation of the embryonic stem cell genome, and their loss impacts differently on gene expression.”
Cohesin dynamics and DNA replication

How the transcription and replication machineries deal with the presence of cohesin on chromatin remains unclear. The dynamic association of cohesin with chromatin depends on Wapl and Pds5, which exists in two versions in vertebrate cells, Pds5A and Pds5B. Using genetic deletion in mouse embryo fibroblasts and a combination of genome editing by CRISPR and RNA interference in human cells, we have analysed the consequences of Pds5 depletion for DNA replication. We found that either Pds5A or Pds5B is sufficient to allow proper cohesin dynamics while their simultaneous removal increases cohesin’s residence time on chromatin and slows down DNA replication. A similar phenotype is observed in Wapl-depleted cells. Normal fork rates are restored in Pds5-deficient cells by cohesin downregulation, suggesting that chromatin-bound cohesin hinders the advance of the replisome. We further showed that Pds5 proteins are also required to recruit Wrnipt, Rad51 and Brca2 to stalled forks and, in their absence, nascent DNA strands at unprotected forks are degraded by the Mre11 nuclease. These findings provide new hints as to how cohesin and its regulators contribute to the response to replication stress, a common feature of cancer cells.

Figure Cohesin variants regulate distinctially the spatial organisation of mESCs. (A) Aggregate analyses of Hi-C interactions between promoters within the Hoxb or Hoxc loci and any other Polycomb-bound promoter in cells with (control) or without SA1 or SA2. (B) As a consequence of decreased interactions between Polycomb domains in the absence of SA2, Polycomb repressed genes are de-repressed, as shown in this box plot. (C) A model for the roles of cohesin-SAI and cohesin-SA2 in intra- and inter-Polycomb domain interactions, which ultimately affect gene repression.

RESEARCH HIGHLIGHTS

Dissecting the role of cohesin-SA1 and cohesin-SA2 in mouse embryonic stem cells

Cohesin consists of 4 core subunits, SMC1, SMC3, RAD21 and SA/STAG. There are 2 versions of the SA subunit in all vertebrate somatic cells, SA1 and SA2. Our recent studies in human cells analysing the genomic distribution of cohesin, gene expression and 3D chromatin organisation in the absence of either variant showed that cohesin-SA1 is important for the organisation of the topological associated domains (TADs) that make up the global structure of the genome and works always alongside the CTFC protein. In contrast, cohesin-SA2 promotes more local chromatin contacts that are relevant for tissue-specific transcription independently of CTFC. In the absence of SA2, a situation that occurs in several tumours, cohesin-SA1 cannot occupy the non-CTCF cohesin sites normally bound by cohesin-SA2, and gene expression is altered.

To confirm these findings, we have now carried out similar analyses in mouse embryonic stem cells (mESCs), as they provide a powerful experimental system to address the functional cross-talk between genome organisation and gene regulation and differentiation. Maintenance of stem cell properties requires a careful balance between self-renewal and differentiation, which is achieved by the active transcription of pluripotency genes under the control of super-enhancers and the repression of lineage specification genes by Polycomb Complex 1 (PRC1) and PRC2. Genes and gene clusters occupied by PRC1 in mESCs, most prominently the Hox loci, define a new class of self-interacting domains of compacted chromatin that is different from TADs, the Polycomb domains. We have found that cohesin-SA2 facilitates Polycomb domain compaction through PRC1 recruitment and in this way promotes the establishment of long-range interaction networks between distant Polycomb-bound promoters and contributes to gene repression (FIGURE). Cohesin-SA1, in contrast, disrupts these networks, while preserving TAD borders. Also in super-enhancers, cohesin-SA2 mediates local, short-range interactions while cohesin-SA1 plays a more important role in defining domain borders. The diverse effects of both complexes on genome topology may reflect two modes of action of cohesin that depend on their dynamic association with chromatin. Fluorescence recovery after photobleaching (FRAP) experiments in mouse cells show that cohesin-SA1 binding to chromatin is more stable than the binding of cohesin-SA2. This is probably due to the lower affinity of SA1 for Wapl, a cohesin releasing factor, and its higher affinity for CTFC. We are currently testing these hypotheses and further exploring the consequences of SA1 or SA2 loss on cell differentiation.
Our laboratory studies the process of genome duplication, which is responsible for many of the mutations and genomic alterations found in human cancer. While the protein machinery responsible for DNA replication is normally very accurate, it becomes error-prone when the DNA displays chemical alterations caused by endogenous reactive species, external drugs or ionising radiation. We are interested in the phenomenon of replicative tolerance, i.e. the mechanisms that allow the progression of the ‘replisome’ proteins through damaged DNA, a step that normally precedes the activation of specific DNA repair pathways. In 2019, we focused on two major areas: (1) studying the efficiency of replication origins in response to replication stress in pluripotent cells, in the context of their three-dimensional positions in the nuclear chromatin; and (2) evaluating the function of DNA primase PrimPol in the tolerance of cytotoxic DNA lesions in normal and cancer cells with different genetic backgrounds.

“We have identified that PrimPol primase counteracts the effect of cisplatin and other DNA crosslinking agents and mediates an adaptive response in cancer cells that could be exploited in chemotherapy.”
RESEARCH HIGHLIGHTS

In previous years, we identified 2 cellular responses to replicative stress (RS), a phenomenon defined by the slowdown of DNA synthesis caused by damaged DNA templates or special DNA secondary structures that are difficult to replicate. The first response involves the activation of extra replication origins, and the second one involves specialised enzymes that promote re-initiation of DNA synthesis downstream of the lesion, leaving it behind and triggering a signal to initiate its subsequent repair. In 2019, we have continued to characterise both pathways.

Mapping of ‘dormant’ origins that react to replicative stress

As one of the early proponents of the role of ‘dormant origins’ in counteracting RS, we are interested in their characteristics as well as their localisation and mode of activation. We led a study to map active origins in embryonic stem cells under normal growth conditions or in the presence of RS (Figure 1), in collaboration with M. Gómez (Centro de Biología Molecular “Severo Ochoa”: Madrid), Alfonso Valencia (Barcelona Supercomputing Center) and V. Pancaldi (Cancer Research Centre of Toulouse). Because origins are not ‘fired’ in every cell in the population, they can be classified according to their efficiency, i.e. the proportion of cells in which they are activated. The most efficient origins tend to be located at regions displaying ‘open chromatin’ epigenetic marks, frequently overlapping with CpG islands and transcriptional start sites. In contrast, RS-responsive origins correspond to less efficient initiation sites and are not enriched in these genomic elements. RS triggers a global increase in origin efficiency, maximising the activation of low-usage origins as a backup for replication. To identify structural determinants of origin efficiency, we integrated origin maps into 3D networks of chromatin contacts, finding that origin efficiency is proportional to their connectivity with other origins (Figure 2). Interconnected origins tend to display similar efficiency and replicate at the same time in 3D, providing a logical framework for the concept of chromosomal ‘replication factories’ (Jodkowska et al., 2019).

Replicative tolerance mediated by PrimPol protein

PrimPol is the only primase in mammalian cells besides the canonical Pol/primase involved in the initiation of DNA replication. In previous work, we reported that PrimPol facilitates replication through UV-induced DNA adducts by synthesising DNA primers downstream of the damaged nucleotides. In 2019, we collaborated with the laboratory of A. Vindigni (Washington University, St Louis, MO, USA) to analyse how PrimPol mediates an adaptive cellular response to DNA damage in human cells. We have started a screening for potential PrimPol small molecule inhibitors, in collaboration with the CNIO Experimental Therapeutics Programme.

DNA replication in other biological contexts

We contributed to the characterisation of TIAR, an RNA-binding protein required for genomic stability that restricts CDK1 activity under RS (Lafarga et al., 2019). We also started a collaboration with Scott Lowe (Memorial Sloan-Kettering Cancer Center, New York, NY, USA) to perform CRISPR-based genetic screenings related to the effect of uncontrollable DNA replication in the process of gene amplification.

Figure 1 Identification of stress-responsive origins. Genome browser regions containing origins mapped by SNS-Seq in two replicates (I-II) of mESCs (WT), or the same cells by SNS-Seq in two replicates (I-II)

Figure 2 Origin connectivity is linked to efficiency. Representation of a subset of the total network of origins located in a 3D chromatin contact map generated by promotor-capture Hi-C. Origin efficiency, indicated by a yellow-to-red colour gradient, is directly proportional to the number of connections (degree) established by each node in the network. The correlation is reflected in the box plots shown in the right panel. Adapted from Jodkowska et al. (2019).

PUBLICATIONS


AWARDS AND RECOGNITION

- Visiting Scientist, Memorial Sloan-Kettering Cancer Center in New York (USA).
- Sponsored by the Fulbright Commission and the ‘Salvador de Madariaga’ Programme (Ministerio de Educación y Universidades, Spain).
- Coordinator of the “Molecular and Cellular Biology” area, Agencia Estatal de Investigación, Spain.
Melanomas are inherently aggressive cancers for which basic and translational research have significantly improved patient prognosis. Nevertheless, clinical responses are still incomplete. The long-term goals of our Group are to identify new progression biomarkers and therapeutic agents. We are particularly interested in mechanisms of cellular stress that, being selectively deregulated in melanoma, define lineage-specific vulnerabilities (publications in *Nature, Cancer Cell, Nature Cell Biology, Nature Communications*, among others). Our laboratory has also generated the first-in-class lymphoreporter mice for non-invasive imaging of pre-metastatic niches in melanoma (*Nature*). These systems have led to the validation of nanoparticle-based treatments that are currently being tested in clinical trials. Our ultimate objective is to improve the management of patients with otherwise refractory metastatic melanomas.

“The long-term goal of the Soengas Laboratory is to translate basic research in melanoma into the clinic, by identifying novel tumour markers and drug targets.”
**RESEARCH HIGHLIGHTS**

**CNIO Melanoma Group: objectives and model systems**

Melanomas are aggressive solid tumours and a paradigm of how basic and clinical research have significantly improved patient prognosis. Nevertheless, despite great success achieved with targeted and immune-based therapies, sustained clinical responses are still limited. Moreover, the field lacks molecular markers of diagnosis, and the knowledge about how melanomas progress is largely incomplete. These are main unmet needs, as melanomas are the only tumours where lesions barely over one millimetre in depth can be at risk for metastasis. One of the main objectives of our Group is to define drivers of this lineage-specific behaviour. In addition, we are interested in imaging and targeting (pre)metastatic niches in vivo. Specifically, we have elected to visualise the tumour-induced expansion of the lymphangiogenic vasculature (neo-lymphangiogenesis), as this is a process that is activated at early stages of melanoma initiation. However, the specific contribution of lymphatic endothelial cells (LEC’s) to melanoma is unclear. LECs can secrete a variety of cytokines, which, depending on the context, may favour or inhibit immune surveillance. Moreover, sentinel lymph node removal does not necessarily extend the overall survival of melanoma patients, suggesting that melanoma cells ‘escape’ very early to distal (pre)metastatic niches, but how this occurs remains poorly defined.

The main aims of our Group are (FIGURE 1):

1. To define when and how melanomas act “at a distance” (on stromal and immune compartments) before tumour cell dissemination.
2. To determine how melanoma cells evade the immune system, and whether distinct mechanisms may be activated at different anatomical sites.
3. To dissect the impact of the microenvironment, particularly alarmins and bacterial response factors.
4. To develop anticancer agents to prevent and eliminate metastatic sites.

**Lineage-specific oncogenic dependencies in melanoma**

One of the long-term objectives of the Melanoma Group is to discover new melanoma drivers. We previously identified a cluster of endolysosomal-associated genes that distinguish melanomas from over 35 additional malignancies (Aloña-Curbelo et al., Cancer Cell 2014). Further analyses of lysosomal-dependent pathways also revealed unique features of autophagy genes (ATG5) in melanoma (García-Fernández et al., Autophagy 2016). Other melanoma-enriched regulatory mechanisms were identified by focusing on RNA binding proteins (RBPs). We selected RBPs (a family of over 1500 members) because they are largely unexplored in melanoma, although this is a tumour characteristically associated with a plethora of changes in mRNA gene expression profiles. Performing a series of genome-wide studies (i.e. genomic, transcriptomic, proteomic and interactomic analyses), we uncovered new roles of the RBPs CPEB4 and CUGBP1 in the modulation of mRNA stability, with unexpected targets involving master specifiers of the melanocyte lineage (Perez-Guijarro et al., Nat Commun 2016; Cifdaloz et al., Nat Commun 2017). We have now identified new roles of the RNA binding protein IGF2BP1 in the control of the half-life of a large set of pro-metastatic factors. These included FERTM2 and FERMT2 as adversative determinants of disease-free survival (Karras et al., Cancer Cell 2019, with the cover highlighting the new signalling cascades identified).

‘MetAlert’ mice for the visualisation of premetastatic niches in melanoma and as a platform for gene discovery and target validation

We previously published lymphoreporter melanoma models to visualise metastatic niches before their colonisation (Olmeda et al., Nature 2017). ‘MetAlert’ animals, in combination with human tissue specimens, revealed growth factor MIDKine as a new driver of lymphangiogenesis and melanoma metastasis. We have now exploited the MetAlert mice to further define immunomodulatory roles of MDK, and to screen for anticancer agents. In particular, we identified an unexpected ability of dsRNA-based mimic BO-110 to blunt neolymphangiogenesis and the associated melanoma metastases (Olmeda et al., BioRev 2019; see comparative analyses with respect to targeted agents or immunomodulatory antibodies in FIGURE 2).

**Figure 1** Main objectives of the CNIO Melanoma Group aimed to identify new expression biomarkers and validate more efficient anticancer agents.

**Figure 2** MetAlert mice for pharmacological testing of anticancer agents. Luciferase-based imaging of drug response in MetAlert mice that reconstitute malignant melanomas driven by oncogenes. Blue/Pink in the context of Pten loss (Vagelakis et al., Proc Natl Acad Sci U S A 2015). Representative examples of mice with no tumours (not induced), and mice with lethal metastases were induced by tamoxifen, but were left either untreated or treated as indicated. (B) Growth curves of treatments as in (A).

**PUBLICATIONS**

- Fritz Anders Cancer Cell 2016 (Top500 Most Influential Spanish Women).
- Selected Member, Academia Galicia de Farmacia, Real Academia Nacional de Farmacia
- Elected Treasurer, Confederación de Sociedades Científicas de España (COSEC)
- Special mention Ciencia y Mujer 2019
- WomenCEO, Jóvenes Investigadoras Gallegas en el Extranjero Event.
- Top100 Mujeres Líderes de España 2019 (Top100 Women Leaders in Spain)
- Muñoz E C.

**AWARDS AND RECOGNITION**

- Alfredo Ferrer Award for Pigment Cell Research (EP Carrera)
- Seagram Award for Influential Women in Science and Innovation
- \( \text{RCina-Fernández樊女士 2019 (Top50} \) Influential Spanish Women (Women CEOWomenCEO, Jóvenes Investigadoras Gallegas en el Extranjero Event.}
BASIC RESEARCH

MOLECULAR ONCOLOGY PROGRAMME

EPITHELIAL CARCINOGENESIS GROUP

We focus on the molecular pathophysiology of pancreatic ductal adenocarcinoma (PDAC) and urothelial bladder carcinoma (UBC), adopting a disease-oriented approach. We use patient samples, cultured cells, and genetically modified mice, giving a similar weight to the 3 model systems. Observations made at either of these levels are then extended through additional work. To translate the findings, we bring this knowledge to a ‘population’ level – leveraging on information and samples from large patient cohorts – in close collaboration with Núria Malats’ Group.

In PDAC, a main hypothesis is that cell differentiation is a potent tumour suppressor mechanism acting early on in carcinogenesis. We use the excellent genetic mouse models available because these processes cannot be readily studied in humans. In mice, PDAC can originate in pancreatic progenitors and in adult acinar and ductal cells. Understanding the contribution of early molecular events is crucial to design better strategies for prevention and early tumour detection.

In UBC, we focus on identifying new genes, using them for improved tumour taxonomy, characterising the mechanisms of action, and applying this knowledge for improved prediction of outcome and therapy.

“Our Group was the initiator of the International Bladder Cancer Molecular Taxonomy Group, which, in 2019, released the Second Consensus Classification.”

OVERVIEW

Francisco X. Real
Group Leader

Miriam Marqués
Staff Scientist

Elena del Pilar Andrada, Irene Felipe, Eleonora Lapi, Santí Pardal, Mark Kalisz (until June), Gabriel Piedrafita (since April)

Post-Doctoral Fellows

Sonia Coral (since September), Ana M. Maldonado, Irene Millán, Catarina Pereira (until September), Monica Pérez

Graduate Students

Elena del Pilar Andrada, Irene Felipe, Eleonora Lapi, Santí Pardal, Mark Kalisz (until June), Gabriel Piedrafita (since April)

Technicians

Miguel Deblas, Natalia del Pozo, Jaime Martínez (TS)

Visiting Scientists

Luís César Fernández Díaz (since October) (Universidad Europea Madrid), Mark Kalisz (since July) (CIBER, Madrid)

“Titulado Superior (Advanced Degree)”

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Pancreatic cancer molecular pathophysiology

The genetic and genomic changes associated with PDAC have been extensively described over the last few years by the genome consortia, and there is increasing interest in defining the contribution of precursor lesions and the molecular changes that precede tumour development. Our lab has pioneered the notion that cell differentiation is the first tumour suppressor process in the pancreas. Focusing on acinar cells, we have identified several novel players - and mechanisms - including GATA6, GATA4, NRS2A, HNF3A, and NFTC. Dysregulation of these transcription factors is associated with a scenario of pre-inflammation or inflammation and with predisposition to PDAC development using mutant Kras-driven genetic mouse models. These studies provide the basis for the pharmacological – or genetic – manipulation of acinar differentiation as a tumour preventative strategy.

We have found that while loss of either GATA6 or GATA4 favours PDAC development in mouse models of chronic inflammation, acinar cells play distinct roles in acinar differentiation and inflammation, and they contribute differently to tumour initiation. We are now focusing on understanding their specific functions and deciphering their transcriptional programmes using a combination of mouse models and genomic approaches (i.e. RNA-Seq and ChIP-Seq). In collaboration with J. Ferrer (CRG, Barcelona), we have developed conditional knockout mouse models of Hopfta that are providing new evidence of the tumour suppressor role of this gene in PDAC initiation. Using a dual recombinase system, we are exploring whether Hopfta affects the tumour suppressor role of this gene in PDAC initiation.

Our recent effort to develop organoids from normal urothelial cells has culminated in the first single cell RNA-Seq analysis of these cells, which provided novel evidence on the role of the NOTCH pathway in urothelial differentiation, and uncovered new genes associated with this process (FIGURE 1). The organoid cultures provide key clues to understanding urothelial stem cell biology and the control of cell proliferation and regeneration in homeostasis and upon cancer.

URETHRAL BLADDER CARCINOMA (UBC) GENETICS, BIOLOGY, AND CLINICAL TRANSLATION

We are interested in refining our understanding of new genes involved in UBC, using organoids and genetic mouse models to unravel their function, and to apply this knowledge in the clinical setting.

Through exome sequencing we identified mutations in STAG2, coding for a cohesion subunit, and in RBM10, coding for a splicing regulator, as new UC genes that are more broadly involved in human cancer. We have generated conditional mouse models for these 2 genes and are exploring their role in development and urothelial biology as well as their cooperation with other bladder cancer genes.

STAG2 is a cohesin complex component. Increasing evidence shows that it acts as a tumour suppressor through rather unique mechanisms, largely unrelated to the canonical role of cohesin in chromosome segregation. Using normal cultured urothelial cells, we have found that the genomic effects of STAG2 loss are largely dependent on the differentiation state of the cells. These findings support the strong association of STAG2 inactivation with a luminal/urothelial phenotype and pave the way for the discovery of new mechanisms leading to UBC.

Our translational studies focus on the prediction of response to cisplatin-based chemotherapy and to immune checkpoint blockade (ICB). In collaboration with an extended group of Spanish uro-oncologists and Núria Malats, we are assessing the value of immune signatures to stratify patients to receive neoadjuvant therapy (cisplatin-based chemotherapy vs. ICB) in a randomised clinical trial.

![Figure 1](image)

**Figure 1** Organoids derived from normal mouse urothelium provide a unique tool to understand tissue biology. (A) Urothelial organoids can be perpetuated for more than 1 year under proliferative conditions (P) and can be induced to differentiate (D), as shown by the down-regulation of basal keratins and the up-regulation of uroplakins. (B) Differentially regulated, but not their proliferative counterparts, acquire barrier function characteristic of the normal urothelium. This is evidenced using FITC-destined loading and fluorescence recovery after photobleaching (FRAP). (C) Single cell RNA-Seq has allowed the identification of the features of normal proliferative urothelial cells as well as the role of the Notch pathway in urothelial differentiation. Upper panel shows the UMAP plots visualizing integrated analysis of cells from P and D organoids as a joint plot (top) or as separate plots (bottom).

**PUBLICATIONS**

Research in the last decade has focused mainly on understanding the functions and roles of newly discovered mutated genes in the development of cancer and associated diseases. With this focus, less attention has been paid to environmental factors leading to the expression of virulent eukaryotic proteins or tissue damage that also present a permanent challenge for an organism. How environmental factors can alter the host’s eukaryotic epithelial cells to cause various pathologies, potentially progressing to cancer, remains largely unknown. The identification of likely causal links between environmental stresses and diseases progressing to cancer will help to elucidate mechanisms of diseases and to identify, and functionally validate, targets with preventive and therapeutic values to treat frequent lethal human disorders with increased worldwide incidence and unmet medical needs.

“We put lots of effort to understand mechanisms of diseases by generating and using new mouse models that recapitulate pathological features of human syndromes in order to guide the design of novel medicines.”
Our laboratory is devoted to the understanding of the molecular mechanisms that link environmental stresses to disease pathogenesis affecting organs of the digestive system, including the liver, intestine, pancreas and stomach (FIGURE).

Based on the integration of experimental mouse models, combined with the use of state-of-the-art technologies and human data, our interest is mainly driven by the discovery of the proteins URI (Unconventional prefoldin RPB5 Interactor) and MCRS1 (Microspherule protein 1), whose expressions are regulated by various environmental factors – radiation, bacteria, viruses, diet, etc. (Djouder et al., 2007; Fawal et al., 2015; Chaves-Perez et al., 2019) – compromising their functions and activating pleiotropic circuits to support non-oncogene addiction functions and dependence, thereby provoking severe outcomes.

In this regard, in the past, we conceptually demonstrated that metabolic alterations initiate tumorigenesis prior to genomic instability (Tummala et al., 2014; Brandt et al., 2017) and thus, are driving forces in cancer development. Our findings indicate that hallmarks of cancer are part of different time-dependent events arising dependently during tumorigenesis.

Moreover, recently, we made the key discovery that URI marks the slow-cycling, label-retaining (LR) cells in the intestinal crypt, which are essential for organ regeneration following ionising radiation. Reduced URI levels render LR cells highly proliferative by activating the β-catenin/c-MYC axis. Consequently, LR cells become radiosensitive, thereby increasing gastrointestinal syndrome severity. We conclude that: (1) URI protects LR cells to promote intestinal tissue regeneration in response to high-dose irradiation; and (2) LR cells represent the facultative stem cell pool essential for organ regeneration following ionising radiation. This work was published in Science (Chaves-Perez et al., 2019).

By employing an interdisciplinary approach, which includes the use of various genetically engineered mouse models (GEMMs) and human data combined with state-of-the art technologies, including cell biology with organoid culture and quantitative imaging, biochemistry and functional genomic methodologies, we intend in the near future to continue deconstructing mechanisms of pathologies associated to the digestive system in response to environmental stressors, with a special focus on understanding the mechanisms of colorectal cancer and liver diseases.

1. Mechanisms of colorectal cancer

By using gain- and loss-of-function GEMMs for URI, we aim to understand the mechanisms of colorectal cancer development and to determine the cells at origin of tumours. Our goal is to track LR cells during tumorigenesis through the use of sophisticated mouse genetic experiments.

2. Mechanisms of liver diseases

We aim to elucidate mechanisms of liver cirrhosis and its role in hepatocellular carcinoma, a frequent lethal liver neoplasm. Our final goal is to identify and functionally validate targets with potential preventive and therapeutic values to treat two deadly human disorders with increased worldwide incidence and unmet medical needs. We will put effort to fulfil the following objectives: (1) to find out what goes wrong in diseased and cancerous tissues; (2) to understand how the organ can regenerate and how regeneration in chronic injury can impact liver cancer development; and (3) to promote healthy liver regeneration and reduce cirrhosis and liver cancer.

Special effort will also be put on developing new approaches for the quantitative assessment and analysis of single cell RNA sequencing. Moreover, we have developed an interest in nanotechnology-based theranostics, and plan to combine conceptual advances arising from my laboratory with this exploding technology in order to develop new therapeutic approaches for the prevention and treatment of liver cancer.
Current therapies for breast cancer and other epithelial tumours are in many cases not effective because of intrinsic or acquired resistance, and tumours often relapse, leading to metastatic disease.

Research in the Transformation and Metastasis Group aims to identify novel therapeutic targets for cancer prevention and treatment, and to elucidate resistance mechanisms to drugs currently available. Tumours exploit and manipulate for their benefit the same mechanisms that work correctly in healthy tissue. Thus, we first aim to understand normal development and identify the key events that lead to tumour initiation, progression and metastasis to avoid and combat them. We work with primary cell cultures (including 3D cultures), genetically modified mouse models, patient derived xenografts and clinical samples.

The main contributions of the Group are within the field of mammary gland biology and breast cancer. Our goal is to translate our basic research findings into relevant clinical results.

“Using a collection of patient-derived breast cancer xenografts and multi-OMIC approaches, we have identified mechanisms of chemoresistance and propose novel strategies to guide the use of the right chemotherapy.”
Amplification of chromosome 12p in triple negative breast cancer is associated with emergent docetaxel resistance and carboplatin sensitivity

Taxanes are standard therapy in clinical practice for metastatic breast cancer, however, primary or acquired chemoresistance are a common cause of mortality. Breast cancer patient-derived xenografts (PDXs) are powerful tools for the study of drug resistance in breast cancer PDX models and residual disease may have predictive value for chemotherapy response in TNBC. IMPlications: Subtype-specific DNA methylation patterns are maintained in breast cancer PDX models, including luminal and triple-negative breast cancer (TNBC) models sensitive to docetaxel, their matched models after emergence of chemoresistance, and residual disease after short-term docetaxel treatment. We found that DNA methylation profiles from breast cancer PDX models maintain the subtype-specific methylation patterns of clinical samples. Two main DNA methylation clusters were found in TNBC PDX and remained stable during the emergence of docetaxel resistance; however, some genes/pathways were differentially methylated according to docetaxel response. A DNA methylation signature of resistance able to segregate TNBC based on chemotherapy response was identified. Transcriptomic profiling of selected sensitive/resistant pairs and integrative analysis with methylation data demonstrated correlation between some differentially methylated and expressed genes in docetaxel-resistant TNBC PDX models. Multiple gene expression changes were found after the emergence of docetaxel resistance in TNBC. DNA methylation and transcriptional changes identified in docetaxel-sensitive and -resistant TNBC PDX models or residual disease may have predictive value for chemotherapy response in TNBC. IMPLICATIONS: Subtype-specific DNA methylation patterns are maintained in breast cancer PDX models. While no global methylation changes were found, we uncovered differentially methylated and expressed genes/pathways associated with the emergence of docetaxel resistance in TNBC. FIGURE 2.

The altered transcriptome and DNA methylation profiles of docetaxel resistance in breast cancer PDX models

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**Figure 1** A pre-existing population harbouring chr12p amplification is associated with the emergence of docetaxel resistance, but carboplatin resistance in TNBC/BRCA1-mutated tumours. These findings indicate that sequential treatment with docetaxel and carboplatin could be more efficient in this subset of TNBC patients than the combination or single treatments.

**Figure 2** Global DNA methylation patterns of breast cancer PDX resemble breast cancer human samples. (A, B) Scatter plot of genomewide mean genome-wide DNA methylation levels analyzed by GenomeStudio between two sensitive TNBC PDX models (A) or between a TNBC and a luminal PDX model (B). Correlations are indicated as r2. (C) Unsupervised hierarchical clustering using 32,264 most differentially methylated CpGis between breast cancer PDX models. Methylation differences between at least one of the groups is equal or higher than 75%. p-value < 0.05. (D) Supervised hierarchical clustering applying 345 selected CpGis that discriminate TNBC vs luminal subtype from TCGA breast cancer to BCCLs. Breast cancer PDX models and human tumours samples of origin and TCGA clinical samples. Breast cancer PDX models are indicated. Chi-square and corresponding p-value indicating association between TCGA breast tumours and PDX models or BCCLs from the same subtype are indicated below.

**Publications at other institutions**


**Awards and recognition**

- Eva González-Suárez: 2019 Research Grant (PIF), the Spanish Association Against Cancer (AECC).
- La Mano Fist Grant (PIF), La Mano Fist Foundation, Spain.
- Alessandra Bartoletti was awarded the pre-doctoral contract FE2019-086522 (MC2O).
- Alejandro Collado received the pre-doctoral fellowship FI2018-086522 (MEIC).
- Jaime Redondo was the recipient of a Severo Ochoa PhD contract (PIE2018-086522, MVIC).
BASIC RESEARCH

OVERVIEW

Our laboratory aims to understand how the microenvironment impacts metastatic behaviour. Most of the efforts in the past focused on defining intrinsic factors involved in tumour progression and metastasis. However, our interpretation of tumour evolution and metastasis has shifted and currently it is widely accepted that extrinsic factors are actively involved in cancer progression. To tackle this question, our laboratory uses melanoma models to define the role of secreted exosomes in cancer progression. To further analyse how obesity induces systemic changes favouring metastasis (e.g., increased vascular permeability, platelet recruitment and immune cell impairment). Furthermore, we are visualizing pre-metastatic niches in vivo by intravital imaging, in collaboration with the CNIO Confocal Microscopy Unit, to understand how breast tumour cells home in metastatic lungs in normal and high fat diet-fed mice, and the mechanisms underlying this process.

RESEARCH HIGHLIGHTS

Novel strategies for diagnosis and treatment of metastatic melanoma

Liquid biopsies provide information about cancers in a non-invasive way. In this context, we explore the use of exosomes circulating in biofluids from melanoma patients for minimal residual disease detection and treatment monitoring. Since an important number of patients are refractory to therapy, we additionally study the tumour-immune system cross-talk to find new therapeutic strategies to defeat melanoma metastasis focused on restoring the sensitivity to targeted therapies and/or anti-tumour immunity. We are also interested in the analysis of matrix remodelling processes and microenvironmental factors that influence melanoma progression and could open avenues for new treatment strategies.

How does obesity impact metastasis?

Obesity is a chronic inflammatory condition associated with enhanced cancer incidence and mortality. In fact, obesity is thought to be responsible for up to 20% of cancer-related deaths in adults. We are currently analysing how obesity induces systemic changes favouring metastasis (e.g., increased vascular permeability, platelet recruitment and immune cell impairment). Furthermore, we are visualizing pre-metastatic niches in vivo by intravital imaging, in collaboration with the CNIO Confocal Microscopy Unit, to understand how breast tumour cells home in metastatic lungs in normal and high fat diet-fed mice, and the mechanisms underlying this process.

• PUBLICATIONS

  • Gabandé-Rodríguez E et al. (incl. Sánchez-Redondo S, Peinado H) (2019). Lipid-induced lysosomal damage after de-myelination compromises microglia protective function in lysosomal storage disorders. EMBO J 38, 49655.
Brain metastasis is the most common neurological complication of cancer. When metastatic cells reach the brain, prognosis is poor given that local therapies (i.e., surgery and radiation) have limited benefits for patients and the disease inevitably progresses. The rise in the number of patients with brain metastasis is partially due to the increasing number of systemic therapies that work extra-cranially but that are unable to provide the same therapeutic benefit in the brain. Consequently, cancer cells present at this secondary site have additional time to evolve and to grow into clinically detectable lesions. In the laboratory, we study how cells from different cancer types in the microenvironment including microglia/macrophages and T cells that infiltrate the brain when affected by metastasis. The newly established networks among different components of the metastasis-associated microenvironment represent an active area of investigation in the laboratory since they are a novel source for therapeutic targets.

Given our unprecedented success obtained with a recent therapeutic strategy targeting the microenvironment both in experimental models and in patients with brain metastasis, we further explored the possibility of applying this rationale earlier in order to prevent brain metastasis instead of just treating it. We found a potential mechanism that could be inhibited right after metastatic cells crossed the blood–brain barrier and that has a major impact on experimental animals by preventing the formation of metastasis.

In addition, our newly developed drug-screen platform (METPlatform) has enabled us to identify new compounds with anti-metastatic activity that have been validated in vivo in experimental models and in patient-derived organotypic cultures. Not only are we interested in developing new treatments, but we also try to understand why classic treatments, such as radiotherapy, do not provide greater benefits to patients. In this sense, we have identified a mechanism that could explain the low responses to this therapy in vivo and an inhibitor that could target it, thus increasing the anti-tumour effects with reduced radiation doses.

“Our ongoing projects are showing us that the untreatable nature of brain metastasis could be questioned by the identification of vulnerabilities that could be exploited therapeutically.”
In the Metabolism and Cell Signalling Lab we study the interplay of nutrients, metabolism and cancer. Every cell in the organism integrates signals emanating from the intracellular nutrients and from the nutritional state of the organism as a whole. Integration of cellular and systemic nutrient abundance and the fluctuations in nutrient levels underpins regulatory T cell control of immune tolerance (2019).

**OVERVIEW**

“In a large fraction of tumors, hijacks the normal responses to the fluctuations in nutrient levels to satiate the need for growth and proliferation, but these alterations also impose exploitable vulnerabilities.”

**RESEARCH HIGHLIGHTS**

**Nutrient signalling in B cell lymphoma**

One of the most rapid proliferation bursts in mammalian cells is that of B lymphocytes upon encountering certain pathogens or antigens. This proliferation suddenly multiplies the energetic and metabolic demands of the activated B cell and, accordingly, precise nutrient sensing and signalling are key to successfully accomplish the energetically onerous rounds of growth and division. Recently, components of the Rag GTPase pathway, a key nutrient signalling pathway that enables the anabolic capacity of the cell for rapid proliferation, were found mutated in follicular lymphoma, an incurable B lymphocyte tumour. By means of novel strains of mice that express mutant variants of the RagC GTPase, we found that these mutations drive B cell activation and development of lymphomas, but underlie an exquisite sensitivity to pharmacological inhibition of the mTORC1 pathway (FIGURE A). Such treatment may be particularly efficacious for 1 out of 6 follicular lymphoma patients with RagC mutations, and also for patients without genetic mutations but with functional deregulation in the nutrient signalling pathway.

**Chronic signalling of elevated nutrients and premature ageing**

In the absence of lymphoma, mice with elevated nutrient signalling show multiple features of premature ageing (FIGURE B), including the thinning of dermal and subcutaneous fat layers of the skin (FIGURE C) and increased senescence-associated β-galactosidase activity in multiple organs (FIGURE D). These mice are the first genetic mammalian system to interrogate the mechanisms that link elevated nutrient signalling to the energetic and metabolic demands of the activated B cell and, accordingly, precise nutrient sensing and signalling are key to successfully accomplish the energetically onerous rounds of growth and division. Recently, components of the Rag GTPase pathway, a key nutrient signalling pathway that enables the anabolic capacity of the cell for rapid proliferation, were found mutated in follicular lymphoma, an incurable B lymphocyte tumour. By means of novel strains of mice that express mutant variants of the RagC GTPase, we found that these mutations drive B cell activation and development of lymphomas, but underlie an exquisite sensitivity to pharmacological inhibition of the mTORC1 pathway (FIGURE A). Such treatment may be particularly efficacious for 1 out of 6 follicular lymphoma patients with RagC mutations, and also for patients without genetic mutations but with functional deregulation in the nutrient signalling pathway.

**PUBLICATIONS**


**PUBLICATIONS AT OTHER INSTITUTIONS**

BASIC RESEARCH

In our laboratory, we use a variety of approaches – both genetic and small molecule drug screenings – coupled with in vivo treatment response will be instrumental for the development of new therapeutic modalities.

Gaining insights into the pathways that determine this poor treatment response will help to define new therapeutic targets for treatment of brain tumours.

GBM mouse models in order to identify genes involved in therapy resistance of gliomas. We reason that these studies will help to define new therapeutic targets for treatment of brain tumours.

“...the overall aim of our Group is to uncover the genetic alterations present in GBM patients that are responsible for the aggressiveness of this tumour type, with particular interest in the identification of the signalling pathways that lead to poor treatment response.”

RESEARCH HIGHLIGHTS

MGMT genomic rearrangements contribute to chemotherapy resistance in gliomas

Temozolomide (TMZ) is an oral alkylating agent used for the treatment of glioblastoma and is now becoming a chemotherapeutic option for patients diagnosed with high-risk, low-grade gliomas. The therapeutic benefits of TMZ depend on its ability to methylate DNA, which takes place at the N-7 and O-6 positions of guanine and the N-3 position of adenine. Although the minor product O-6-methylguanine (O6-meG) accounts for less than 10% of the total alkylation, it exerts the greatest potential to induce apoptosis. The O-6-methylguanine-DNA methyltransferase (MGMT) is responsible for the direct repair of the O6-meG lesion by transferring the alkyl group from guanine to a cysteine residue. Epigenetic silencing, due to promoter methylation of the MGMT gene, prevents the synthesis of this enzyme and consequently increases tumour sensitivity to the cytotoxic effects induced by TMZ and other alkylating compounds. Still today, MGMT promoter hypermethylation is the only known biomarker for TMZ response. However, the discordance between promoter methylation and protein expression detected in a subset of patients limits the prognostic value of methylation assessment. This evidence suggests that other mechanisms, in addition to promoter methylation, could contribute to MGMT upregulation in recurrent tumours.

By analysing a large cohort of IDH wild-type and mutant recurrent gliomas treated with TMZ, we have discovered that a subset of patients carries distinct MGMT genomic rearrangements. By leveraging CRISPR/Cas9 technology, we generated some of these MGMT rearrangements in glioma cells and demonstrated that the MGMT genomic rearrangements contribute to TMZ resistance, both in vitro and in vivo. Lastly, we showed that such fusions can be detected in tumour-derived exosomes and could potentially represent an early detection marker of tumour recurrence in a subset of patients treated with TMZ.

• AWARDS AND RECOGNITION

- Miguel Jiménez Alcázar has been awarded an EMBO long-term fellowship.

• PUBLICATION

Programme’s research areas and strategic goals

The goal of the Structural Biology Programme (SBP) is to provide mechanistic insights at the molecular level of proteins and macromolecular complexes that contribute to cancer progression. A better understanding of how these macromolecules work, together with knowledge of their three-dimensional structures, provide information to guide the design of new strategies against cancer. The groups at SBP are currently focused on the study of protein kinases as well as complexes involved in the DNA damage response. A special emphasis has been placed on setting up high-resolution cryo-electron microscopy (cryo-EM) methods, a powerful technique for high-resolution structural characterisation of individual molecules that is reshaping biological research.

SBP is composed of 1 Senior Group, 2 Junior Groups and 4 Units. During 2019, 2 new Junior Groups joined the Programme to reinforce the computational studies applied to cancer research.

Summary of milestones & major achievements during 2019

It has been roughly two years since the Structural Biology Programme was restructured to incorporate 3 new Groups and high-resolution cryo-EM technologies. 2019 was the year when these changes were firmly consolidated. The new cryo-EM microscope was installed and started to generate high-resolution data; we also set up all the computational resources and methodologies essential for high-resolution image processing. The new Groups are fully operational having published remarkable results in *Nature*, *ACS Chemical Biology*, *Journal of the American Chemical Society*, and *Proceedings of the National Academy of Sciences of the USA*. In addition, the ongoing activity of the Units contributed to the research conducted at CNIO, resulting in publications in *Nucleic Acids Research*, *Journal of Experimental Medicine*, *Bioinformatics*, and *Cancer Cell*, among other journals. During 2019, the Groups and Units at SBP also secured access for data collection, based on competitive applications, to the eBIC Biological Cryo-Imaging - Diamond Light Source (UK) and the ALBA synchrotron Light Source (Spain).

In 2019, SBP was deeply engaged in organising scientific meetings. Groups and Units at SBP participated in the organisation of four meetings: two CNIO “la Caixa” Frontiers Meetings (on ‘Structural and Molecular Biology of the DNA Damage Response’ and ‘Heterogeneity and Evolution in Cancer’), the ‘CCP-EM High Resolution EM Model Building and Validation Workshop’ and the ‘Workshop in Advances in the R2TP / URI-Prefoldin Complex in Cancer’. These meetings were an excellent opportunity to discuss the latest advances in these areas, but also to advertise the good science performed at SBP and the CNIO as a whole. In addition, excellent speakers were invited to our seminar series on topics connecting Structural Biology and cancer research, of particular interest was the visit of Sjors Scheres (MRC-Laboratory of Molecular Biology, Cambridge, UK), one of the main references in cryo-EM applied to biomedical research.

Finally, 2 new Groups, led by Solip Park and by Geoff Macintyre respectively, recently joined the CNIO to strengthen computational science in SBP. They will combine high-throughput technologies, big data and computational modelling to characterise the complexity of tumours and to develop better diagnostic and therapeutic tools for personalised medicine.

“SBP provides structural and mechanistic understanding of macromolecules relevant in cancer, which is a first step towards developing new therapies. To achieve this goal, cryo-EM technologies were made fully operative in 2019.”
Our key mission is to provide in-depth structural and molecular understanding of how macromolecular complexes implicated in cancer work. This information is essential to comprehend why and how some proteins are involved in the development of cancer. This fundamental knowledge is the basis to start the search for potential strategies to interfere with the function of these macromolecules. To accomplish this, we make use of several biochemical and molecular biology tools in combination with cryo-electron microscopy (cryo-EM). Cryo-EM is used to visualise large macromolecular complexes, and to observe their motions. Two main objectives drive our current research: (i) the study of macromolecular complexes that function in the cellular response to DNA damage; and (ii) an HSP90 co-chaperone network implicated in the assembly, activation and regulation of several complexes that are essential for cancer progression. In addition, we also address other relevant questions about human disease, in collaboration with other groups.

“R2TP/URI Prefoldin-like complex is a molecular chaperone that contributes to cancer by poorly understood mechanisms. In 2019, we showed how 2 essential ATPases in this complex are regulated.”

OVERVIEW
Regulation of RUVBL1-RUVBL2 ATPases in the R2TP co-chaperone

Activation and assembly of several protein complexes implicated in cancer require the assistance of Heat Shock Protein 90 (HSP90), a molecular chaperone; thus, HSP90 inhibitors are being evaluated as potential anticancer agents. HSP90, working in concert with the R2TP/URI Prefoldin-like complex, is needed for the activation and stability of the PI3-kinase–like family of kinases (PIKKs), regulating the DNA damage response and cell growth. R2TP/URI Prefoldin-like complex is the most complex HSP90 co-chaperone yet described; it is involved in cancer progression and is the focus of several studies looking for potential inhibitors.

We are using cryo-EM to fully understand the structure of this co-chaperone complex and how it works. R2TP forms a core sub-complex containing 2 ATPases, RuvB-like protein 1 (RUVBL1) and RuvB-like protein 2 (RUVBL2). These ATPases form a hexameric ring that interacts with RNA polymerase-associated protein 3 (RPAP3) and PHD domain-containing protein 1 (PHD1) to assemble the R2TP complex. Several studies have demonstrated that the ATPase activity of RUVBL1 and RUVBL2 is required for their biological functions in vivo, but how this is controlled and regulated is still mysterious.

In our new study, cryo-EM is used to reveal one of the mechanisms regulating these ATPases. RUVBL1 and RUVBL2 cannot efficiently hydrolyse ATP because the access to their nucleotide-binding site is obstructed by hexamerization, making ATP/ADP exchange more difficult. Cryo-EM of RUVBL1 and RUVBL2 in complex with PHD1D1, one of the components of the R2TP complex implicated in client recruitment, reveals that the interaction of PHD1D1 with RUVBL2 induces large conformational rearrangements that lead to the destabilization of an N-terminal segment of RUVBL2 acting as a gatekeeper to nucleotide exchange (FIGURE 1). These results identify PHD1D1 as a factor that regulates the accessibility to the nucleotide-binding site in RUVBL2, thereby facilitating nucleotide exchange and activation.

Architecture of the Type VII secretion system in mycobacterium

Tuberculosis is an infectious disease and one of the 10 leading causes of death worldwide. The mycobacterium causing this disease uses a membrane–embedded secretion system (Type VII secretion system, T7SS) to inject virulence factors required for infection into the host immune cells, some of which block the defensive response. Targeting the function of this secretion mechanism has been proposed as a way to stop infection, but the lack of information on how T7SS works at the atomic level has prevented progress in designing these new therapeutic strategies. In a joint effort between our group and the group headed by Sebastian Giebel at the University of Würzburg, we managed to describe in detail the structure of T7SS at the atomic level.

We used M. smegmatis as a model to study M. tuberculosis, a bacteria that shares the same secretion system. Our work showed that T7SS is a sophisticated nanomachine in which several proteins cooperate to inject the virulence factors produced by the bacterium into the cells of the immune system (FIGURE 2). Most interestingly, EccC3, one of the proteins in the cytosolic side of the membrane, comprises 4 linked but flexible ATPase domains involved specifically in recruiting the virulence factors and energising secretion. Our structure shows that this ATPase protein makes direct contact with an alpha helix from the periplasmic pore protein, which inserts all the way into the cytoplasm. The architecture of T7SS and the experiments performed suggest that conformational changes induced by ATP hydrolysis most likely regulate the opening and closing of the secretion pore.

**Figure 1** Cryo-EM structure of the RUVBL1-RUVBL2 hexameric ring, revealing conformational changes in RUVBL2 after PHD1D1 binding (left panel). Structures of one RUVBL2 subunit in the ADP-bound conformation (cyan) and an open ADP-empty conformation (green) are shown in the right panels. ADP is shown in blue. The N-terminal segment of RUVBL2 (residues 8 to 481) is coloured in red (adapted from Muñoz-Hernández et al., 2019).

**Figure 2** Side and top views of the hexamer model for T7SS built from 3 dimers, each coloured differently. One monomer in the hexamer is selected to colour each of the constituent proteins. EccB3 protein is periplasmic, and its conformational changes can regulate the opening and closing of the pore. EccC3 is a flexible cytoskeletal ATPase that engages close to the membrane with a helix from EccB3 to possibly regulate the opening of the secretion pore (adapted from Famelis, Rivera-Calzada et al., 2019).
We established 4 main research lines in 2019, and at the same time the lab expanded with the arrival of 2 ‘CNIO Friends’ fellowship recipients: Rubén Julio Martínez Torres (postdoctoral contract) and Moustafa Ahmed Shehata (Carmen Gloria Bonnet predoctoral contract).

- Structural and molecular determinants of RET catalytic activity and signalling, both in cis by intrinsic elements and in trans by effector kinases and adaptor proteins. We paid special attention to the crosstalk between RET and non-receptor tyrosine kinases (NRTKs).
- Structure-function studies of RET oncoprotein variants, i.e. point mutations targeting the kinase domain and oncogenic fusions generated by DNA rearrangements, with a special emphasis on the latter in the context of aggressive types of cancers.
- Structure-based drug-discovery for new (allosteric) RET inhibitors.
- Histidine phosphorylation and structure-function studies of histidine kinases.

We also focused on less known phospho-specific modifications such as histidine phosphorylation and the regulation of histidine kinases. The current understanding of this type of phosphorylation is poor. Together with T. Schirmer’s group at the Biozentrum (University of Basel), we directly contributed to the first crystal structure of a full-length hybrid histidine kinase and the molecular dissection of its full catalytic cycle (FIGURE). This work was recently published in PNAS (Dubey et al., 2020).

OVERVIEW

Rational and precise targeting of oncogene-driven signalling is a crucial and, yet today, outstanding challenge in cancer research. Understanding the structural and molecular bases of oncogene activation and signalling is key for the design and development of better therapeutics. Our research focuses on the structural and molecular understanding of protein kinase function: (i) how protein kinases are activated and regulated by posttranslational modifications and allosteric inputs, and (ii) how they assemble into macromolecular protein complexes to transmit signals inside the cell. We put a special emphasis on how these mechanisms are corrupted in cancer and disease due to oncogenic mutations and other oncogenic insults. Crucially, such atomic and molecular information can be translated into the design and development of more potent and specific protein kinase inhibitors, eventually leading to more effective drugs for the treatment of cancer patients.

RESEARCH HIGHLIGHTS

- Structural and molecular determinants of RET catalytic activity and signalling, both in cis by intrinsic elements and in trans by effector kinases and adaptor proteins. We paid special attention to the crosstalk between RET and non-receptor tyrosine kinases (NRTKs).
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“Understanding protein kinase function and inhibition for better cancer therapeutics.”

PUBLICATION


AWARDS AND RECOGNITION

- Rubén Julio Martínez Torres was the recipient of a ‘CNIO Friends’ Postdoctoral Contract.
- Moustafa Ahmed Shehata was awarded the ‘CNIO Friends’ Carmen Gloria Bonnet Predoctoral Contract.
OVERVIEW

Safeguarding genetic information is essential to all forms of life. Two key cellular processes keep it free from errors: DNA replication and repair. Importantly, when they do not work correctly, genetic information may be damaged or lost, ultimately leading to disease. Deregulation and malfunction of the protein machinery that safeguards our genome are a hallmark of cancer, but it remains unclear how this happens at the molecular level. The devil is in the detail, and we aim to understand what and when something goes wrong with these molecular machines, so we can act to correct it and prevent it from happening.

These macromolecules are like real-life machines, with intricate mechanisms that allow them to perform their activities. To understand how they work, we use cryo-electron microscopy and biochemistry in an integrative approach. Beyond fundamental research, this structural information provides the necessary detail for drug development.

DNA replication and repair – focus on mitochondria

Eukaryotic cells have 2 genomes: nuclear and mitochondrial. However, how the integrity of the mitochondrial genome is maintained through the equilibrium between DNA replication, repair and degradation, as well as organelle dynamics, remains unclear. We are interested in understanding these pathways because of their implications for ageing and disease, and, in particular, their relation to cancer.

Cryo-electron microscopy (cryo-EM)

Combined with many other approaches already established at the CNIO, we use cryo-EM to study diverse macromolecular complexes involved in cancer. Recent technological developments in microscopes, detectors and image processing tools have significantly improved the resolution of the technique, enabling the structural analysis of many elusive macromolecules to an unprecedented level of detail. Last year, we worked together with Oscar Llorca’s Group and the EM Unit to bring the cryo-EM facility at the CNIO to a state-of-the-art level. Moreover, we were awarded access to high-end microscopes at the Biological Electron Bio-Imaging Centre (eBIC) in Oxford (UK).

Mismatches repair

DNA mismatch repair (MMR) is critical for genome stability. The DNA mismatch repair machinery loads onto newly synthesised DNA and searches for mismatches. The recognition of an error in DNA by the MutS protein leads to an ATP-dependent conformational change that transfers MutS into a sliding clamp state. Only this MutS state can activate the MutL·ATPase that in turn promotes the removal of the DNA for repair. These protein complexes are incredibly dynamic and flexible, and many steps of the cycle have remained elusive to structural analysis. Using cryo-EM, we captured multiple functional steps and we have studied the conformational changes that these proteins undergo in order to recognise the mismatch and license downstream events that lead to repair. These studies were carried out in collaboration with Titia Jinxma (Netherlands Cancer Research Institute) and Meinert Lamers (Leiden University).

RESEARCH HIGHLIGHTS

**Mismatch repair**

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**Publications**


**Awards and Recognition**

- Maria Dolores Moreno was the recipient of a ‘CNIO Friends’ Postdoctoral Contract. Alberto López-Francos López-Romero received a fellowship from the summer training programme of the Spanish Association Against Cancer (AECC).

**Figure**: High-resolution reconstruction of a protein structure from the lab to 3.5 Å resolution (in press). (A) Shows the overall atomic density of the protein, and (B) shows close-ups of density and model with clear signal for amino-acid side-chains.
During 2019, we: (1) set up 3 collaborations to identify novel cancer predisposition genes based on our own developed method; and (2) established a new research line for understanding the context-dependent cancer fitness landscape.

Finding novel cancer predisposition genes

We established 3 collaborations (2 in Spain and 1 in South Korea) to find novel cancer predisposition genes using our previous method (Park et al., 2018, Nature Communications). We applied it to 3 different cancer studies and this will increase the scientific impact of our method.

Cancer-type specific fitness landscape

To understand the comprehensive cancer fitness landscape, we established the dosage (by copy-number changes)-fitness function when it is mutated (either somatic or germline), for each gene in each cancer type. We applied it to all possible human genes (~20,000 genes) across more than 30 cancer types. Based on this analysis, we could classify many different classes of cancer genes, including unexpected, novel cancer types. We expect to validate our observations by computational (independent dataset) and experimental analysis in 2020.

OVERVIEW

Cancer is one of the most complex human diseases, involving genetic, environmental and even unknown factors. Over the past several decades, large-scale genomics analyses of cancer patients have been made in order to understand this complex disease. One of the most striking findings of large-scale cancer genomics is the remarkable heterogeneity in cancer driver (oncogene or tumour suppressor gene) alterations across different patients and cancer types. However, even though various important biological characteristics are commonly measured in cancer patients, little is currently known about the cancer type- or context-specific tumour progression for each gene in each cancer type. Furthermore, by analysing large-scale cancer genomics data, many exceptions have been observed, including haploinsufficiency in tumour suppressor genes, or amplification-linked mutations in oncogenes and even in dual-functional genes. Clearly, activity levels of genomic alterations in cancer genes are disparate across cancer types, and their optimal models for tumour progression may also vary depending on contexts or cancer types.

"Large-scale public cancer genomics has provided new insights to understand the contribution of inherited mutations to cancer risk."

"The phenotypic outcome of a reduction (tumour suppressor genes) or induction (oncogenes) in gene expression is differentially manifested depending on the cancer type. (A) Large-scale cancer genomics data will be analysed to understand the cancer fitness landscape in each cancer gene across different cancer types. (B) All possible tumour progression mechanisms by using genomics data. (C) Multi-dimensional cancer fitness landscapes will be measured by many different phenotypic factors."

"Large-scale public cancer genomics has provided new insights to understand the contribution of inherited mutations to cancer risk."

"The phenotypic outcome of a reduction (tumour suppressor genes) or induction (oncogenes) in gene expression is differentially manifested depending on the cancer type. (A) Large-scale cancer genomics data will be analysed to understand the cancer fitness landscape in each cancer gene across different cancer types. (B) All possible tumour progression mechanisms by using genomics data. (C) Multi-dimensional cancer fitness landscapes will be measured by many different phenotypic factors."
Different types of chromosomal instability leave distinct “scars” in the DNA of a tumour which we can detect using whole-genome sequencing. These genetic scars, or “signatures of CIN”, represent a way to detect and quantify different causes of CIN in a tumour.

**Using tumour organoids to target CIN**

Tumour organoids can be treated in vitro providing a way to link genomic features with drug response. By determining the activity of different types of CIN and linking them to drug response we are building a rational framework for therapy selection in the clinic using CIN as a biomarker.

**Predicting therapy response in patients**

Our lab is performing a series of retrospective clinical studies looking at predicting response to therapies using signatures of CIN (FIGURE A). The long-term goal is to predict response in prospective clinical trials in order to improve patient stratification and trial success.

**Single cell DNA sequencing to detect ongoing CIN**

Standard “bulk” whole-genome sequencing does not allow us to separate CIN that is ongoing in a tumour, from CIN that is historical (occurred during the evolutionary history of the tumour). We are using single cell DNA sequencing to interrogate the changes unique to each cell, which enables us to separate ongoing CIN from historical CIN (FIGURE B). Our lab is applying this technology to premalignant lesions allowing us to observe CIN at its earliest stages in tumour development, before it causes aggressive, resistant tumours, with the goal of developing chemo-preventive treatment strategies.

**OverView**

In the Computational Oncology Group we are tackling some of the deadliest cancers by targeting the causes of chromosomal instability. Pancreatic, oesophageal, lung and ovarian cancers have the lowest survival rates, but they also share a common trait which we can exploit – extreme chromosomal instability (CIN). By therapeutically targeting CIN, we aim to improve outcomes in these tumours.

Our main research areas include:

- Using tumour organoids to develop therapeutic strategies to target CIN.
- Predicting therapy response using genomic signatures of CIN in patient biopsies.
- Developing single cell/nucleus sequencing approaches to detect ongoing CIN.

We are applying these technologies at the earliest stages of tumour development in patients with premalignant lesions, with the goal of preventing aggressive, difficult to treat cancers.

“Tackling some of the deadliest cancers by targeting the causes of chromosomal instability.”

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**Figure (A)** An overview of the workflow for predicting drug response from clinical samples.

**Figure (B)** A schematic outlining how a normal cell can acquire ongoing CIN through TP53 mutation and NF1 deletion. The plots on the right show genome-wide copy number profiles obtained from bulk or single cell sequencing approaches. As the bulk is an average across cells, the newly acquired CIN cannot be detected.
The Unit provides a broad range of instrumentation for the biophysical characterisation of biomolecules and their interactions, including spectrophotometers, a fluorimeter, isothermal titration and differential scanning calorimeters, a circular dichrograph, dynamic and multi-angle static light scattering devices, and a surface plasmon resonance (SPR) instrument. Research groups mostly from, but not limited to (i.e. the Haematological Malignancies Clinical Research Unit, the Epithelial Carcinogenesis Group and the Experimental Therapeutics Programme – ETP), the Structural Biology Programme extensively used these technologies throughout 2019.

The Unit hosts a 700 MHz NMR spectrometer that is equipped with probes and a sample changer to run up to 120 samples automatically. This provides medium throughput for the screening of small molecule protein binders (together with the CNIO’s Structural Biology and ETP Programmes), as well as for metabolite quantification that in 2019 was done in collaboration with the CNIO-Lilly Cell Signalling and Immunometabolism Section, from the ETP; and the Cell Division and Cancer and the Metabolism and Cell Signalling – MCS – Groups, from the Molecular Oncology Programme. As an example, in collaboration with the MCS Group, we conducted 13C tracing intracellular metabolite measurements by NMR to characterise the metabolic changes associated with exposure to a small molecule chemical inhibitor (FIGURE). Collectively, with this and other groups, we continue to implement sample preparation protocols and to develop spectroscopic and analytical tools to characterise the metabolites present in different biological samples.

“In 2019, we conducted NMR experiments in cell media and extracts to quantify metabolite changes induced by gene silencing or by chemical inhibitors, thereby contributing to the elucidation of the cellular function of the silenced genes and the specificity and mode of action of the inhibitors.”

Figure NMR quantification of inhibitor-affected 13C-labelled polar intracellular metabolites derived from 13C-glucose in MDA-MB468 breast cancer cells. Each colour-coded square corresponds to the relative variation of each metabolite in a particular sample upon inhibitor treatment (INH) relative to the average value of the 3 independent control (DMSO) experiments. The putative metabolic enzyme inhibitor was discovered in a cell phenotypic screening performed by MCS and ETP. With the exception of the glutamates in glutathione, the compound produces a decrease of the metabolic flux from glucose to most metabolites, including citrate, α-ketoglutarate (αKG) and malate; and the glutamic and aspartic acids that are proxies for αKG and oxalacetate, respectively.
BIOINFORMATICS UNIT

BASIC RESEARCH

Bioinformatics is a key discipline for understanding the cancer genome and for the future of cancer therapeutics. Bioinformatics-based approaches have the ability to transform the huge amount of biological data into comprehensive models that provide an in-depth understanding of cancer disease and the complex relationships among genotype and phenotype that are needed to identify cancer driver molecular alterations and new therapeutic targets.

The CNIO Bioinformatics Unit (BU) has several goals: (i) to develop new computational methodologies and bioinformatics tools to enable the integration of biological and clinical data; (ii) to achieve genome analysis in cancer patients’ data in order to identify new biomarkers and mechanisms of drug response; (iii) to provide bioinformatics support with data analysis and interpretation using computational and statistical methods; and (iv) to maintain the scientific computing facilities at the CNIO and provide training in bioinformatics tools and methods.

In 2019, the CNIO Bioinformatics Unit published 19 peer-reviewed articles (see full list on our web site https://bioinformatics.cnio.es/) generated from our ongoing research projects and scientific collaborations. We studied the impact of inter- and intra-tumour heterogeneity using our tool PanDrugs and its predictive power of clinical outcome (Piñeiro-Yáñez E et al., 2019). Our results showed that patients labelled as responders according to PanDrugs predictions had significantly increased overall survival compared to non-responders. Additionally, PanDrugs’ usefulness was assessed considering spatial and temporal intra-tumour heterogeneity and showed that it can propose drugs or combinations to target clonal diversity. Additionally, we published vulcanSpot (Perales-Patón J et al., 2019) for detecting and targeting cancer genetic dependencies. All our tools are freely available and have been used in our scientific collaborations, such as the use of PanDrugs in a case of T-ALL (Fernández-Navarro P et al., 2019) or mutualistic analysis during tumour clonal evolution (González-Rincón J et al., 2019).

Additionally, the Unit extended its analysis of misannotated coding genes (Frankish et al., 2019) from the human genome to the mouse genome, and manual annotators are currently revising the annotations of coding genes in Ensembl/GENCODE for both genomes. Finally, the Unit analysed the importance of SINE Ali transposable elements in the human genome and found that these elements are preferentially incorporated into human coding genes.

The Bioinformatics Unit, as a node of INB/ELIXIR-ES, is also involved in the organisation of events and training activities. During 2019, we organised the ONCONET- SUDE Workshop on Innovative IT for Healthcare as well as a Software Carpentry workshop. With regard to training, we co-organised the Master en Bioinformática Aplicada a Medicina Personalizada y Salud (ISCIII-ENS) (visit our web page for a full list of activities).

OVERVIEW

“PanDrugs predictions can be correlated with clinical outcome and can be useful to manage intratumour heterogeneity in patients while increasing therapeutic options and demonstrating their clinical utility.”

SELECTED PUBLICATIONS


Please see BU’s web site for a list of all publications.
Nowadays, cryo-electron microscopy (cryo-EM) has become a main structural biology method to study macromolecules in more ‘native,’ i.e. biochemically functional, buffer conditions. At the CNIO, we use our 120 kV Tecnai G2 Spirit microscope, equipped with the TVIPS CMOS detector, to screen cryo-samples and to carry out low resolution analysis of different biological specimens. For high-resolution data collection, CNIO’s Structural Biology Programme has been granted access to high-end cryo-EM microscopes at the Electron Bio-Imaging Centre (eBIC) (Oxford, UK) through a peer-reviewed Block Allocation Group (BAG). In addition, we are performing the final set-up of our new cryo-electron microscope (JEM-2200FS) equipped with a K3 direct electron detector for medium-high resolution data collection.

During 2019, our scientific activity was developed through collaborations with all the research groups of the Structural Biology Programme, as well as with several groups from other Programmes and with scientists outside the CNIO. For instance, in collaboration with the Kinases, Protein Phosphorylation and Cancer Group (Structural Biology Programme), we worked on the structural characterisation of an oncogenic fusion of RET tyrosine kinase; in collaboration with the Macromolecular Complexes in DNA Damage Response Group (Structural Biology Programme), we were involved in the structural characterisation of several protein complexes (e.g. DNA repair and RUVBL1/2 complexes), together with M. Palacín’s Group (IRB Barcelona), we collaborated on the high-resolution structural characterisation of heteromeric amino acid transporter complexes; with the Genome Integrity and Structural Biology Group (Structural Biology Programme), we collaborated to set up a pipeline to use cryo-EM as a tool for drug discovery; with the Experimental Oncology Group (Molecular Oncology Programme), we worked on optimising, for cryo-EM, the purification of c-Raf’s protein complex; and, lastly, together with the Cell Division and Cancer Group, we analysed how the mutations in a centrosomal protein affect the architecture of centrioles.

The aim of the Electron Microscopy (EM) Unit is to help researchers to solve their biological questions using various transmission electron microscopy techniques. We have extensive knowledge in sample preparation, negative staining and cryo-electron microscopy, as well as experience in image processing, 2D analysis and 3D reconstruction. We offer guidance for selecting suitable techniques, specimen preparation and training on the use of our microscopes and support equipment. More advanced studies are usually provided through research collaboration.

“Over the past year, we devoted our efforts to provide technical and scientific support to the users of the Unit in addition to fine-tuning the recently installed high-resolution cryo-electron microscope.”

**OVERVIEW**

**ELECTRON MICROSCOPY UNIT**

**Unit Head**

Jasminka Boskovic

**Technicians**

Carmen García (TS)**

Pilar Redondo

(Título Superior Advanced Degree)

*(Titulado Superior Joven (since October, Youth Employment Plan)*

## RESEARCH HIGHLIGHTS

**Figure** Proof-of-concept for single-particle cryo-EM as a drug discovery tool. (a) Representative micrograph; (b) Reference-free 2D averages; (c) Preliminary 3D reconstruction at 2.6 Å resolution; (d) Zoom-in detail of cryo-EM density.

**Publication**

**OVERVIEW**

The Crystallography and Protein Engineering Unit (XTPEUnit) is a core facility that provides on-demand services at different levels, from protein cloning to the determination of its 3D structure, with the purpose to fulfill the demands of our users and to comprehend how their protein targets work. Thus, we produce proteins for different types of biochemical/biophysical/in vitro/in vivo assays, for monoclonal antibody generation, and we also offer macromolecular structural determination at low resolution by small-angle X-ray scattering (SAXS) or at atomic resolution by X-ray crystallography. The latter includes protein co-crystallisation in the presence of inhibitors or small fragments – a method that we routinely combine in parallel with the quantification of protein thermal stability (thermofluor assay) – during the guided drug discovery process.

**CRYSTALLOGRAPHY AND PROTEIN ENGINEERING UNIT**

**Unit Head**

Inés Muñoz

**Staff Scientist**

Jorge L. Martínez

**Postdoctoral Fellows**

Rafael S. Correia (since April), Johanne Le Coq

**Technicians**

Aida Contreras (since October), Letícia Martin (until January), Miguel A. Navarro (since January), Álvarez Otero (since June)

**RESEARCH HIGHLIGHTS**

Fragment-based screening service was recently included in our portfolio. It is a well-established and powerful approach to early drug discovery. The purpose of this method is to expose protein to libraries of fragments and to solve the crystal structures of the complexes. Our first target was the dimerization domain of TRF1, a project in which we joined efforts with the Telomeres and Telomerase Group. The work was financially supported after approval of an XChem proposal by the synchrotron Diamond Light Source (UK) in the context of an H2020 INEXT European project. As in previous years, we worked closely with the Experimental Therapeutics Programme on several projects that have since led to the production of recombinant proteins (full-length human MASTL, tyrosine kinase domain of human DDR1, full-length mouse TRF1 and human TRF1 dimerization domain) for biochemical and structural analyses. Also, in support of drug discovery projects, we performed several thermal shift assays (thermofluor) in the presence of compounds developed in the Medicinal Chemistry Section.

We have also continued our work on the production of proteins for the generation of antibodies by the Monoclonal Antibody Unit (Biotechnology Programme), including several cancer-related proteins such as POT1A, HIPXA, Syncytin1, CDK6, TRB2, TRB1, and FNIP2, among others. Furthermore, we have combined efforts with the Haematological Malignancies Clinical Research Unit in the structural and biophysical characterisation of bdnRNPK. Additionally, we undertake a number of international collaborations with other CNIO Groups and Units, providing them with recombinant proteins for biochemical and/or cell-based functional assays, for example, with the Telomeres and Telomerase Group, the Experimental Oncology Group, the Genomic Instability Group, the Cell with the Telomeres and Telomerase Group, the Experimental Therapeutics Programme on several projects that have since led to the production of recombinant proteins (full-length human MASTL, tyrosine kinase domain of human DDR1, full-length mouse TRF1 and human TRF1 dimerization domain) for biochemical and structural analyses. Also, in support of drug discovery projects, we performed several thermal shift assays (thermofluor) in the presence of compounds developed in the Medicinal Chemistry Section.

The Unit also has ongoing collaborations with external groups such as the Environmental Biology Department (CIB-CSIC), the Pharmacology and Therapeutics Department (Roswell Park Cancer Institute, USA), the Department of Biomedicine (University of Bergen, Norway), the Department of Crystalllography and Structural Biology (Instituto Quimico-Fisico Roosolano, CSIC), the Protein-Tools Unit (CNB-CSIC), the Biomedical Application of Radioisotopes Unit (CIEMAT), the Department of Molecular Engineering (Aarhus University, Denmark) and the Division of Pulmonary and Critical Care Medicine, Fibrosis Research Center, and the Center for Immunology and Inflammatory Diseases (Harvard Medical School, USA).

During 2019, the Unit also continued with its own scientific projects. We worked on targeting the function of the Mdm2-MdmX E3 complex activity, in the context of an NIH-funded collaboration with the Department of Pharmacology and Therapeutics at Roswell Park Cancer Institute. Moreover, we solved by SAXS the structure in-solution of 2 new bipecific mAbs. Our collaborators (Aarhus University) verified their high inhibition potency against tumours in vivo. Finally, the Unit is taking part in a collaborative project with the Biomedical Application of Radioisotopes Unit of CIEMAT and the Molecular Imaging Unit to develop new antibody-based positron emission tomography (immunoPET) imaging tools for tumour visualisation; this work is supported by a grant from the BBVA Foundation.

**PUBLICATIONS**


**AWARDS AND RECOGNITION**

- Member of the Board of Directors, Asociación de Ciegos de la Comunidad de Madrid
- Fellow of the American Association for Cancer Research
- Member of the Board of Directors, Asociación de Ciegos de la Comunidad de Madrid
- Fellow of the American Association for Cancer Research
- Member of the Board of Directors, Asociación de Ciegos de la Comunidad de Madrid
- Fellow of the American Association for Cancer Research
Translational Research

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H12O-CNIO Lung Cancer Clinical Research Unit 122
The Human Cancer Genetics Programme (HCGP) is a translational research programme working on areas related to genetics, genomics, pharmacogenetics, molecular cytogenetics and the environmental bases of human cancer. The HCGP works in close collaboration with the clinical community. Our main objectives are to: (i) discover genes responsible for familial cancer; (ii) decipher the genetic bases of sporadic cancer; (iii) analyse the role of modifier factors (genetic and non-genetic) in cancer development; (iv) understand the relationship between genes and drug response; (v) implement new strategies for the cure of genetic disorders, e.g., genome editing; and (vi) translate this knowledge into clinical practice through genetic diagnostic studies and genetic counselling.

Currently, the HCGP is composed of 3 Research Groups and 3 Units: the Human Genetics Group, led by Javier Benítez; the Hereditary Endocrine Cancer Group, led by Mercedes Robledo; and the Genetic and Molecular Epidemiology Group, led by Núria Malats. The Genotyping Unit, headed by Anna González-Neira, supports our 3 research groups from a technical point of view, and provides support to other CNIO groups as well as to external users. The Molecular Cytogenetics and Genome Editing Unit, headed by Sandra Rodríguez-Perales, contributes to this provision of technical support. Finally, the Familial Cancer Unit coordinates the clinical part of the HCGP through the CNIO Familial Cancer Consultancy, which is located at the Hospital de Fuenlabrada. Miguel Urioste is responsible for these activities. In addition, the 3 Units conduct their own research activities.

The HCGP collaborates closely with the clinical community, not only to foster cooperation in genetic diagnosis but also to promote training and education. In 2019 the Familial Cancer Consultancy carried out around 570 consultancies, and the HCGP performed 1,410 genetic diagnoses and 1,230 cytogenetic studies. In addition, the HCGP’s Groups hosted 10 medical residents from different Spanish hospitals, who rotated between the Groups and Units for 3-month intervals. We also offer professionals from different national and international research centres the opportunity to join us, either as visitors or for training visits consisting of short-term stays of 1-3 months; a total of 6 international and 14 national visitors and students were hosted in 2019. In terms of education, 14 national PhD students worked on their research projects, 2 of whom already successfully defended their theses.

Finally, one of the main objectives of the HCGP is to establish research collaborations with national and international groups; this is well demonstrated by our publication record as well as the key roles held by several of the Programme’s members in consortia and projects, both nationally and internationally. Currently, we collaborate with 14 international consortia representative of the main tumour types on which we focus. In addition, we lead or participate in 15 national and 3 international European projects.

Milestones and major achievements of the HCGP in 2019 include:

- Javier Benitez: the discovery of a group of solute carrier genes that explain several autoimmune pathologies.
- Mercedes Robledo: Group Leader of the 706 Unit, CIBERER (Centro de Investigación Biomédica en Enfermedades Raras).
- Javier Benitez: became member of the International Consortium of Testicular Cancer.

“We are entering a new era of medicine: the study of healthy people based on risk algorithms, in order to identify groups at high-risk of developing cancer and to perform individualised follow-up.”
We continue to decipher the genetic bases of hereditary and sporadic breast and ovarian cancers. In addition, we have participated in a project that combines the genotype and phenotype in order to stratify and select women at high risk of developing breast cancer (BC). Other families with rare tumours are also object of our studies, for example, testicular cancer whose genetic bases are unknown. More recently, we started a study to elucidate the common genetic origin of different autoimmune-polyendocrinopathies (APs), such as chronic gastritis atrophy, thyroiditis, diabetes or arthritis. We have identified several genes (most of them solute carriers) opening the way for new diagnoses and treatments. Finally, we have progressed in understanding the role of glycosylase genes as modifiers of hereditary breast cancer and their role along the cell cycle.

“We continue working to solve new challenges associated with hereditary BC diagnosis and treatment, but in parallel have extended our studies to discover new genes that explain families with rare tumours. In this regard, a whole pathway, including solute carrier genes associated with APs, has been identified.”
Looking for new breast cancer susceptibility genes

Deciphering the role of rare variants in breast cancer

The European project BRIDGES, aims to build a panel of high and moderate susceptibility genes to identify families with breast cancer having a genetic aetiology. For this purpose, we have analysed 36 candidate genes in 60,000 breast cancer cases and controls and have confirmed 20% of them as susceptibility genes. The second step comprises the whole exome sequencing of these 60,000 cases, aiming to discover new susceptibility genes. This part of the work was conducted throughout the year. We will translate this knowledge — the new genes plus the previous (already confirmed) genes — to several cancer consultancies throughout Europe in order to analyse their value in clinical practice.

Identification of RECQL5 as a new candidate moderate-risk gene in breast cancer

As a complementary approach to the BRIDGES project, we conducted another study using next-generation sequencing (NGS) technologies to identify new BC susceptibility genes in a few, very well selected families. This approach led to our identifying RECQL5, a member of the RECQL-helicase family, as a new breast cancer susceptibility candidate deserving further study. We used a combination of whole exome sequencing in a family negative for mutations in BRCA1/2 (BRCAX) — in which we found a probably deleterious variant in RECQL5 — as well as targeted NGS of the complete coding regions and exon-intron boundaries of the candidate gene in 699 BC Spanish families with BRCA mutations and 665 controls. Functional characterisation and in silico inference of pathogenicity were performed to evaluate the deleterious effect of detected variants. These results prompted us to propose RECQL5 as a gene that would be worth analysing in larger studies in order to explore its possible implication in BC susceptibility (Taveza-Faigia et al., 2019).

Filtering genes in BRCA1/2 genes

Single nucleotide polymorphisms (SNPs) in DNA glycosylase genes involved in the base excision repair (BER) pathway can modify breast and ovarian cancer risk in BRCA1 and BRCA2 mutation carriers. We previously found that SNP rs34259 in the uracil-DNA glycosylase (UNG) might decrease ovarian cancer risk in BRCA2 mutation carriers. Now, we have validated this finding in a larger series of patients with familial breast and ovarian cancer and gained insight into how this UNG variant exerts its protective effect. We found that rs34259 is associated with significant UNG downregulation and with lower levels of DNA damage at telomeres. In addition, we found that this SNP is associated with significantly lower oxidative stress susceptibility and lower uracil accumulation at telomeres in BRCA2 mutation carriers (Baquero et al., 2019).

Familial cancer exome project

Autimmune polyendocrine syndrome (APS)

In 2015, we published research identifying the ATP4A gene as responsible for families with gastric endocrine tumours (Calvete et al., 2015). In 2017, we extended this study to a new family that presented the same lesion along with hypothyroidism and arthritides. The family presented 2 mutations in ATP4A and PTHHR1 following a digenic model that explained the 3 concurrent autoimmune pathologies (Calvete et al., 2017). In 2019, we published a model that involves the uncovered genetic landscape with the acid-base balance malfunction and explained the autoimmune response activation that triggers malignant progression (Benitez et al., 2019).

We are further investigating the apparent relation of gastric autoimmune disease (gastric neuroendocrine tumour or chronic atrophic gastritis) with other autoimmune diseases such as thyroid pathology, arthritis, diabetes type 1, vitiligo, etc. Through targeted sequencing, using a custom panel containing 12 solute carrier genes and some receptors involved in the previously described mechanism, we found several mutations in new genes involved in homeostasis function (solute carriers) — not only in stomach parietal cells but also in other tissues (epithelium, pancreas, thyroid) — altering the acid-base balance and explaining the presence of different autoimmune pathologies (apparently unrelated) in a family or an individual. Several gastroenterologists, pathologists and endocrinologists are collaborating in this project (FIGURE).

Testicular Germ Cell Tumour (TGCT)

During the past year, we completed the first part of our study by performing whole exome sequencing (WES) in familial testicular cancer and described 3 new low susceptibility genes (PLEC, EXD3 and INHAP7) that contribute to cancer development (Pauwmar et al., 2018). We have revised the data using different selection criteria and filtering of the variants in order to look for moderate-high susceptibility genes. Additionally, we are exploring the genetic landscape and somatic contribution that drives different tumour histologies (seminomas and non-seminomas) in different hereditary models (familial, bilateral and sporadic TGCT). The preliminary results are being validated in newly recruited cases. Finally, we have also joined The Testicular Cancer Consortium (TECAC), led by Dr Katherine Nathanson, to contribute with our data and compare our results in a bigger cohort.

Ovarian cancer

Endometrioid (EOC) and clear cell (CCOC) ovarian carcinomas are considered refractory to chemotherapy and present a poor outcome once disseminated. Defects in mismatch repair (MMR) and microsatellite instability (MSI) are predictors of immunotherapy response. During 2019, we compiled 180 EOC and CCOC that are being characterised using a comprehensive approach that integrates assessment of global microsatellite instability (MSI), mutation burden and tumour-infiltrating lymphocytes. In order to maximise the potential translatable of our results, we designed an “ad hoc” NGS ovarian cancer panel (OvaSeq-MSI) that specifically includes a large set of MS markers to determine MSI status and that generates information about mutations in ovarian carcinogenesis genes, ovarian cancer susceptibility genes or therapeutic targets. We have already sequenced 95 tumours of our series. Altogether, we expect to find markers to enable more rational therapeutic decision-making for patients with EOC and CCOC.

Publications

- Calvete O, Garcia-Pavia P, Domínguez JC (2019). RNA-Seq perspectives to improve MSI determination and that generates the potential translatability of our results, we designed an “ad hoc” NGS ovarian cancer panel (OvaSeq-MSI) that specifically includes a large set of MS markers to determine MSI status and that generates information about mutations in ovarian carcinogenesis genes, ovarian cancer susceptibility genes or therapeutic targets. We have already sequenced 95 tumours of our series. Altogether, we expect to find markers to enable more rational therapeutic decision-making for patients with EOC and CCOC.

Conclusion

We are further investigating the apparent relation of gastric autoimmune disease (gastric neuroendocrine tumour or chronic atrophic gastritis) with other autoimmune diseases such as thyroid pathology, arthritis, diabetes type 1, vitiligo, etc. Through targeted sequencing, using a custom panel containing 12 solute carrier genes and some receptors involved in the previously described mechanism, we found several mutations in new genes involved in homeostasis function (solute carriers) — not only in stomach parietal cells but also in other tissues (epithelium, pancreas, thyroid) — altering the acid-base balance and explaining the presence of different autoimmune pathologies (apparently unrelated) in a family or an individual. Several gastroenterologists, pathologists and endocrinologists are collaborating in this project (FIGURE).
OVERVIEW

Our Group is mainly interested in identifying genetic risk factors involved in endocrine tumour susceptibility. Through a comprehensive analysis of tumour genomic features, we have been able to propose diagnostic and prognostic markers, to identify altered pathways that could be therapeutically targeted, and to identify new major susceptibility genes.

We are also interested in defining markers associated with differences in anticancer drug response and toxicity. We are applying targeted and whole-exome next-generation sequencing to a large series of clinically well-characterised patients. The aim is to identify new therapeutic approaches to personalise cancer treatment. These efforts will collectively improve the diagnosis, prognosis and treatment of patients.

“We identified a miR-21-3p/TSC2/mTOR axis with predictive value for mTOR inhibitor sensitivity in pheochromocytoma and showed that PTEN expression and TSC1/TSC2/mTOR mutations predict response to rapalogs in renal cancer.”
Integrative multi-omics analysis identifies a prognostic miRNA signature and a targetable miR-21-3p/TSC2/mTOR axis in metastatic pheochromocytoma

Metastatic pheochromocytoma and paraganglioma (mPGLG) represent major clinical challenges due to its accurate diagnosis and effective treatments. For this purpose, we carried out a comprehensive analysis of miRNomes from 443 patients, the largest discovery cohort explored so far thanks to the participation of an International Consortium of Reference Centres with expertise on this disease.

First, we succeeded in identifying in tumour tissues a miRNA signature related to metastatic risk and to shorter time to progression. Higher levels of these miRNAs were also detected in mPGLG patients’ liquid biopsies compared with controls. Using a prognostic predictive model, we built a miRNA-based classifier, which was further studied in an in vitro model, concluding that the classifier’s miRNA overexpression induces aberrant levels of mesenchymal and neuroendocrine markers and enhances cell migration capability.

The miRNA/mRNA data integration of the same tumours revealed a link between miR-21-3p and TSC2. Moreover, a pan-cancer TCGA integrative study, also including proteomics data, further elucidated TSC2 as a potential target for miR-21-3p, being able to uncover a non-previously identified regulatory miRNA/mRNA network. To address this challenge, we performed a molecular and immunohistochemical characterisation of key mTOR pathway components in a series of 105 renal cell carcinoma patients treated with mTOR inhibitors, and recruited by the Spanish Oncology Genitourinary Group (SOUGJ) and the University Hospitals Leuven. We demonstrated that response to these drugs occurs more frequently in cases with mTOR pathway mutations than in those without mutations (p < 0.003). Negative PTEN immunohistochemistry staining was detected in 58% of the tumours, and it was more frequent in rapapder responders (p < 0.0029). Furthermore, mutations and negative PTEN protein expression were not mutually exclusive events, and their combined improvement response prediction (p = 0.008).

In conclusion, our findings suggest that mTOR pathway mutations, negative PTEN immunohistochemistry staining, and their combination, are potential markers of mTOR inhibitor response. These results provide a step forward with regard to guiding treatment with mTOR inhibitors and personalising renal cancer treatment.
OVERVIEW

The scope of the research carried out by our Group ranges from the identification of aetiological 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 cancer types through a case-control approach, and further evaluated the less explored association between PC and autoimmune diseases (AIDs) through an epidemiological analysis. Fifteen morbidities shared at least 1 gene with PC based on public databases. 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 subsequently 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 an international consortium initiative on the molecular classification of muscle-invasive BC based on transcriptomics data that enabled us to identify 6 subgroups, namely, basal-squamous, luminal papillary, luminal unstable, luminal non-specified, stromal-rich, and neuroendocrine. This workpaves the way for future analysis on the specific aetiology of each BC subtype. The Group was also involved in the risk assessment of BC associated with air pollution. Finally, we contributed to the discovery and validation of both urine- and tumour-predictive and prognostic markers in large Spanish and European studies of both non-muscle and muscle invasive BC.

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 far from being straightforward and all corresponding connections. A Network of diseases that share genetic component with PC based on public databases. Based on common genes, several morbidities shared at least 1 gene with PC and further evaluated the less explored association between PC and different morbidities through a computational approach, progressing in the characterisation of pancreatic cancer risk (FIGURE 2).

Translational activities

The Group actively provides methodological support to several clinical trials on immunotherapy and vitamin D in BC. We continue to support the Spanish Familial PC Registry (PanGen-FAM) and the European Registry of PC (PancreoFr). We also lead the Research Work Stream of the Pancreatic Cancer Europe (PCE) multistakeholder platform. By joining efforts and participating in the European Alliance of Personalized 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.

**METHODS**

**Data sources**

OnO data were integrated usingwares for i) omics (OnO, i.e., gene expression, metabolomics, proteomics and clinical data; ii) non-omics (OnO, i.e., epidemiological and clinical data). The core data sources involved the PAMOKAM database (CIBERehd) and the European Registry of PC (Pancreos). The Group was also involved in the risk assessment of BC associated with air pollution. Finally, we contributed to the discovery and validation of both urine- and tumour-predictive and prognostic markers in large Spanish and European studies of both non-muscle and muscle invasive BC.

**FIGURE 1**

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

**FIGURE 2**

Challenges found in the integration of omics and non-omics (OnO) data and analytical frameworks for building hybrid models containing OnO data.
FAMILIAL CANCER CLINICAL UNIT

Miguel Urioste
Clinical Unit Head

Laura Pena
Graduate Student

Technicians
Verónica García-Lencara Juárez, Maika González-Norte, Falma Herradorín

OVERVIEW

CRC is the third most frequent type of cancer and the third cause of cancer-related deaths in most developed countries. Age is the main risk factor. The median age at diagnosis is 68 years in men and 72 in women. Since the mid-2000s, CRC global incidence and mortality in the USA and Europe have been decreasing at an annual rate of 2-3% for both sexes. This decrease is probably related to the extended use of the faecal occult blood test and colonoscopy, which facilitates the removal of precursor lesions, and to the increased awareness among the general population of the preventive and risk factors.

Recent epidemiological studies indicate that CRC incidence in people under 50 is increasing, which is the opposite situation for individuals over 50 years of age. The greater increase was observed in the age range of 40 to 49 years, in which the incidence changed from 18.2 cases population per 100,000 in 1992, to a rate of 26.5 per 100,000 in 2015. This caught the attention of researchers and the general media. Several causal hypotheses were contemplated – new exogenous factors, epigenetic modifications, low-penetrance gene variants and their interactions – and there is a proposal to launch a research agenda to advance knowledge about the aetiological factors and diagnostic methods of early-onset CRC (EOCRC). Since 2010 the Familial Cancer Clinical Unit (FCCU), together with the Surgery Department of the Fundación Jiménez Díaz University Hospital and the Institute for Biomedical Research of Salamanca, has been committed to investigating EOCRC.

The aim is to: (1) accelerate research to address unanswered questions about the causes of the increase in EOCRC; and (2) increase the adoption of evidenced-based practices to identify and manage younger adults at risk for CRC and to facilitate early diagnosis.

PUBLICATIONS


CLINICAL, DIAGNOSTIC AND RESEARCH HIGHLIGHTS

Our clinical and diagnostic activities in 2019 can be summarised as: 538 patients visited our consultancy at ICF (6.00% increase over 2018), and 572 genetic diagnostic studies were performed in the FCCU laboratory (12.59% increase). Among these studies, we identified 17 cases of CRC in individuals younger than 45, of whom were patients younger than 30 (14 and 28 years old). The FCCU also focuses its research efforts on less frequent cancer predisposition syndromes. One of these is the PTEN hamartoma tumour syndrome (PHTS), in which the high clinical heterogeneity is a major obstacle to establishing an early diagnosis. We studied this pathology at the clinical and molecular level in the largest series of Spanish patients with PHTS (145 probands). Our findings are consistent with the syndrome descriptions in other populations, with few exceptions such as a higher proportion of carriers of mutations in PTEN exon 1 who apparently have an increased risk of developing renal cancer. We discussed the usefulness of the different diagnostic criteria proposed to date and made recommendations based on our results (FIGURE).

Figure: Proportion of individuals showing each clinical manifestation in our PHTS series, excluding carriers of variants of unknown significance.

Noteworthy is that we highlight a novel risk for patients with PHTS, namely the development of cancer at young ages, for which we suggest to anticipate cancer screening in these individuals. Moreover, we demonstrated that the presentation of cancer types within the PHTS spectrum criterion alone is not sufficient to refer patients for PTEN screening, at least as a first measure. In collaboration with the groups of Dr Pulido (Herbesa) and Dr Cid (UCM), we functionally demonstrated the deleterious effect of several PTEN variants of unknown significance. However, about half of our PHTS patients could not be explained by alterations in PTEN, and therefore we also focused our efforts on the search for other genes possibly involved in this disease, using a gene panel (including PIK3/AKT/mTOR pathway genes) and whole genome sequencing.

Future directions will focus on unravelling the relevance of these findings. Our study continues to contribute to a better definition of PHTS and to accelerate its diagnosis.
Recurrent chromosomal rearrangements – changes in the structure of native chromosomes – are very common and well-known hallmarks of cancer. Recent technological advances have improved our ability to detect and understand these rearrangements. A better understanding of these cancer-causing mechanisms will lead to novel therapeutic regimens to fight cancer. The research activity of the Molecular Cytogenetics and Genome Editing Unit focuses on increasing the knowledge about the role of chromosomal rearrangements in cancer development and progression and the discovery of new therapeutic targets. With the combined use of CRISPR genome editing and cytogenetic technologies, we are creating in vivo models that recapitulate chromosomal, genetic, and epigenetic cancer alterations. The goal of the Unit is to provide the CNIO and external researchers with the latest and epigenetic cancer alterations. The goal of the Unit is to provide the CNIO and external researchers with the latest and epigenetic cancer alterations. The goal of the Unit is to provide the CNIO and external researchers with the latest

We apply genome engineering approaches to reproduce and eliminate chromosomal rearrangements and gene alterations. We provide access to the latest cytogenetic and CRISPR technologies. We apply genome engineering approaches to reproduce and eliminate chromosomal rearrangements and gene alterations. We provide access to the latest cytogenetic and CRISPR technologies. We apply genome engineering approaches to reproduce and eliminate chromosomal rearrangements and gene alterations. We provide access to the latest cytogenetic and CRISPR technologies. We apply genome engineering approaches to reproduce and eliminate chromosomal rearrangements and gene alterations. We provide access to the latest cytogenetic and CRISPR technologies. We apply genome engineering approaches to reproduce and eliminate chromosomal rearrangements and gene alterations. We provide access to the latest cytogenetic and CRISPR technologies. 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Efficient methodologies for recreating cancer-associated chromosome aberrations and gene mutations are in high demand as tools for investigating how such events initiate cancer. We recently demonstrated, by generating chromosomal rearrangements, the feasibility of utilising gRNA/Cas9 ribonucleoprotein (RNP) complexes to model cancers driven by fusion genes. We optimised new strategies to enhance the efficiency of CRISPR-mediated translocation induction in human stem cells, including mesenchymal and induced pluripotent stem cells. The CRISPR-Cas9-mediated generation of targeted translocations in human stem cells opens up new avenues to modelling cancer. We are also working on an efficient approach to selectively eliminating cancer-associated fusion oncogenes.

Technological and translational activities

The Unit makes available a complete suite of tools for cellular and genetic manipulation to research groups; these tools can be used interchangeably with an array of delivery vehicles, offering a flexible, modular platform for precision genome manipulation. The Unit offers molecular genome engineering. The Unit is continuously implementing technologies used in the fields of molecular cytogenetics and genome editing. We also participate in collaborative projects with clinical and basic science investigators at the CNIO and other institutions.

Modeling cancer using CRISPR/Cas9 genome editing technology

Efficient methodologies for recreating cancer-associated chromosome aberrations and gene mutations are in high demand as tools for investigating how such events initiate cancer. We recently demonstrated, by generating chromosomal rearrangements, the feasibility of utilising gRNA/Cas9 ribonucleoprotein (RNP) complexes to model cancers driven by fusion genes. We optimised new strategies to enhance the efficiency of CRISPR-mediated translocation induction in human stem cells, including mesenchymal and induced pluripotent stem cells. The CRISPR-Cas9-mediated generation of targeted translocations in human stem cells opens up new avenues to modelling cancer. We are also working on an efficient approach to selectively eliminating cancer-associated fusion oncogenes.
The most abundant types of genetic variation are single nucleotide variants (SNVs) and copy number variants (CNVs). Association studies involving the large-scale analysis of both SNVs and CNVs in thousands of patients can help to identify nucleotide variants (SNVs) and copy number variants (CNVs) in thousands of patients. After replication in an independent cohort, the implementation of these biomarkers in the clinical practice may allow to discriminate those breast cancer patients with a high risk of developing AIC.

Genetic factors underlying the risk of persistent chemotherapy-induced alopecia in patients treated with docetaxel. Persistent chemotherapy-induced alopecia (pCIA) appears in its more severe grade (grade 2) in up to 10% of breast cancer patients treated with docetaxel-based therapies, and has severe psychological impact on these patients. We conducted a genome-wide association study (GWAS) to identify variants associated with the risk to develop this adverse effect. A regulatory variant located in an enhancer element that interacts with the ABCB1 promoter was found to be associated with pCIA appearance, this finding was validated in the replication cohort (ORcombined 4.05; 95% IQR, 2.46-6.67; P=3.946 x 10^{-8}). This variant affects ABCB1 mRNA expression and is the risk allele associated with decreased ABCB1 expression levels (P=1.64 x 10^{-5}). To our knowledge, this is the first study to identify a genetic factor related to this adverse effect.

Mutational characterisation of glioblastomas for the identification of prognostic markers and therapeutic alternatives. Glioblastoma (GBM) is the most common and aggressive malignant brain tumour in adults. Despite the advances in surgical resection, the prognosis for patients with GBM remains poor, with a median survival of 15 months, and tumours generally recur after standard multimodal treatments. We have performed the genomic characterisation of 89 primary GBMs including 26 genes significantly mutated in GBMs in the Cancer Genome Atlas Project, and also 22 actionable genes to identify clinically relevant mutations in these patients. We identified a total of 339 pathogenic variants having an average of 4.3 (1-26) mutations per tumour. We found that PTEN mutations are strongly associated with shorter survival in patients with GBM (P=0.00041). We also found mutations in several actionable genes, such as PARP and BRAF genes. Our results demonstrate that the molecular characterisation of GBM tumours using NGS multigene panels could be a good strategy to improve the management of these patients.

![Image of a brain with arrows indicating different areas]
TRANSLATIONAL RESEARCH

CLINICAL RESEARCH PROGRAMME

MIGUEL QUINTELA-FANDINO Acting Programme Director

The Clinical Research Programme (CRP) has 2 main aims: 1) to translate preclinical research into novel clinical care standards; and 2) to address novel clinical oncology challenges with preclinical research. The specific areas of work include: 1) development of novel agents; 2) study of mechanisms of action of novel compounds and tackling drug resistance; and 3), moving forward in the field of biomarkers, functional taxonomy and precision medicine.

Currently, 2 functional objectives summarise the CRP’s new operating model: i) generating synergies with ongoing research lines in the basic research programmes; ii) constituting a bi-directional bridge to facilitate closer interactions between the CNIO and tertiary cancer hospitals. There are 4 agreements in place with tertiary hospitals (Hospital 12 de Octubre, Hospital de Málaga, Hospital de Fuenlabrada and Hospital Quirón Pozuelo), where the clinical activity of the CRP’s Clinical Units takes place. These agreements foster the interaction between clinicians and scientists, and allow scientists from all CNIO Programmes to participate in translational research studies. The number of ongoing collaborations between the CRP Units and CNIO Research Groups have increased to 39 projects and 3 coordinated grants, which account for the high translational research activity of the institution. Nine medical oncology residents from different Spanish hospitals completed their 3-month optional stays at CNIO during 2019.

The Breast Cancer Clinical Research Unit, led by Miguel Quintela-Fandino, published a major finding about the role of fatty acid synthase as a key factor eliciting transformation of the breast epithelium. This is of importance for the development of prevention strategies for populations at high risk of developing breast cancer. The Lung Cancer Clinical Research Unit, led by Luis Paz-Ares, completed a pivotal clinical trial to register the immunotherapy combination nivolumab and ipilimumab for lung cancers with high mutational burden, where the risk for disease progression was almost halved compared to standard chemotherapy. The Haematological Malignancies Clinical Research Unit, headed by Joaquín Martínez-López, enhanced our understanding of hnRNP K as a bona fide oncogene. The Prostate Cancer Clinical Research Unit, under David Olmos’ supervision, expanded the PROCURE network and confirmed the role of ATM in hereditary prostate cancer, which led to the publication of a seminal manuscript in the field; the Unit was recently awarded the prestigious ‘Proyectos AECC Grant’ to strengthen this pioneering line of research. Finally, the Molecular Diagnostics Unit, led by Luis Lombardía, continued to provide support to hospitals in the diagnosis of haematological malignancies. With the large number of ongoing translational research collaborations, the arrival of novel immuno-oncology drugs, and the search for novel groups for the CRP, we face an exciting year 2020 for patient-oriented oncology research at CNIO.

“The Clinical Research Programme aims to improve cancer care by developing novel agents and personalising therapeutic approaches on the basis of biomarkers.”
BREAST CANCER JUNIOR CLINICAL RESEARCH UNIT

OVERVIEW

The Breast Cancer Clinical Research Unit (BCCRU) focuses on the translational interface of therapeutic development. Breast cancer is a heterogeneous disease and, thus, there are large inter-patient variations in terms of disease course, prognosis, relapse and resistance to conventional or targeted therapeutics. Our activities are directed towards personalised treatment, which disrupts the mitochondrial respiratory supercomplexes and results in cell death. These findings open up therapeutic opportunities in the preventive phase of breast cancer.

In vitro and in vivo models of breast carcinogenesis cannot undergo transformation in the absence of FASN; however, its deletion after the cancer is established has little effect. Mechanistically, this preventive role is independent of its biosynthetic product. FASN consumes acetyl-CoA, which unlocks reductive isocitrate dehydrogenase-dependent carboxylation. This allows the production of the reductive power necessary to quench the reactive oxygen species (ROS) produced during the 2D-to-3D growth transition. This necessary hallmark of cancer is abrogated in the absence of FASN due to intramitochondrial ROS accumulation, which disrupts the mitochondrial respiratory supercomplexes and results in cell death. These findings open up therapeutic opportunities in the preventive phase of breast cancer.

Our previous findings about the metabolic adaptation of tumours in response to metabolic-normalising antigens were confirmed in a clinical trial, where patients with early HER2-negative breast cancer were treated with bevacizumab alone or bevacizumab plus a mitochondrial inhibitor. The latter patients experienced a 3-fold decrease in the Ki67 replicative fraction.

Finally, we searched the world for predictive markers of activity of anti-PD-L1 agents. In patients with advanced breast cancer, we found that those with a baseline higher quotient of T-effector/T-memory populations had a higher chance of response to durvalumab.

RESEARCH HIGHLIGHTS

Contrary to what was previously known, we have found that fatty acid synthase (FASN, an enzyme with low expression in healthy tissue but high expression in epithelial malignancies) exerts a key role during the early steps of cancer initiation, but not when the cancer is established. In vitro and in vivo models of breast carcinogenesis cannot undergo transformation in the absence of FASN; however, its deletion after the cancer is established has little effect. Mechanistically, this preventive role is independent of its biosynthetic product. FASN consumes acetyl-CoA, which unlocks reductive isocitrate dehydrogenase-dependent carboxylation. This allows the production of the reductive power necessary to quench the reactive oxygen species (ROS) produced during the 2D-to-3D growth transition. This necessary hallmark of cancer is abrogated in the absence of FASN due to intramitochondrial ROS accumulation, which disrupts the mitochondrial respiratory supercomplexes and results in cell death. These findings open up therapeutic opportunities in the preventive phase of breast cancer.

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In 2019, the BCCRU finalised its characterisation of fatty acid synthase as a key mediator of breast epithelium transformation. This opens up an unprecedented opportunity for cancer prevention.

PUBLICATIONS


FASN: PyMT

Figure 1C staining of FASN in the mammary gland of an MMTV-PyMT mouse with incomplete systemic KO for FASN. This system provides an ideal context for appreciating the role of FASN. FASN-positive areas can form tumours (characterised by invasive growth, distorting acini architecture and breaking basement membrane), as opposed to FASN-negative areas.

**OVERVIEW**

Prostate cancer (PrCa) is one of the most heritable human cancers. Inherited mutations in several genes involved in DNA damage response and repair have been reported to predispose men to PrCa, including mutations in *BRCA2*. Seminal work from our Group has established that these mutations are an independent prognostic factor for the disease.

The Prostate Cancer Clinical Research Unit remains a major contributor to CNIO’s scientific productivity, with a total IF > 90 and an accumulated IF > 500 since the Unit’s creation in 2012. These figures include 15 manuscripts led or co-led by the Group in 2019, and an accumulated IF > 90 contributor to CNIO’s scientific productivity, with a total IF > 90.

**PUBLICATIONS**


- SMEI, E1355.


**RESEARCH HIGHLIGHTS**

During 2019, our Group made significant progress in its multiple projects, with the following highlights:

- **We demonstrated that ATM gene aberrations associate with a higher frequency of advanced disease and metastatic spread. Similarly, in TRAMP® model of metastatic prostate cancer, ATM knock-out or silencing translated into increased aggressiveness and a higher rate of metastasis.**

- **Previously, we had shown that germline BRCA2 mutations are associated with worse prognosis in different stages of prostate cancer and may be predictors of response to certain standard therapies. In 2019 we demonstrated that somatic BRCA2 and RB1 co-deletion as well as MYC amplification occur more frequently in gBRCA2 mutant tumours. The addition of these events progressively increases the risk of metastasis and death from prostate cancer in both sporadic and gBRCA2 mutant associated prostate cancer.**

- **We established a methodology for developing prostate cancer metastatic xenograft models using both cell lines and patient derived xenografts, in which we can trace biomarkers of treatment sensitivity and resistance (using circulating tumour cells –CTCs– and metastasis). As proof of concept, we identified a biomarker of both docetaxel efficacy and resistance. First, we observed an early (post-24h) increase of pH3 (mitosis arrest) in CTCs derived from tumours that responded to docetaxel and, then, an increase in the aneuploidy index in tumours that did not respond to docetaxel. The early increase of pH3 in CTCs was associated with docetaxel response in advanced prostate cancer patients undergoing treatment with docetaxel.**
Expanding our support

During 2019, we expanded our catalogue by adding one new molecular diagnostic test based on bi-directional Sanger sequencing. This assay detects activating mutations in exons 4, 5, 6 and 8 of the runt-related transcription factor 1 (RUNX1), a key regulator gene required for the differentiation of myeloid progenitor cells to granulocytes. The RUNX1 gene is the most frequent target for chromosomal translocations associated with human leukaemias. However, loss-of-function RUNX1 mutations have also been identified in patients with de novo AML. These alterations could coexist, or be mutually exclusive, with mutations in other genes included in the assays already available in our portfolio (i.e. FLT3, TP53, IDH1, IDH2, TET2, NPM1, CEBPA, etc.). Consequently, even if patients with RUNX1 mutations were classified as high-risk group due to adverse prognostic outcomes (i.e. shorter relapse-free survival), depending on coexisting detected mutations, they could benefit from specific targeted therapies (FIGURE).

Additionally, MDU started several project collaborations with the CNIO Microenvironment and Metastasis Group. Thus, for the purpose of evaluating the clinical utility of liquid biopsies for molecular testing, we designed allelic discrimination assays that make qRT-PCR detection of BRAF V600E and GNAQ Q209L/P mutations possible in different biological fluids (plasma, circulating exosomes, lymphatic fluids) from patients with, respectively, cutaneous or uveal melanomas. Another collaboration with this Group aims to analyse, by whole exome sequencing, primary tumours and lymph nodes from melanoma patients to understand the genomic evolution of nodule metastasising tumours. The objective is to establish a mutational signature that could help to determine risk groups that have residual disease using plasma samples and/or post-lymphadenectomy lymphatic fluids.

Tutoring

In 2019, we hosted one secondary school student, and a postgraduate student carried out her Master’s degree project at MDU.
Haematological malignancies include a myriad of heterogeneous diseases with high frequency, such as non-Hodgkin’s lymphoma, or with high mortality rates, such as multiple myeloma and acute myeloid leukaemia. In the laboratory, we dissect the biology of haematological cancers by investigating: (i) novel diagnosis and prognosis biomarkers; (ii) innovative tools and techniques to identify and monitor the disease; (iii) original therapeutic targets and treatments against haematological malignancies; and (iv) how to decipher the biological processes underlying the diseases and characterise the drivers, oncogenes and tumour suppressors.

The following main lines of research define our laboratory:

- Role of hnRNP K, a novel driver of lymphoma and leukaemia in tumorigenesis.
- Molecular fingerprint in clonal evolution, heterogeneity and drug resistance.
- Liquid biopsy and next-generation sequencing.
- Immunotherapy: NK-CAR and T-CAR in haematological and paediatric cancers.

“We have identified a novel master regulator of cancer, hnRNP K, a tumour suppressor now characterised as an oncogene. Lymphoma patients might benefit from more personalised therapies based on targeting hnRNP K.”
Uncovering the oncogenic role of hnRNP K in B-cell lymphomas

Heterogeneous nuclear ribonucleoprotein K (hnRNP K) is an RNA-binding protein that is aberrantly expressed in cancer. Recently, biallelic (“double hit”) TP53 mutations have been associated with a median survival of <2 years. The proliferation of MM cells can lead to the expansion and domination of the affected clones within a patient’s bone marrow. To test this hypothesis, we established fluorescence-activated cell sorting (FACS) and flow cytometry to investigate the safety and efficacy of the oral combination of ruxolitinib and bortezomib in patients with myelofibrosis. Haematologica. PMID: 30315025.

Clonal evolution and estimate competitive advantages of both mono- and biallelic TP53 variants. Strikingly, we demonstrated that subclones with TP53 wild-type double hit outcomes and overgrow other TP53 variants. Reflecting these results, a meta-analysis, including publicly available data sets, confirmed single- and double-hit myelomas to be significantly enriched in patients who relapsed (work published in Blood).

Mitochondrial activity plays a key role in multiple myeloma fitness

Mitochondria control several key biological pathways involving cell proliferation and apoptosis. Many studies have implicated a functional role for mitochondria in tumour formation and development; however, our impact on the pathogenesis of multiple myeloma (MM) remains largely unexplored. We investigated the impact of mitochondrial loss and activity on the progression and relapse of MM. RNA-seq data from 770 newly diagnosed patients with MM revealed overexpression of mitochondrial activity-associated genes correlating with poor outcome. The expression of mitochondrial genes and proteins were elevated in patients who relapsed with bortezomib compared with previous stages, concomitant with an increase in mitochondrial activity. In proteasome inhibitor-relapsed MM patients, an elevation in c-Myc and CD38 expression, both involved in metabolic activation, could explain the consequent increase in mitochondrial activation triggered by proteasome inhibitor treatment. In vitro and in vivo studies with primary MM cells and the JNJ-3-Luc-GFP cell line showed the efficacy of the mitochondrial inhibitor tigecycline, alone and in combination with the frontline treatment bortezomib, reversing the bortezomib resistance induced by mitochondrial activation. Our findings provide a strong rationale for investigating tigecycline and other mitochondrial inhibitors in combination with current MM therapies (work published under review in Blood).

Figure 1 hnRNP K is a bona fide oncogene when overexpressed and represents a novel mechanism for c-Myc activation.

Figure 2 Clonal evolution and competitive advantages of TP53 variants. (A) Experimental flow chart. (B) Clonal competition assays of TP53-biallelic (red), TP53 monoallelic (yellow) and TP53WT/AMO1 cells (purple).

References:
1. Chań A et al. (incl. Martínez-López J) (2019). Detection of sequential subclones with TP53 with bortezomib compared with previous stages, concomitant with an increase in mitochondrial activity. In proteasome inhibitor-relapsed MM patients, an elevation in c-Myc and CD38 expression, both involved in metabolic activation, could explain the consequent increase in mitochondrial activation triggered by proteasome inhibitor treatment. In vitro and in vivo studies with primary MM cells and the JNJ-3-Luc-GFP cell line showed the efficacy of the mitochondrial inhibitor tigecycline, alone and in combination with the frontline treatment bortezomib, reversing the bortezomib resistance induced by mitochondrial activation. Our findings provide a strong rationale for investigating tigecycline and other mitochondrial inhibitors in combination with current MM therapies (work published under review in Blood).

Figure 1 hnRNP K is a bona fide oncogene when overexpressed and represents a novel mechanism for c-Myc activation. A (left) and murine (right) cells. (H) G4K expression. (I) OS hnRNP K expression. (J) OS hnRNP K expression. (K) OS hnRNP K expression. (L) OS hnRNP K expression. (M) OS hnRNP K expression. (N) OS hnRNP K expression. (O) OS hnRNP K expression. (P) OS hnRNP K expression. (Q) OS hnRNP K expression. (R) OS hnRNP K expression. (S) OS hnRNP K expression. (T) OS hnRNP K expression. (U) OS hnRNP K expression. (V) OS hnRNP K expression. (W) OS hnRNP K expression. (X) OS hnRNP K expression. (Y) OS hnRNP K expression. (Z) OS hnRNP K expression. (AA) OS hnRNP K expression. (BB) OS hnRNP K expression. (CC) OS hnRNP K expression. (DD) OS hnRNP K expression. (EE) OS hnRNP K expression. (FF) OS hnRNP K expression. (GG) OS hnRNP K expression. (HH) OS hnRNP K expression. (II) OS hnRNP K expression. (JJ) OS hnRNP K expression. (KK) OS hnRNP K expression. (LL) OS hnRNP K expression. (MM) OS hnRNP K expression. (NN) OS hnRNP K expression. (OO) OS hnRNP K expression. (PP) OS hnRNP K expression. (QQ) OS hnRNP K expression. (RR) OS hnRNP K expression. (SS) OS hnRNP K expression. (TT) OS hnRNP K expression. (UU) OS hnRNP K expression. (VV) OS hnRNP K expression. (WW) OS hnRNP K expression. (XX) OS hnRNP K expression. (YY) OS hnRNP K expression. (ZZ) OS hnRNP K expression. (AA) OS hnRNP K expression. (BB) OS hnRNP K expression. (CC) OS hnRNP K expression. (DD) OS hnRNP K expression.
Lung cancer continues to be the most frequent cause of cancer-related deaths worldwide. Our Unit focuses on the study of lung cancer, from fundamental research proposals to other more clinically oriented ones, always aiming to solve the problems of lung cancer patients. We are particularly interested in 2 research areas: (i) the identification of new molecular biomarkers for diagnostic, prognostic and predictive purposes; and (ii) the development of novel treatment strategies, including targeted therapies and immunotherapeutics. For example, we have contributed to elucidating the molecular determinants of EGFR or FGFR oncogenicity and have discovered biomarkers that may guide the efficacy of inhibitors of those receptors in lung cancer. We have developed an extensive platform of patient-derived xenografts of non-small-cell lung cancers to test new therapeutic strategies. Finally, our Unit has extensive experience in taking new drugs to the clinic, as well as in conducting practice-changing phase II/III trials in the fields of personalised cancer care and immuno-oncology. “Our Unit has significantly contributed to the development of novel biomarkers that have impacted the currently available selection of targeted therapies (e.g. EGFR mutation in the clinic) and novel immunotherapeutics (e.g. tumour mutational burden). We have led randomised clinical trials with novel agents as well as combinations of targeted therapies (e.g. Ramucirumab plus Erlotinib) or checkpoint inhibitors (e.g. chemotherapy plus Pembrolizumab or Nivolumab plus Ipilimumab) in lung cancer that have impacted clinical practice worldwide.”
The Lung Cancer Clinical Research Unit has led phase III trials in non-small cell lung cancer (NSCLC) and to develop new biomarkers with a predictive role for anti-EGFR therapy in NSCLC (Quintanal-Villalonga A et al. 2019). In addition, this PDX platform has contributed to the discovery of novel therapeutic targets, such as VEGF (Garmendia I et al., AHRCCM 2019) or Notch (Bousquet Mur E et al. 2019). Recently, we published a phase II trial demonstrating a strong correlation among them. Additionally, biomarker analysis beyond angiogenesis: "Best in Class (BIC)" 2019 in Lung Cancer patients with previously treated advanced non-small cell lung cancer, gastro-esophageal reflux disease (GERD), or esophageal cancer. (incl. Paz-Ares L.) (2019).

Early clinical trials
Our Group has significantly expanded its activities regarding the testing of new molecules and combinations in solid tumours, particularly in the field of immune-based approaches. In 2019, we participated in more than 40 projects in this research area, including 9 new trials. Recently, we published a phase II trial of Lurbenecitin, a novel transcription inhibitor, in small cell lung cancer. The results showed encouraging activity in the second-third line setting (Response rate: 34%), particularly in patients with sensitive relapse (median survival: 11.8 months) (Trigo JM et al. Lancet 2020). Based on encouraging activity, the drug is now being tested in a phase III registrational study.

Changing standard-of-care in treatment clinical practices
The Lung Cancer Clinical Research Unit has led phase III trials whose results have significantly impacted the clinical practice in the stage IV lung cancer, such as the combination of chemotherapy plus Durvalumab in small cell lung cancer (SCLC) patients (Paz-Ares L et al. Lancet 2019). The novel regimen was shown to significantly improve survival when compared to the current standard of care and survivors of stage IV NSCLC patients, regardless of the expression of PD-L1 in their tumours (Hellmann M et al., NEJM 2018, Hellmann M et al., NEJM 2019).

Figure 1 (A) A effect of numetstat and A2O4547 (FGFR inhibitor) on tumour growth of the lung adenocarcinoma PDX model. (B) Effect of FGFR4 mRNA expression on progression-free survival (PFS) of patients with resection or gefitinib- treated lung adenocarcinoma, showing that patients with high FGFR4 expression had a shorter PFS period.

Figure 2 Results of the CASPIAN study (NCT02320464). (A) Comparison of survival between durvalumab plus platinum-etoposide, when compared to platinum-etoposide (HR 0.73, p=0.0047), in treatment-naïve patients with extensive-stage small-cell lung cancer (ES-SCLC).

Biomarker discovery and implementation
We currently own an extensive PDX platform that has led to deciphering the role of the tyrosine kinase receptors FGFR1 and FGFR4 in non-small cell lung cancer (NSCLC) and to develop new biomarkers with a predictive role for anti-EGFR therapy in NSCLC (Quintanal-Villalonga A et al. 2019). In addition, this PDX platform has contributed to the discovery of novel therapeutic targets, such as VEGF (Garmendia I et al., AHRCCM 2019) or Notch (Bousquet Mur E et al. 2019). Recently, we published a phase II trial demonstrating a strong correlation among them. Additionally, biomarker analysis beyond angiogenesis: "Best in Class (BIC)" 2019 in Lung Cancer patients with previously treated advanced non-small cell lung cancer, gastro-esophageal reflux disease (GERD), or esophageal cancer. (incl. Paz-Ares L.) (2019).

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CAROLINA POLA
Director of Innovation

“Through our innovation activities we boost our impact and foster public-private alliances that contribute to bringing value and novel health solutions to society.”

From the identification of an idea to the transference of our product to the market, the Department of Innovation aims to improve the process every step of the way. Our close collaboration with investigators and to protect their research interests and assets are the main drivers to obtain results and boosts our indicators of innovation.

This optimised process has allowed us to identify four main areas of innovation potential that we have supported in 2019: drug discovery capabilities, biotechnological potential and novel basic discoveries in cancer, ageing and regenerative medicine, and computational biology. Boosting these areas has been a main objective of the Innovation Department and in this regard, we focused on identifying synergies and potential translational projects that can move forward by channeling collaborations between CNIO investigators and other institutions. Consequently, the CNIO obtained a substantial net return in royalties derived from licenses totalling €674,894, a growing amount compared to the last two years.

Our collaborations with the University Hospital H12O have started to yield important results with great impact for the health and biomedical ecosystem. In 2019, we closed an agreement with a spin-off company from the H12O called Altum for the diagnosis of residual disease and we co-developed an antibody against one type of cancer. This antibody promises to have a great impact at a societal and clinical level. Additionally, two patent applications were submitted in collaboration with industry, which highlights our partnerships with the private sector to advance translational research.

Maintaining our contact with the national and international industry and life sciences investors is crucial for the development of long-term agreements and to keep up to date on new developments and companies that are important players in the field of small molecules and advanced therapies. Our presence in the Milner Therapeutics Symposium held in Cambridge every year is testament of our international activities to stay in contact with the biopharmaceutical industry.

In 2019, a Caixaimpulse was awarded to an exciting project on cell therapy in diabetes regeneration led by Maria Salazar and Marcos Malumbres, and we worked on a proposal for the development of telomerase gene therapy in lung and heart disease. As CNIO positions itself in the competitive field of gene and cell therapy with novel approaches, our Department will keep exploring potential partners and providing understanding and input to contribute to development plans of our assets.
The main mission of the Biotechnology Programme Core Units is to provide expert technical and scientific support to CNIO Research Groups in a number of disciplines and technologies widely used in biomedical research, as well as to implement and develop state-of-the-art biotechnological tools and protocols. The Programme consists of 9 Core Units covering major areas in Biotechnology, namely Genomics, Proteomics, Monoclonal Antibodies, Histopathology, Flow Cytometry, Confocal Microscopy, Molecular Imaging and Mouse Genome Editing, as well as an Animal Facility. Although the Core Units are mainly focused on providing support and collaborating with the CNIO Research Groups, they also work with groups from other public research institutions as well as with private companies.

Faithful to its mission, a number of different technological innovations have been explored or implemented by the Core Units during 2019, often in collaboration with CNIO Groups. Among the new technologies introduced at the CNIO this year, it is particularly worth mentioning the Histopathology Unit’s implementation of the RNAScope system for the detection and visualisation of specific mRNAs by microscopy directly on tissue samples. Likewise, this year the Genomics Unit set up a new technology for single cell gene expression analysis (scRNAseq), based on a cell encapsulation system (Chromium 10X) acquired in late 2018. Moreover, the technological capabilities of the Units have been upgraded during 2019, with the acquisition of an Illumina NextSeq550 instrument for deep sequencing at the Genomics Unit, and a new ultrasound VisualSonics Vevo 3100 system at the Molecular Imaging Unit, among other equipment. Finally, the purchase process of a STED platform for super-resolution microscopy, co-funded with support from a call for scientific infrastructures from the Ministry of Science, Innovation and Universities (MCIU), has been initiated. The system will be deployed in 2020.

As an indication of our strong commitment to training, education and outreach, the Programme has been deeply involved in the organisation of courses, workshops, student visits, and meetings. We collaborated with the ‘CNIO & the City’ project, coordinated by the CNIO Institutional Image and Outreach to Society Office. The EuroMabNet network, chaired by the Head of the Monoclonal Antibodies Unit, held a workshop on the validation of antibodies, and specific training courses and workshops were organised by diverse Units (Confocal Microscopy, Flow Cytometry, Molecular Imaging, Animal Facility). Moreover, several members of our staff participated in various Masters courses and other training activities at the CNIO and elsewhere.

As usual, the Core Units were active in attracting funding from external sources through activities related to innovation, including contracts and agreements with private companies and public institutions based on the technologies mastered by several of our Core Units. Also, the royalties derived from the sales of the antibodies produced by the Monoclonal Antibodies Unit continue to represent a significant funding source for the CNIO, with an increase of 10% compared to the previous year; in addition, several new agreements have been signed with different companies to sell and distribute those antibodies.

Last but not least, 2019 was again a very productive year scientifically for the Programme. The contribution of the Units to the overall scientific performance of the CNIO is reflected in nearly 30 publications co-authored by members of the Units, many of them in top journals.

“The capability to maintain and upgrade state-of-the-art core facilities is one of the key elements behind the success of CNIO and its outstanding track record of scientific achievements.”
The Genomics Unit provides on-demand services in the genetics/genomics fields to CNIO researchers and the wider research community. Technologies are put in place with the capacity to interrogate genomes and their activities in a single assay. These methodologies contribute to dissecting molecular hierarchies and pathways. Processes such as functional activation states, as delineated by transcriptomic profiles (mRNA, miRNA) or protein factor interplays at the gene level, and structural features, such as mutation landscapes or variations in chromatin structure, can all be examined to study the quick-paced lives of cancer tumours. We cover a broad range of applications, including solutions such as exome study the quick-paced lives of cancer tumours. We cover a broad range of applications, including solutions such as exome, whole genome and whole exome tumour characterisation, transcriptomic analyses and location of chromatin interacting protein factors or RNA binding. This year we acquired and installed 2 pieces of equipment that enrich our capacity in this field: a Chromium Controller from 10x Genomics, suitable to perform single-cell genomics studies and a sequencer (NextSeq, Illumina), a necessary element for the readout of NGS applications.

Some of our contributions led to the following research reports being published in 2019, with the co-authorship of some of the Unit’s members: Fernández-Barral et al. report the presence of the vitamin D nuclear receptor (VDR) and stem cell markers (LGR5) in the human intestinal mucosa. Transcriptomics and ChIP-seq data support a direct effect of calcitriol, the active metabolite of vitamin D, in colon mucosa crypt stem cells. Vitamin D was found to display both pro-stemness and antiproliferative effects on the intestinal mucosa and is therefore proposed to contribute to the homeostasis of healthy intestine. The other report by Santos et al. describes organoids that recapitulate urothelial features in vitro. 90% of bladder cancer cases originate in the urothelium, and its growth and differentiation characteristics are poorly understood. The single-cell transcriptomics platform of 10x Genomics revealed cellular heterogeneity in different organoid culture conditions, and common and distinct cellular programmes under differentiation or proliferative responses. In addition, the study uncovered the involvement of Notch signalling in urothelial differentiation, which is consistent with the reported findings of mutated Notch pathway components in bladder tumours, and with the down regulation of NOTCH1 transcript levels in transformed bladder cells.
Genetically modified mice represent one of the basic pillars that sustain cancer research at the CNIO. The term ‘cancer’ includes a variety of extremely complex diseases in which malignant cells communicate with different body systems, such as immune cells or blood vessels, that modulate tumour growth, expansion and invasion. Such complexity cannot be sufficiently well studied by using in vitro systems alone. The Mouse Genome Editing Unit is dedicated to the design, generation and cryopreservation of genetically modified mouse models of cancer, using state-of-the-art technology for the controlled modification of the mouse germ line. In collaboration with CNIO groups, we have created hundreds of genetically engineered mouse strains that are crucial for understanding the molecular basis of tumour development and for the preclinical validation of new and more efficient cancer therapies. The Unit currently maintains a collection of more than 1000 cryopreserved mouse strains from which the entire scientific community may benefit for the advancement of Science in many different research disciplines.

**RESEARCH HIGHLIGHTS**

CRISPR/Cas based gene editing tools have revolutionised the way we approach genetic studies both in cells and in animals. The Unit has incorporated the CRISPR/Cas gene editing system for mouse germ line precise modification, replacing, in many cases, gene targeting in embryonic stem cells (ES cells) to generate knockout and knockin alleles with high efficiency. CRISPR reagents, introduced directly in mouse zygotes by pronuclear injection or electroporation, replace, in many cases, difficult and time-consuming ES cell culture and manipulation. The efficiency of knockout allele generation with CRISPR is often around 80-90% and bi-allelic knockout animals are frequently obtained. CRISPR-mediated homologous recombination directly in mouse embryos, using single stranded oligodeoxynucleotides as donor DNA for repair, leads to the efficient generation of point mutations or small tag insertions, thereby allowing precise and reliable genome editing. We have also developed strategies to increase the efficiency of CRISPR-mediated large (more than 3 Kb size) knockin integrations using, in this case, circular plasmids as donor DNA. As many as 40% of the pups born after zygote electroporation carry targeted knockin inserts (FIGURE). Zygote electroporation is a good alternative to microinjection for gene knockout generation. It is a much faster and easier process than embryo microinjection. Moreover, zygotes may also be obtained by in vitro fertilisation (IVF) and edited, on the same day, by CRISPR electroporation, increasing the chance of having a large number of fertilised mouse embryos. As many as 40 zygotes can be electroporated simultaneously in a single pulse and no embryo alteration (removing the zona pellucida) before electroporation is required. However, not all embryos are equally tolerant to the electroporation process. C57Bl6 zygotes exhibit a much lower viability than embryos of other genetic backgrounds, such as hybrid F1(B6.CBA) embryos, upon electroporation. We have also optimised protocols for electroporation of pure C57Bl6 embryos without compromising embryo viability.
The production of monoclonal antibodies has had a profound impact on multiple branches of biomedical research, and has driven a fundamental shift in the analysis of biological problems. Monoclonal antibodies allow a better understanding of life processes, and can help in the discovery and elucidation of new pathways for the diagnosis, prevention and treatment of cancer.

The Monoclonal Antibodies Unit provides CNIO Research Groups with a la carte generation of mAbs. We are highly specialised in the production of mouse and rat monoclonal antibodies. The Unit also offers mAb characterisation and tailored services. We are highly committed to improving the education and training of junior scientists in the field of antibody validation. Members include internationally distinguished academic laboratories that generate and validate mAbs. EuroMAbNet is strongly committed to improving the education and training of junior scientists in the field of antibody validation.

During the last 19 years, the Monoclonal Antibodies Unit has generated a large number of mAbs, directed against more than 100 different antigens, mostly targeting molecules for which mAbs are not commercially available. Many of those mAbs have been licensed to external companies, generating royalties that represent an important source of revenue for the CNIO.

Each year, we prepare and update a detailed CNIO mAbs catalogue, which contains the datasheets of more than 100 thoroughly validated high-quality mAbs (accessible at http://www.cnio.es/ing/servicios/anticuerpos/default.aspx). This catalogue is offered to specialised companies that are looking for licensing opportunities.

**RESEARCH HIGHLIGHTS**

**Figure** Expression of CD85A mAb in diffuse large B-cell lymphoma (DLBCL), angioimmunoblastic T cell lymphoma (AITL), modular sclerosis and mixed cellularity Hodgkin lymphoma (HD). Members include internationally distinguished academic laboratories that generate and validate mAbs. EuroMAbNet is strongly committed to improving the education and training of junior scientists in the field of antibody validation. We achieve this aim by organising annual Antibody Validation Workshops in different venues across Europe.

The final goal of EuroMAbNet is to strengthen European leadership in mAb technology, improve education in the field on an international level, and actively engage with industrial partners to ensure the optimum benefits from using mAb technology to improve human health.

**Research activities**

In collaboration with P. Engel from the Universidad de Barcelona, we have produced and characterised several new mAbs against the leukocyte immunoglobulin-like receptor family (LILR, LIR, ILT, CD85). LILRs are widely expressed in haematopoietic-lineage cells and mediate activation or inhibition of the functions of various immune cells, primarily myeloid cells. It is becoming clear that LILRs, with their capacity to regulate immune responses and mediate protumour functions, represent a new class of receptors that can be targeted for the treatment of a variety of immunologic disorders and cancer.

Targeting one member of the LILR family with mAbs, however, is extremely complex due to the high homology shown among family members. The use of nonspecific antibodies might trigger the function of other members, which may complicate the interpretation of the biologic effects. The study of the functional role of LILRs in cancer is challenged by the lack of suitable mAbs able to specifically recognise each family member. For this reason, we developed and extensively validated novel mAbs specific for CD85A and CD85G that will help to study how LILRs regulate myeloid function and tumour progression, as well as to test the therapeutic efficacy of targeting LILRs for the treatment of malignant, autoimmune, and inflammatory diseases.

**EuroMAbNet, a European consortium of experts in monoclonal antibody technology**

In 2008, in collaboration with Oxford University, we founded EuroMAbNet (www.euromabnet.com), a non-profit organisation that currently spans 11 European countries.
In 2019, we installed a new ultrasound system with better resolution to perform diagnosis and follow-up of tumours, as well as to phenotype different models and organs. The system improves the quality of ultrasound diagnosis by increasing the image resolution and signal-to-noise ratio (FIGURE).

The Molecular Imaging Unit continues to provide CNIO researchers with state-of-the-art molecular imaging equipment and human resources in order to guarantee the highest quality studies and to develop and update protocols and imaging techniques that optimise tumour visualisation in both the preclinical and clinical fields. The Unit also assesses and advises researchers on the best-suited imaging modality for their research projects.

As a result of a collaboration with the CNIO Breast Cancer Clinical Research Unit, we contributed to establishing the clinical usefulness of 18F-FDG PET as a tool to assess patients’ tumour responses in clinical trials.

The Molecular Imaging Unit continued to work on 2 main projects. Granted in collaboration with the CIEMAT group, one focuses on developing and labelling nanobodies produced by camelids based on the ImmunoPET strategy; this strategy combines the high specificity and selectivity of the antibodies with the high sensitivity and quantitative capabilities of PET. We also continued our participation in the RENIM Network. Our project focuses mostly on developing nanoparticles for optical and multimodality (optical-MRI or PET-MRI) imaging to detect primary tumours and distant metastasis. The results of this research will directly benefit CNIO scientists, who will be able to use and test these new imaging tools.

**OVERVIEW**

Molecular imaging is defined as the in vivo measurement of biological processes at the cellular and molecular levels. These techniques can visualise pathophysiological processes noninvasively in real time, with the potential for serial monitoring, and provide information about specific molecular alterations underlying the disease status of individual subjects. By complementing conventional ‘anatomical or physiological’ imaging, molecular imaging enables early detection of disease, disease staging, and quantitative assessment of therapeutic response.

“Molecular imaging with tumour-specific probes acts as a virtual biopsy, providing biological characterisation in a non-invasive way.”

**PUBLICATIONS**


**AWARDS & RECOGNITION**

- Project evaluator of the Junta de Andalucía and Generalitat Valenciana: Investigación, Desarrollo e Innovación Biomedica y en Ciencias de la Salud 2019.
FLOW CYTOMETRY CORE UNIT

Lola Martínez
Core Unit Head

November (P-E-L)**, Tania López
(unti April) (TS)'

Technicians
Renan Antoniali (until March) (TS)*,
Julia García (TS)*, Sara García (since
November)

SPANISH NATIONAL CANCER RESEARCH CENTRE, CNIO
ANNUAL REPORT 2019

BIOTECHNOLOGY PROGRAMME | FLOW CYTOMETRY CORE UNIT

RESEARCH HIGHLIGHTS

We provide state-of-the-art equipment and software packages in flow cytometry and collaborate with CNIO investigators in setting up and optimising flow cytometry techniques of their interest. Some of the applications developed and validated at our Unit are:

- Cell proliferation studies (CFSE, Cell Trace Violet, BrdU or EdU, DNA content, etc.)
- Apoptosis studies (Annexin V, Mitochondrial Membrane Potential, Caspase 3, etc.)
- Multicolour immunophenotyping panels (B and T cell development, Tregs, Inflammation, etc.)
- Functional assays (side population detection, Ca\textsuperscript{2+} flux, intracellular pH, etc.)
- Cytometric bead arrays to measure several cytokines from cell extracts and plasma
- Platelets studies

We further optimised our multicolour flow cytometry panels to characterise immune response in various samples from haematopoietic tissues, pancreas, skin, liver, lung, brain, as well as different tumour types. Single cell deposition into 96 or 384 PCR plates to perform single omics techniques is now part of our routine portfolio. We perform 4-way sorting based on DNA content on live stained samples and are advancing to separate even further to isolate 6 different fractions of DNA content. Additionally, we are also pushing the power of our analytical tools by moving towards high dimensional analysis, performing ‘unsupervised’ clustering analysis on our multiparametric panel assays.

OVERVIEW

Flow Cytometry is an indispensable tool in the oncology field. It allows multiparametric analysis for the identification, quantification and isolation of defined subpopulations of cells, based on the levels of expression of fluorescent markers and their relation to each other.

Our aim is to provide CNIO groups with technical and scientific advice regarding the use of cytometric technologies, collaborating with them in the design, acquisition, data analysis and interpretation.

We have 4 analysers and 3 high-speed cell sorters, with different configurations of lasers and detectors, to cater to all our users’ needs. We also have an automated magnetic bead separation system (AutoMACS), 2 automated cell counters and a tissue homogeniser (GentleMACS). Analysts are user-operated upon appropriate training, and cell sorters are operated by the Unit staff. Our sorters can separate up to 4- or 6-defined populations simultaneously, as well as perform single cell cloning. We can accept human samples to sort according to Biosafety regulations.

“To further push the development and optimisation of immunophenotyping panels, we have installed a fifth laser line into our LSR Fortessa. We also developed a 16-colour panel to characterise immune subsets in human blood samples.”

CNIO LSR Fortessa X20

Deep Multicolor Immunophenotyping

Human 18 marker Immune panel

Murine 20 marker Immune panel

AWARDS AND RECOGNITION

Vice-Treasurer of the European Association ‘Core Technologies for Life Sciences (CTLS)’.

Re-elected Member of the Board of Directors of the Iberian Cytometry Society (SIC).
The Confocal Microscopy Unit is equipped with 3 laser scanning confocal systems (Leica SP8) that incorporate UV and multiphoton excitation, as well as a white light laser and hybrid detection, and 2 wide-field systems (a Deltavision 4D deconvolution station and a Leica DMR6000 system, equipped with microinjection and microfluidics control). All the microscopes are automated and equipped with incubators for live cell imaging.

In addition, the Unit has implemented high throughput technologies applied to confocal microscopy using 2 different systems:

→ An Opera (Perkin Elmer) High Content Screening (HCS) system, which allows HCS experiments to be run on fixed and live cells in multiwell plates, and enables the monitoring of cell dynamics (translocation, cell division, etc.) through the use of fluorescent markers.

→ A Matrix Screening Application integrated into the SP8 confocal systems, enabling high throughput feeding of the instrument, not only in multiwell plates but also in tissue sections.

These advances enable us to increase the level of information obtained from a sample as well as to carry out the automated screening of cell behaviour under different treatments.

The Confocal Microscopy Unit continues to dedicate significant effort towards developing and implementing High Content Screening technology at the CNIO. In 2019, we further developed new advanced Machine Learning solutions oriented towards data mining and classification, thus allowing us to manage multiple object features applied to, for example, HCS multi-parametric treatment activity classification. Our activity in this field has been recognised and has led to the publication of several articles in journals as well as scientific book chapters.

**PUBLICATIONS**


The Unit promotes and helps with the protocol development for novel sample preparation, bringing knowledge in tissue clearing as well as in expansion microscopy. Moreover, the demand for the performance of Microfluidics, used for live cell assays in perfusion chambers, has increased greatly. Experiments in the field of intra-vital microscopy are available and we are now running several projects for studies of metastasis, skin alterations and immune system response.

In 2019 the Unit was awarded an infrastructure grant for the acquisition of new equipment.
Proteomics act as the molecular effectors of cells and catalyse virtually all biological processes. In this regard, proteomics aims to characterise the complete repertoire of proteins to better understand how cells function at the molecular level. Global analysis of proteins is challenging, owing to their high complexity (>12,000 genes transcriptionally active in mammalian cells) and high dynamic range (9 orders of magnitude between high- and low-expressed proteins). Furthermore, proteins are post-translationally modified (e.g. phosphorylation) and interact with each other to form complexes; both processes are highly divergent in time and (e.g., phosphorylation) and interact with each other to form complexes. surrogate markers of melanoma progression. We found that seroma-derived exosomes are enriched in proteins mimicking melanoma progression. Along the same lines, in collaboration with the Genes, Development and Disease Group, we applied this strategy to perform proteomic analysis of exosomes in a mouse lung fibrosis model and found that they are enriched in collagen-related proteins secreted by macrophages. Finally, the Unit continues to implement new technologies to the catalogue of available services. Throughout 2019, we optimised protocols for the global analysis of protein methylation, including mono- and di- methylation of lysines as well as mono- and di-methylation can be purified through highly specific monoclonal antibodies. "In the last decade, mass spectrometry-based proteomics has emerged as the most powerful technique to explore proteome structure and function."
Pathology is the branch of science devoted to the study of the structural, biochemical and functional changes in cells, tissues and organs underlying disease. The Histopathology Unit offers support and expertise throughout a full range of services covering from paraffin embedding and tissue sections to histochemical stains, research and diagnostic immunohistochemistry (IHC) testing, antibody validation, immunohistochemistry staining, double stains to detect both mRNA and protein, or any other marker of interest.

The high quality of the techniques run by the Unit continues to be endorsed by External Quality Assessment Schemes. Thus, our histochemical techniques were evaluated by UK NEQAS. On the other hand, NordiQC and SEAP has evaluated a subset of our IHC techniques under different modules, including general markers, breast cancer markers and PD-L1; these all obtained very high scores.

Training and outreach activities are also a critical component of the Unit’s activity. This includes our participation in modules of Formación Profesional for pathology technicians, mentoring of high school students during short-term stays at the Unit, conducting guided visits to the laboratories for students and other audiences, as well as offering practice sessions on the different technologies run by the Unit in Masters and other courses, among other activities.

In line with the activity carried out over the last few years, the Unit has maintained the portfolio of services demanded by its users in accordance with the needs of their projects. Thus, about 30,000 paraffin blocks of tissue samples were generated, and c. 25,000 techniques performed, including histological and IHC techniques, in situ chromogenic hybridisation, tissue microarrays, slide scanning, etc. Also, during this time we introduced new IHC markers useful for the study of tumour development, as well as new chromogenic substrates for the visualisation of those markers.

During 2019, the Unit implemented RNAScope technology for in situ hybridisation, using the Ventana-Roche automatic platform for IHC stains. This new technique allows the efficient detection of specific mRNAs directly on sections from formalin-fixed paraffin-embedded (FFPE) tissues, thus providing a spatial dimension to gene expression analysis. The applications of this new technology are expected to be manifold, e.g., as an alternative to IHC whenever it is difficult to find specific antibodies that work well on FFPE tissues, or to validate results from other technologies, among others. Also, sometimes it is feasible to combine this technique with IHC, allowing for double stains to detect both mRNA and protein, or any other marker of interest.

The implementation of the in situ hybridisation technology RNAScope and multiplexed immunohistochemistry staining, to enable the detection of several protein markers and mRNAs on the same tissue section, is an example of the Unit’s commitment to innovation to facilitate the progress of research projects at CNIO.”

“*The implementation of the in situ hybridisation technology RNAScope and multiplexed immunohistochemistry staining, to enable the detection of several protein markers and mRNAs on the same tissue section, is an example of the Unit’s commitment to innovation to facilitate the progress of research projects at CNIO.*”

Pathology expertise. Also, the Unit offers its portfolio of services to other institutions, including hospitals, research centres and private companies.

- **Publications**
The CNIO’s Animal Facility was established to assist researchers in the development and analysis of in vivo models. We are currently collaborating with as many as 27 Research Groups, Sections and Units from different Research Programmes. Our Animal Facility has the capacity to house 19,000 type I11 cages. Our mouse lines are maintained and bred in the Facility’s barrier area, which assures Specific Pathogen Free (SPF) health status through a comprehensive health surveillance programme. Microbiological and environmental parameters in the animal areas are constantly monitored. All mouse strains housed in the barrier are either generated within the barrier or introduced by rederivation. We also have an additional area with a capacity for 1,800 type II1 cages dedicated for the use of non-replicative strains of adenovirus, lentivirus and retrovirus, as well as for xenograft models. In this area, mice are housed in ventilated racks with integration of Individually Ventilated Caging (IVC) units in the building ventilation systems. Mice are always manipulated in Type II biosafety cabins.

Daily operations and husbandry procedures are highly automated in order to safe-guard our personnel from any associated risks; robotic devices perform the potentially hazardous tasks such as the processing of dirty bedding, the washing and filling of cages and bottles, etc. These automated systems maximise the productivity and ensure the quality standards in our washing and sterilising areas. All records concerning breeding protocols and animal inventory are computerised and stored in a web-based application accessible via the CNIO intranet.

The Animal Facility currently harbours more than 40,000 mice representing more than 3,000 genetically modified mouse lines, either as live animals or as cryopreserved embryos or sperm, carrying close to 400 gene targeted alleles and more than 200 transgenic integrations. The Facility also provides access to more than 50 tool strains, including constitutive and inducible Cre strains, Flp strains, reporter strains, Tet transactivator strains and others.

The Animal Facility offers the possibility of running a broad number of experimental procedures in the premises, including the use of gamma irradiation, UV light and volatile carcinogenic agents, as well as surgical procedures, some behavioural studies, a non-invasive blood pressure system, and a lab animal monitoring system (Oxylet) that enables measuring a number of physiological parameters for metabolic profiling and phenotyping of mouse models.

Additionally, the monitoring of the mouse models through non-invasive imaging technologies is provided by the Molecular Imaging Unit, which has integrated all its image acquisition instruments within the Animal Facility. Likewise, the work of the Mouse Genome Editing Unit is performed in a laboratory inside the SPF barrier. Finally, the necropsy laboratory is equipped with instruments for the haematological and biochemical analysis of blood and urine, which complement the pathology and clinical diagnostics.

In addition to mice, the Animal Facility hosts a colony of rats for the generation of monoclonal antibodies directed against mouse antigens, as well as for a project of the Experimental Therapeutics Programme that aims to test the safety of some specific anti-tumour compounds.

**ANIMAL FACILITY**

Isabel Blanco  
Core Unit Head

Management  
Vivoteca Management & Services
The following highlights summarise some of the achievements of the Experimental Therapeutics Programme (ETP) during 2019.

**CDK8 inhibitors.** ETP-18, a highly selective orally bioavailable CDK8 inhibitor, demonstrated good results after PO administration in pharmacokinetics and pharmacodynamics (PK/PD) studies in MOLM13 xenografts. ETP-18 is well tolerated and efficacious in this model. The lead compounds ETP-93 and ETP-18 were scaled up for toxicity studies in rats. The corresponding PK experiments were carried out to identify the dosing for those studies.

**Haspin and MASTL Inhibitors.** (In collaboration with Marcos Malumbres, CNIO Cell Division and Cancer Group). We previously generated 2 distinct chemical series of highly potent and selective Haspin inhibitors. In 2019, we evaluated combinations of our Haspin inhibitors with a library of 114 antitumour drugs. Additionally, we performed RNAseq experiments with both inhibitors, detecting the upregulation of certain genes. The results of both approaches could position Haspin inhibition as an interesting antitumour therapeutic option in combination treatments (confidential).

We also designed 2 additional series of potent MASTL inhibitors with higher commercialisation potential due to their chemical novelty. Currently, we are assessing their kinase selectivity to trigger and guide their further optimisation. Importantly, we undertook the development of PROTACs against MASTL kinase. We have already identified some molecules with low nanomolar affinity for the protein, and are performing MASTL degradation studies in cells.

**TRF1.** (In collaboration with Maria Blasco, CNIO Telomeres and Telomerase Group). We are still embarked on the target deconvolution of ETP-946. Previous pull-down experiments with reversible and irreversible affinity probes, using ‘click chemistry’ for their conjugation to a biotin-based tag, did not identify any validated target for ETP-946. This was due to inconsistent results between biological replicates. We have now designed new affinity probes that will not require the click chemistry step, a potential interference in our previous assays. We continued the SAR (Structure-Activity Relationship) exploration of ETP-946. Several analogues blocking metabolism hotspots have demonstrated good TRF1 activity together with better metabolic stability. Selected analogues are being evaluated in PK and distribution studies. Furthermore, we contributed to identifying additional signalling pathways involved in TRF1 modulation. One of them, the RAF/MEK/ERK pathway, was further validated as a key regulator of TRF1 in M. Blasco’s laboratory.

During the year, the ETP also helped other CNIO groups with several research activities such as screening campaigns and the synthesis of key tool compounds.

Importantly, the Singapore-based biotech company AUM Biosciences acquired from Inflection Biosciences an original ETP-CNIO multi-kinase inhibitor series. We are hopeful that AUM Biosciences will facilitate their clinical development.

“The first PROTAC has reached the clinic in 2019. In drug discovery projects, it is time to consider this avenue as an upfront option and not as a ‘nice to have’ complement to classical inhibitors.”
The Medicinal Chemistry Section is part of the interdisciplinary Experimental Therapeutics Programme dedicated to early Drug Discovery. Our activities consist of the design and synthesis of potential drugs with a therapeutic use in the field of cancer. Other activities integrated in our Section include the synthesis of high-quality chemical probes—potent, selective and cell-permeable compounds that are essential for target validation activities and the early stages of the drug discovery process. Additionally, we help CNIO’s basic research groups to decipher the mechanism of action that mediates an observed phenotype in cancer cells after screening for small organic molecules. Identifying the molecular target is essential to increase our knowledge about cancer and is a great aid to start drug discovery activities. To do this, we synthesise affinity chemical probes that enable cellular localisation of the target through imaging techniques and target identification through pull-down experiments coupled with proteomics.

“We implement PROTAC-target degradation strategies in our projects. The first PROTAC-like molecules have been synthesised that will be used to search for MASTL protein degraders.”
During 2019, we were involved in several different projects:

Cyclin-dependent protein kinase 8 inhibitors (CDK8i) project

We scaled-up our 2 lead compounds, ETP-93 and ETP-18, for additional biological characterisation. Proof-of-concept studies in MDML13 xenografts with ETP-93 and ETP-18 were completed, showing positive results. Additionally, pharmacokinetics (PK) studies in rats with both compounds were carried out. These compounds will be used in further toxicity studies in rats.

Microtubule-associated serine/threonine kinase-like (MASTL) inhibitors

In collaboration with the CNIO Cell Division and Cancer Group, we continued the exploration of the chemical series identified to obtain potent and selective compounds. We identified 2 chemical series of novel inhibitors, in a new chemical space, and in the low nanomolar range. We are currently performing selectivity studies against a panel of 468 kinases (KINOMEscan) in order to determine the selectivity profile, an important aspect for a compound. As a complementary strategy to target inhibition, we are also exploring the field of target degradation. More than 20 PROTAC-like molecules have been synthesised, among which some have been identified as having low nanomolar activity at the biochemical level. We are currently performing degradation studies with them.

Telomeric repeat binding factor 1 (TRF1) inhibitors

This project is undertaken in collaboration with the CNIO Telomeres and Telomerase group (TTG). We continued our efforts around the ETP-946 chemical series to expand Structure-Activity-Relationships (SAR). On the one hand, we wanted to improve the bioavailability parameters of our lead compound. For this purpose, we explored the molecule by blocking all the potential unstable positions through introduction of halogenes or other stable frames. The new compounds proved to be TRF1 inhibitors, and in vitro ADMET (absorption, distribution, metabolism, excretion and toxicity) studies were carried out. PK studies with these compounds showing a positive ADMET profile will be performed. A second approach in this chemical series is the exploration of different scaffolds and linkers to generate new chemical space and novel chemical series. So far, we have identified some modifications that retain TRF1 activity.

As part of the target deconvolution activities, our previous affinity probes synthesized using click chemistry did not allow us to identify a target. Now, we are applying several strategies in order to get new affinity probes while avoiding the click chemistry step. One of the first approaches that we took is to synthesise biotinylated compounds that preserve TRF1 activity and that will be used in pull-down experiments by direct binding to streptavidin beads (FIGURE). Finally, in order to get molecules that disrupt dimerization of TRF1 or binding of TRF1 to double-stranded (ds) telomeric DNA, the corresponding assays were set up and validated in the Biology Section, and small screenings are being run.

Discoid domain receptor (DDR) 1/2 inhibitors

As a result of a 4-year PhD project, we worked on searching for DDR1/2 inhibitors. Discoid domain receptors, DDR1 and DDR2, are 2 members of the collagen receptor family that belong to the tyrosine kinase receptor subgroup and are potential targets for human cancer and inflammation-related diseases. During 2019, we generated a novel chemical series of potent inhibitors in the low nanomolar range, at the biochemical and cellular levels. The chemical series presents an interesting selectivity profile and promising in vitro ADME data. The next step will be to perform PK studies to evaluate the in vivo levels after oral and IV administration with the most advanced compounds, in order to determine their use in efficacy studies.

Collaborations with other CNIO Groups

We gave support to different groups by synthesising tools or reference compounds, for example, to Miguel Gallardo, from the H22-CNIO Haematological Malignancies Clinical Research Unit, to the Metabolism and Cell signalling Group, to Hector Peinado, from the Microenvironment and Metastasis Group, and to Vanesa Lafarga, from the Genomic Instability Group.

| ![Figure Molecular docking of one of our first PROTAC-like molecules with TRF1 protein using the reported X-ray crystal structure of the hGWL-kinase domain in complex with STU (PDB: 5olh). Our molecular fits in the catalytic site of the protein (surface in green colour; the chemical structure is confidential), and the linker and CDBN moieties are extended into the solvent areas to be able to interact with the E3 ligase.](https://example.com/figure) |

**RESEARCH HIGHLIGHTS**

**Publications**


**Patent**

In the Experimental Therapeutics Programme, we perform both phenotypic and targeted-based drug discovery. The Biology Section is devoted to the biochemical, cellular, and in vitro/in vivo pharmacological characterisation of the compounds synthesised within the Programme.

At the biochemical assay level, we have developed a panel of different biochemical assays and optimised them for the targets used in our screening campaigns. We have currently established more than 30 different types of biochemical assays, mainly focused on kinase activities and covering a broad range of sensitivities and technologies (FI, FP, FRET, TR-FRET, chemiluminiscence, coupled enzymatic reactions, binding assays, etc.) adapted to the targets that we have been working on.

Recently, in order to identify inhibitors of relevant cancer targets with no enzymatic activity, we have started to develop biochemical assays to measure protein/protein interaction and protein/DNA interactions. These assays are based on AlphaScreen and AlphaLISA technology.

“HASPIN inhibitors could have potential antitumour activity in combination with different approved drugs.”
RESEARCH HIGHLIGHTS

During 2019, our Section was involved in several projects:

Cyclin-dependent kinase 8 (CDK8)
We finished proof of concept studies in mouse models with ETP-18, a selective, advanced, orally bioavailable lead compound that was safe in mice and has shown efficacy in MOLM13 xenographs. We also performed pharmacokinetic (PK) studies in rats with ETP-93 (dual CDK8/HASPIN-i) and ETP-18 (selective CDK8-i) compounds compared with known inhibitors at efficacious doses in mice. The results of the toxicity studies will be reported accordingly.

Microtubule-associated serine/threonine protein kinase-like (MASTL) and HASPIN
These projects are undertaken in collaboration with the CNIO Cell Division and Cancer Group. For MASTL, we tested in our biochemical assay with active human full-length MASTL protein, around 150 new compounds, both MASTL-i and MASTL PROTAC-like molecules. We are characterising those with nanomolar biochemical activity at the cellular level, evaluating both the modulation of P-E2NSA, a direct substrate of MASTL, and the degradation of MASTL with MASTL PROTAC-like molecules. For HASPIN, we obtained 2 highly selective chemical probes with nanomolar biochemical and cellular modulation of HASPIN. After testing them in a panel of 38 tumour cell lines, we evaluated their potential in combination with a library of 114 antitumour drugs and validated the results both by determination of the combination index and in dose response experiments (FIGURE). Moreover, we performed RNAseq experiments with both chemical probes in order to predict possible combinations. At that point, the results were confidential.

Telomeric repeat binding factor 1 (TRF1)
This project is carried out in collaboration with the CNIO Telomeres and Telomerase Group. We have continued our efforts to deconvolute the molecular target of our hit ETP-946. After triplicate pull-down experiments with reversible and irreversible chemical probes of ETP-946, we could not validate any target. Interestingly, we identified a molecule with a single change in one atom with respect to ETP-946 that was not able to modulate TRF1 and that is being used to help in deconvolution studies. The results of RNAseq experiments with ETP-946 and its inactive analogue are being analysed to try to identify the molecular target of ETP-946. Moreover, we tested in a phenotypic assay to measure the association of TRF1 to telomeres, 77 compounds that analogue of ETP-946 to improve its bioavailability and to try to expand chemical diversity. The metabolic stability of the active compounds has been determined and we are performing PK and distribution studies with stable compounds. Furthermore, by using a chemical biology approach, we validated that the RAF/MEK/ERK pathway modulates TRF1 levels at telomeres. Finally, we set up 2 assays based on AlphaScreen and AlphaLISA technology to identify small molecules that disrupt dimerization of TRF1 or binding of TRF1 to telomeric DNA; in parallel, we established their corresponding counter-screen. After virtual/wet screening and analogue searching, we identified several low micromolar hits that disrupt TRF1 dimerization and that are being validated. Furthermore, we started virtual screening to identify disruptors of TRF1 binding to ds telomeric DNA that will be tested in our wet assay.

Collaborations with other CNIO Groups
ETP-Biology provided ongoing support to follow-up on the results obtained from the screenings performed by the Brain Metastasis Group and the Metabolism and Cell Signalling Group. We also provided support for in vitro studies performed by the Microenvironment and Metastasis and the Experimental Oncology Groups, and by setting up and carrying out a screening to identify Protein inhibitors in collaboration with the DNA Replication Group. We conducted the analyses to determine compound levels in several biological samples from the Telomeres and Telomerase Group. Moreover, we collaborated with Experimental Oncology Group, testing and analysing the ETP-antitumour library to identify novel treatments of mutant KRas NSCLC mouse cell lines that was safe in mice and has shown efficacy in MOLM13 xenographs. We finished proof of concept studies in mouse models with ETP-18, a selective, advanced, orally bioavailable lead compound that was safe in mice and has shown efficacy in MOLM13 xenographs. We also performed pharmacokinetic (PK) studies in rats with ETP-93 (dual CDK8/HASPIN-i) and ETP-18 (selective CDK8-i) compounds compared with known inhibitors at efficacious doses in mice. The results of the toxicity studies will be reported accordingly.

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Cancer can be defined as the uncontrolled growth and division of cells, leading to tumour formation, invasion, and metastases. Unlike normal cells that require growth factor signals, tumour cells often have mutations that result in constitutively active (‘always on’) signalling pathways that drive aberrant cell growth and division. In order to fulfil the high nutrient demand required for their continuous growth, tumour cells have reprogrammed their basal metabolism from an oxidative to a more glycolytic/anabolic one, even in the presence of oxygen. Otto Warburg proposed in the early XX century that, ‘this altered metabolic state was the underlying cause for cancer’ (Warburg 1956). The past decade has been a period of very active research in the area of tumour metabolic reprogramming, and major molecular mechanisms involved in the process have been identified and characterised. It was found that both oncogenes (Ras, Myc) and tumour suppressor genes (p53, RB, LKB1) impart an altered metabolic phenotype in cancer cells through the regulation of genes involved in central metabolic pathways such as glycolysis, fatty acid metabolism, oxidative phosphorylation, nucleotide synthesis and the one carbon pool (reviewed by Gilmour & Velasco, 2017). All these alterations have led tumours to rely heavily on specific metabolic pathways to obtain their energy, while using other pathways to grow in order to give tumour cells a growth advantage. This situation may leave tumour cells in a frail position under certain treatments or circumstances, while normal cells may be able to compensate, adapt and survive. Our laboratory is searching for this metabolic weakness in order to stop tumour growth.

Furthermore, the high requirements of nutrients and other soluble factors as well as the release of metabolites with immunosuppressive properties, together with the hypoxic conditions found in tumours, create a ‘non-friendly’ microenvironment for an anti-tumour immune surveillance, while facilitating the growth of other tumour-promoting cells such as stroma and myeloid cells (FIGURE A, B). Thus, the mechanistic understanding of cancer metabolism has led to renew interest in developing therapeutics that target key enzymes involved in this process. Checkpoint-blockade immunotherapy has been one of the most exciting advances made in cancer treatment in recent years. Metabolic interplay in the local microenvironment can mediate T cell differentiation and function. ‘Checkpoint-blockade’ antibodies can also influence cellular metabolism. Finally, recent clinical trials have shown that combination immunotherapy, based on immune checkpoints blockade and targeted and non-targeted therapies, provides even higher response rates than either approach alone. Several clinical trials are currently using this approach, however, not all patients respond to immunotherapy and it is, therefore, necessary to determine which patients would be good candidates for the treatment. It has been found that an inflammatory tumour microenvironment – ‘hot’ tumours - greatly increases patient survival. One of the objectives of our laboratory has been to identify, and characterise the expression of novel and known tumour markers that may enable a better patient stratification for future therapies. This approach has shown that, in addition to the levels of expression of an immunotherapy target, the type of cells that express the marker may also be a feature to consider.
Our office is strongly committed to translating new discoveries in cancer research for the benefit of patients and the health care system. To this end, we identify, protect and develop projects with commercial potential, always with the mindset of co-developing them with private and public entities to increase the value of potential products.

At the CNIO, the best science and research efforts join in the desire to make a great impact for cancer patients and the health care system. The Technology Transfer and Valorisation Office (TTVO) contributes to this purpose by ensuring appropriate protection of intellectual property and by channeling the technologies that arise from our research to companies and entrepreneurs in order to develop them further and thereby impact society.

The TTVO proactively monitors the progress of the CNIO's scientific activity to identify projects with high transfer potential. In 2019, 15 new ideas were incorporated into the technology transfer portfolio, of which 2 turned into priority patent applications and 9 are under patentability analysis. These cover a wide range of products, including a method for determining the presence or absence of minimal residual disease in patients treated for a proliferative disease, a combination of an antibody with activated and expanded natural killer cells for cancer immunotherapy, drug inhibitors, new biomarkers, a monoclonal therapeutic antibody, a cell therapy, and an approach to screening of molecules.

CNIO patents constitute an active portfolio of assets that are carefully prosecuted according to a patent strategy and licensing efforts. In coordination with national and international patent agents, TTVO manages a portfolio of 34 patent families, and provides advice and assistance during the drafting of the patent document, filing and prosecution process. Four PCT (Patent Cooperation Treaty) applications for international extension were filed in 2019, and 2 patents with proven commercial interest entered the national phase. Licensed patents make up a remarkable 37% of the CNIO portfolio. Among the licences signed in 2019, a license agreement with the company Alumara signed in 2019, a license agreement with the company Altum, a remarkable 37% of the CNIO portfolio. Among the licences signed in 2019, a license agreement with the company Alumara, Sequencing represents a milestone for the associated CNIO-H12O Clinical Research Units.

To ensure that scientific ideas and results are transferred to the private sector, a proof-of-concept phase is usually necessary to validate its potential application in the market. The TTVO supports the preparation, coordination and advice of CNIO scientists so that their ideas reach the point of development necessary for potential companies to decide to invest and co-develop.

This is the case of calls aimed at technological development projects such as Caixa Impulse and FET-OPEN, among others. Besides from the 2 Caixa Impulse projects launched in 2018, a new cell therapy project for type 1 diabetes was awarded a Caixa Impulse grant in 2019, and thereby benefits from funding and mentoring by experts of the national bio-ecosystem. A FET-Open grant was awarded to a Consortium in which CNIO researchers will focus on the use of probes for discriminating between different types of cancer and heat generation in order to increase the permeability of the blood-brain barrier.

The experience and financial support of the value chain’s actors, from specialised investors to large multinationals in the biopharmaceutical industry and start-up companies, are necessary to develop technologies. The TTVO identifies these partners, negotiates technology transfer agreements, and manages the relationship with licensees, including the payment of royalty fees. In 2019, the TTVO managed 281 technology transfer records related to industrial and intellectual property generated by CNIO’s researchers, 231 correspond to agreements (MTAs, CDAs, Research Collaborations, licenses, etc.). Among these industrial partnerships is worth noting the collaboration with Lilly, which has been extended for 3 more years to incorporate new scientific studies that include work on immunomodulation, oncogenic drivers, resistance, platforms, and knowledge of resistance in immuno-oncology. Other collaborations include the IRONMAN-ES study funded by the Movember Foundation, in which 30 to 15 hospitals participate and in which the CNIO and Institute of Oncological Research (VHIO) are co-promoters; the extension of the collaboration contract with the Spanish company Lipotrue; and a collaboration contract with the Istituto Scientifico Romagnolo per lo Studio e la Cura dei Tumori.

The majority of these agreements (68%) were established with international entities, which is an indicator of the internationalisation of the CNIO’s research activity. Through research collaborations with industry, up to 1.7 million euro were secured for research activities. Moreover, 4% of the agreements are licences to commercial partners. Patents and unpatented research tools are licensed. The net income derived from licences in 2019 increased to €674,900. This income reverts back to CNIO research activities as well as to the inventors themselves. A total of 40 inventors and 10 research groups have contributed towards and benefited from this achievement.

Effective transfer of research results to the productive environment requires intensive networking and asset promotion. In addition to attending international forums on advanced therapies in cancer and regenerative medicine, in 2019 TTVO participated in the ASEBIO Investors Day in Madrid and the Milner Therapeutics Symposium in Cambridge.

All the above-mentioned achievements stand testament to the excellence and hard work of the CNIO scientists and to the CNIO’s unwavering encouragement of innovation and technology transfer activities.
Biobank
CNIO Biobank - authorised by the Health Authorities of the Comunidad Autónoma de Madrid (CAM) and registered in the National Registry of Biobanks with reference B.000848 - is a ‘biobank for biomedical research purposes’, as defined by the Spanish Law 14/2007 and the Royal Decree RD 1716/2011. It is therefore defined as a public, non-profit organisation that hosts several collections of human biological samples for biomedical research, specifically in cancer and related diseases. The main objective of the CNIO Biobank is to facilitate access to human samples for researchers, ensuring that both the acquisition and use of human samples complies with all the legal and ethical principles that protect donors’ rights.

In addition to this biobanking activity, a number of services have been implemented, both for sample processing and for supporting different aspects of the management of human samples for biomedical research, in order to facilitate the use of human samples for CNIO researchers.

CNIO Biobank is a founder member of the Spanish Biobank Network, a project funded by the Instituto de Salud Carlos III, ISCIII, currently through the Acción Estratégica en Salud - AES 2017 supportive platforms for research programmes. CNIO Biobank leads and/or participates in many different projects such as: centralised request management system (design and development), ethical, legal and social issues (ELSI); harmonisation; biospecimen science; and marketing plans.

Therefore, CNIO Biobank is a cross-service platform for CNIO researchers, as well as the general scientific community, and is geared towards the promotion of biomedical research in cancer and related diseases.

**Ethical and legal services**

CNIO Biobank supported 3 CNIO project submissions for ethical evaluation by the Instituto de Salud Carlos III (ISCIII) Research Ethics Committee.

CNIO Biobank is participating in 3 multicentre research projects:

- Optimar (PI16/00946) (led by the CNIO Biobank): focused on identifying quality markers for tissue samples sensitive to pre-analytical variables.

**Teaching activities**

During 2019, we actively participated in 3 guided school visits (as part of CNIO’s educational activities) and hosted a graduate student for a short-term stay.

CNIO Biobank in collaboration with Lund University (Sweden), University of Copenhagen and the Danish National Biobank (INB) organised and led a PhD course and Symposium in November entitled “The Future of Biobanking” in Copenhagen and Lund (Sweden).

**Research highlights**

**Biobanking**

In 2019, CNIO Biobank coded tissue samples from 468 cases to support 7 research projects. The return in impact related to this activity resulted in 5 (Q1) publications acknowledging CNIO’s Biobank contributions, with a mean impact factor (IF) of 9.077:

> Management of project-driven and diagnostic collections:
  - CNIO Biobank holds responsibility for management of 3 different collections. This year’s activity accounted for a turnover rate of 659 human samples.
  - CNIO Biobank collaborated with the Familial Cancer Unit in the acquisition of 37 new cases.

> The CNIO Biobank’s Virtual Catalogue includes 269 images, 139 of them histological H&E staining. We continue expanding this catalogue to include whole section paraffin-embedded samples.

**Publications**


Book Chapter

### Communication

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For yet another year, the CNIO’s Communications Department brought the research activity of the Centre closer to those who benefit most—patients, their families and society in general—using the available communication channels. This is an essential task, for our society to be more and better informed on science issues, especially in the current information environment in which fake news often prevail.

Media coverage of CNIO activities and discoveries continues to grow each year. In 2019, we appeared more than 4,400 times in the press, both on paper and online (34% more than in 2018), and we were mentioned 340 times on radio and television. In general, media coverage increased by 28% compared to the previous year.

Scientific news of the CNIO attracted the interest of the main Spanish media and those of other countries, such as the BBC and Clarín, and also made it to the front page of local and regional national newspapers, such as El Mundo and La Razón. News items included the confirmation of the link between the most aggressive prostate cancer and hereditary breast cancer (David Olmos, Journal of Clinical Oncology); the elimination of some types of pancreatic cancer in animal models (Mariano Barbadic, Cancer Cell); the discovery of a new immunotherapy treatment that improves survival in a type of aggressive lung cancer (Luis Paz-Ares, The Lancet); and the resolution of the 3D structure of the molecular mechanism that gives virulence to tuberculosis (Óscar Lleó, Nature).

Around February 11 (the International Day of Women and Girls in Science), the #YoRompoTechoCristal [#BreakTheGlassCeiling] social media campaign was run to make the obstacles faced by professional women scientists visible using the video ‘Women and Science’ by CNIO & The City as a starting point. With this activity, 2 proposed objectives were exceeded: on the one hand, in terms of video views—it was the most-watched video of 2019 and the all-time 5th of our YouTube channel—and, on the other hand, in terms of use of the hashtag beyond the campaign: many users used it, mainly on Twitter, in their demands for female visibility in science. Moreover, the initiative was picked up by media outlets such as TVE, El País, Voz Pópuli and Yo Dona.

As part of our efforts to reach society, in September we again kept our commitment to International Cancer Research Day. With the support of “la Caixa”, we brought scientists and the general public together at CaixaForum, Madrid, for the conference ‘New horizons in cancer research—from bench to bedside.’ The event was attended by researcher and theoretical physicist Raúl Rabadán, Professor of the Department of Systems Biology and Director of the Program for Mathematical Genomics at Columbia University (USA), he gave the keynote lecture ‘The Genomic Revolution in Cancer.’ Afterwards, a round table, moderated by journalist and author Cristina Villanueva, was held in which María Blasco (CNIO Director), Manuel Valiente (Head of the Centre’s Brain Metastasis Group), Yolanda Fernández (Head of the Breast Cancer Section of the Central University Hospital of Asturias, HUCA), and former patient and ‘CNIO Friend’ Mila García Calvo participated.

Also during 2019, a collaboration agreement with L’Oréal Spain was formed to launch, together with La Roche Posay, the #ResearchIsLife [InvestigaciónEsVida] campaign on the occasion of World Cancer Day. The two-week campaign was aimed at raising awareness of the ‘CNIO Friends’ initiative to seek new supporters for cancer research at the CNIO. The campaign was present in pharmacies throughout Spain, to which activities in social networks and informational mailings to customers, consumers and the media were added.

In addition, the CNIO Arte project that, with the collaboration of the Banco Santander Foundation, explores the common areas of scientific research and artistic creation, brought together in its second edition the quantum physicist Ignacio Cirac and the photographer Chema Madoz, winner of the National Photography Award. Once again, the reception of the project in the media was exceptional, attracting the interest of cultural programmes such as ‘La Maestra, obra!’ of the Spanish TV channel La 2, the news programme of the Spanish national television channel TVE, National Geographic, the magazines ‘El Cultural’ and ‘GQ’ and Canal Metro, of the Madrid metro—to mention just a few.

In our effort to bring science to spaces where it is not usually present, in November CNIO Director María Blasco was interviewed in the programme ‘El Intermedio’ of the Spanish TV channel La Sexta. Also at this time, researchers María Blasco and Mariano Barbadic participated in the advertising campaign #ValoremusAlosCientíficos [#Let’sValueOurScientists] through which ‘Constantes y Vitales’, the corporate responsibility campaign of la Caixa and AXA, wanted to recognise the work and image of Spanish scientists.

These are some of the initiatives in which the CNIO participated that give value to the researchers’ work, and to the importance of science and research as a driving force to build a better society.

“Only a well-informed public will defend scientific knowledge as key to address global challenges.”
PRESS CLIPPINGS

1. BBC News Mundo, January 14, 2019
2. La Mañana, La 1, February 4, 2019
3. La Razón, February 4, 2019
4. ¡Atención obras!, La 2, March 4, 2019
5. ABC, March 6, 2019
6. El País, March 29, 2019
7. El Mundo, April 4, 2019
8. La Sexta Noticias, La Sexta, April 11, 2019
9. El Mundo, April 27, 2019
10. Telecinco, La 1, May 31, 2019
11. El Correo Gallego, September 14, 2019
12. Gaceta Médica, September 9, 2019
13. El Correo Gallego, September 14, 2019
14. Gaceta Médica, September 9, 2019
15. Diario 24 Horas, October 10, 2019
Our most shared and commented news on the CNIO social network channels offer a good overview of the issues that most interest society with regard to cancer research, but also with regard to science in general.

In 2019, some of the highlighted topics were the work of the teams of Mariano Barbacid about pancreatic cancer (Cancer Cell, April), Nabil Djouder on the side effects of radiotherapy (Science, May), and Maria Blasco about the longevity of species (PNAS, July); interviews such as Maria Blasco in ‘El Intermedio’ of La Sexta, Sandra Rodríguez in El Mundo, and Manuel Valiente in El País; the awards and recognitions to our scientists; the outstanding position of the CNIO in the international rankings of research centres; and events such as the CNIO’s ‘Frontier Meeting on Heterogeneity and Evolution in Cancer’, and the ‘European Researchers’ Night’.

2019 SOCIAL NETWORK DATA FOLLOWERS

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2019 SOCIAL NETWORK DATA CHANNELS

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2019 SOCIAL NETWORK DATA VIDEOS

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SOCIAL EVENTS

CNIO and the Moross Integrated Cancer Center (MICC) of the Weizmann Institute of Science held in Rehovot, Israel, an international symposium on the newest approaches in cancer research and the development of new joint projects. This was the second of the biennial events that take place alternately in Spain and Israel following a cooperation strategy agreed upon in 2017 by CNIO and the Weizmann Institute of Science – two of the world’s top cancer research centres – and Ramón Areces Foundation. September 4-5, 2019.

Scientists from CNIO and the Spanish National Centre for Cardiovascular Research (CNIC), both affiliated with the National Institute of Health Carlos III (ISCIII), organised a Joint Meeting at CNIO headquarters to share knowledge and promote synergies and future collaborations. Raquel Yotti, Director of the ISCIII, opened the meeting, and Maria Blasco and Valentín Fuster, Directors of CNIO and CNIC, respectively, presented an overview of some of the most innovative research lines of each of their institutions and underscored the vital importance of collaborative research. September 20, 2019.

With the support of “la Caixa” Foundation, we celebrated the World Cancer Research Day at CaixaForum Madrid, with an event entitled ‘New Horizons in Cancer Research: from Bench to Bed’. Raúl Rabadán, from Columbia University, gave the keynote speech ‘The Genomic Revolution in Cancer’. Afterwards, a roundtable was held with the participation of Maria Blasco, Manuel Valiente, Yolanda Fernández (Central University Hospital of Asturias), and Mila García Cairo (former cancer patient and CNIO Friend). September 24, 2019.

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CNIO addressed its commitment with the European Researchers’ Night, which is funded by the EU Framework Programme for Research & Innovation, Horizon 2020 - Marie Skłodowska-Curie actions. In the region of Madrid, it is promoted by the Department of Education and Research and coordinated by Fundación madri+d. More than 40 CNIO volunteers and 200 visitors participated in the event, aimed at showing the reality of a collective - the science community - that is key for the development of society. September 27, 2019.

CNIO renewed its commitment with the European Researchers’ Night, which is funded by the EU Framework Programme for Research & Innovation, Horizon 2020 - Marie Skłodowska-Curie actions. In the region of Madrid, it is promoted by the Department of Education and Research and coordinated by Fundación madri+d. More than 40 CNIO volunteers and 200 visitors participated in the event, aimed at showing the reality of a collective - the science community - that is key for the development of society. September 27, 2019.

The SOMM Alliance held its first meeting on gender equality policies at CNIO. Directors of SOMMa Centres discussed the network’s best practices in gender equality, to implement a change of culture that allows gender equality to be integrated into strategic science decisions. Invited speaker Cheryl Smythe, gender equality expert from the Babraham Institute, talked about the gender policies implemented by her centre. The British Embassy in Spain took part in the event, which was closed by Ana Puy, Director of the Women and Science Unit at the Ministry of Science, Innovation and Universities. October 29, 2019.
International Affairs
The combined efforts of different departments spearheaded by the Department of International Affairs (IAs) translate into outputs for the institution that have an impact at a science and institutional level. In collaboration with our Projects Office, we continue to explore funding opportunities to propel the research impact of our investigators and the CNIO. In 2019, we continued participating in strategic working groups organised by the Spanish Ministry of Science, Innovation and Universities (MICIU) and the Centre for the Development of Industrial Technology (CDTI), as a fundamental action to maintain our engagement with funding and influencing institutions at the National and European level. Our institutional strategy to boost the coordination of H2020 consortia projects by CNIO investigators has resulted in an increase in 67% in proposals submissions for coordinated projects.

Since its launch in 2017, the CNIO has been a member of the Severo Ochoa and Maria de Maetzu Alliance (SOMMa). This year, CNIO Director Maria Blasco held the position of Vice-Chair of the Alliance, directly contributing to its performance and governance. The IAs led the WP of Outreach and actively participated in the organisation of the second ‘100xCiencia’ conference held in November at the Tabakalera in San Sebastian that focused on how science can bring value to society. During this event, the CNIO Director Maria Blasco shared with the lay audience the advancements in gene therapy for age-related diseases, and AIAs brought a stand in which we gamified different biomedical innovation projects from CNIO.

Continuing with our approach to promote cooperation with international research institutions, in 2019 we led a proposal for an interdisciplinary project in collaboration with institutions from three different countries. The Accelerator Awards call from CRUK and AECC is a key framework for developing a competitive consortium in alliance with 3 European countries. These and other opportunities have been leveraged to boost our visibility and cooperation beyond our borders.

One of our main successful alliances is the one we keep nurturing with the Weizmann Institute of Science and the Ramon Areces Foundation. In 2019, this successful partnership has translated into a collaborative project for the development of new immunotherapies and knowledge in the field of melanoma, and a cancer research symposium held in Rehovot, Israel. This partnership is a true example of collaboration and commitment between international institutions devoted to the advancement of science.

As the new European framework programme becomes a reality, the IAs has been actively involved in the scrutiny of the working documents for the upcoming Horizon Europe. This aims to facilitate the involvement, participation and influence of CNIO in future calls in order to harness our expertise and leadership in key fields in cancer and ageing-related diseases. We expect 2020 will help us achieve more outputs from the groundwork that we strive to build and strengthen every year.

“We align our scientific and institutional strengths with Europe’s vision for research and innovation to maximise our outputs through collaborative projects and public-private alliances.”
Institutional Image & Outreach to Society
In 2019, the CNIO Cancer Research Centre was transformed into a venue for mutually beneficial encounters between the worlds of science and art. Its walls were given over to multimedia works curated by visual artist Amparo Garrido, who also serves as Coordinator of Institutional Image and Outreach to Society at the CNIO. Prominent among the participants was Ignacio Cirac, who heads the Max Planck Institute of Quantum Optics in Garching (Germany). He was paired off with Chema Madoz, winner of Spain’s National Prize for Photography and the sparks given off materialised in an edition of 30 signed, limited copies of a print by Madoz, the proceeds of which were earmarked for projects funded by the ‘CNIO Friends’ philanthropic initiative.

The photographs by Chema Madoz remained on display from February to April. During that time, Madoz’s work was also exhibited at the ARCO and JUSTMAD contemporary art fairs, while the CNIO also kept its profile high during the ‘Quantum’ exhibition at the Centre for Contemporary Culture in Barcelona (CCCB). Beogota Gómez, co-director of the Masters Programme in Fundraising Management at Madrid’s Complutense University, was present for the Barcelona event as was Carlos Jiménez, emeritus professor at the European University of Madrid, a specialist in art history and critical theory, along with Maria A. Blasco, Director of the CNIO, and Amparo Garrido, project curator and presenter of the event. CNIO Arte is an initiative created by CNIO, with support from the Banco Santander Foundation.

It was the CNIO’s turn to host some of the big players in philosophy and ethics on occasion of the Centre’s annual Symposium on Science and Philosophy. The scientists involved included Maria A. Blasco, Director of the Centre, Lluis Montoliu, Head of the Department of Molecular and Cellular Biology at the Biotech Center (CNB-CNIC) in Barcelona, and Alfonso Valencia, Head of the Bioinformatics and Life Sciences programme at the Barcelona Supercomputing Center. A formidable array of thinkers was mustered to keep the arguments lively, including Antonio Diéguez, distinguished Professor of Logic and Philosophy of Science at the University of Málaga, author of Transhumanism: The Technological Quest for Human Improvement. Also present was Ibígo de Miguel, inter-university research Professor of Legal Aspects of the Human Genome at the University of the Basque Country; Arantza Etxeberria, Professor of Philosophy and Science at the same institution UPV/EHU; Henrik Vogt, Physician and Philosopher at the Centre for Medical Ethics at the University of Oslo (Norway); and Maria Cerezo, Professor of Logic and Critical Theory.

In 2019, our redesigned institutional web received an honorary mention in the Prisma Prize for the Advancement of Science, the most prestigious award of its kind in Spain. In their citation, the judges singled out CNIO’s “innovative proposal for presenting the content and activities of a major research institution directly to the public in a format that is both modern and accessible to all.” All told, the CNIO produced a series of custom videos and held numerous science outreach events throughout the year.

Thanks in part to our new website launched in 2018, the CNIO has been able to consolidate its profile. The roughly 190 events scheduled last year were open to the public, and it was a particular satisfaction to be involved in the ‘International Day of Women and Girls in Science’ on February 11 and other diversity initiatives highlighting the obstacles facing young women who have demonstrated their qualifications to study and build a career in the traditional WISE (women in science and engineering) disciplines.
During one’s school years, there are doubts and important decisions to think about: which career to choose, what to work on... CNIO & The City is an educational and science outreach project established in 2017 to strengthen the bridges between CNIO scientists, the educational community, and society as a whole. It was released to impact and inspire them with our science!

After the success of CNIO & The City’s first editions (May 2017 - March 2018; May 2018 - June 2019), funded by the Spanish Foundation for Science and Technology (FECYT) - Ministry of Science, Innovation and Universities, the CNIO decided to incorporate this project and its values as an essential core of the CNIO outreach strategy.

New standards of scientific excellence are reached thanks to these initiatives. This is widely known here at the CNIO, and over 140 CNIO scientists are involved in our activities: principal investigators (32%), staff scientists (15%), post-doctoral fellows (17%), graduate students (7%) and technicians (29%). Thanks to them, we organised lab immersions and scientific projects with secondary and high school students (EDUCA CNIO); training courses for teachers (FORMA CNIO); and scientific workshops in classrooms (DIVULGA CNIO), which were a unique opportunity for the more than 1,200 participants (students and teachers) over the last 2 years.

We also want to go one step further and get closer to the whole of society. This is why we dedicate time to think about and create educational videos, which can be played everywhere: in class, in a large auditorium and even on smartphones!

In 2019 we launched 2 cartoon videos about general topics in cancer science (‘History of Cancer’ and ‘Cancer Risk Factors’). Another video related to the ‘Women in Science’ issues was released to empower our CNIO & The City female participants (78%) and raise awareness about gender balance in science and breaking the glass ceiling. This video was very well received by the media thanks to our February 11th #YoRompoTechoCristal [I Break the Glass Ceiling] Challenge (International Day of Women and Girls in Science) and was one of the ‘Science Film Festival’ #LabMeCrazy! finalist videos.

CNIO & The City must be a stimulus for young generations and their families too. The inspirational video ‘Changing the World’, which was directed by Amparo Garrido, invited CNIO scientists and their kids to talk about future scientific careers and passions. “I have seen monkey cells!”, explained Diego Megías, Head of the Confocal Microscopy Core Unit, to his son. Science is not only about discovering, but also about getting fascinated and trying new things!

All these activities have transformed ‘CNIO & The City’ into an innovative, inclusive and STEAM education committed project with gender issues as a transversal theme. We have also found that our participants’ knowledge and perceptions about cancer, research and innovation are evolving in a positive way, which suggests that we are helping new generations grow up with a more critical, reflective and no-barriers view of the world around them. This is our mission, and we hope to accomplish it in the coming years!

“CNIO & The City wants to present science as an attractive profession. Despite its difficulties, Science is an option for the future!”

Photo & video by visual artist Amparo Garrido.
Development & Philanthropy
The Development and Philanthropy Office, established in September 2019, is key to achieving two of CNIO’s strategic goals: attracting new sources of funding to ensure financial sustainability and connecting CNIO to society.

The Office was established to enable the CNIO to proactively build a variety of funding sources to support the Centre’s strategic goals. Sources of funding will include the establishment of new collaborative partnerships with corporate organisations, foundations and high net worth individuals. It will also build upon our existing programme of charitable bequests and donations from society at large. Diversifying and increasing our funding sources is critical to enable the CNIO to continue to perform in the top tier of cancer research worldwide.

In late December, Jessica Rose, an expert in fundraising, joined the Development and Philanthropy Office as Director of the office, bringing many years of experience in sponsorship and philanthropy from a global perspective. Together with the CNIO Director and Mercedes Antona – a philanthropy professional who established the office in 2019 – Jessica will work on a global fundraising strategy to develop a comprehensive philanthropic programme for the CNIO.

The Office will manage the giving platform ‘CNIO Friends’, which started in 2014 and until September of this year was collectively administered by different areas of the CNIO. The initiative was a success from the start, growing each year to reach nearly €1.4 million in total donations thus far, which have been channelled into 12 research contracts opening new lines of research across the CNIO. In 2019 alone, CNIO Friends raised €315,000, which will be used to engage more scientific talent in 2020. In addition, the Office will manage the legacy programme which continues to grow and has received a cumulative total of €888,000 since 2015. In 2019, CNIO received charitable bequests of €284,000 with €844,000 pending to be executed.

Since the establishment of the Development and Philanthropy Office, a strategy to raise awareness has been designed to implement in the first half of 2020. Leading figures have been contacted in a variety of spheres to become CNIO ambassadors, sharing the Centre’s values and mission with larger sectors of the population. This work will support the ‘Outreach to Society’ and ‘Communications’ Offices in creating a bridge between the CNIO and society.

Although very new, the Philanthropy and Development Office has already made an impact at the CNIO and has successfully started to build strong alliances with companies and foundations to collaboratively create a positive impact on people and society. In a positive sign for the future of philanthropy for the CNIO, contacts were made with several foundations that are expected to bear fruit in 2020, with at least two €100,000 donations already in solicitation. We look forward to working together with industry and society to enable the CNIO to be the very best it can be.

“We want to develop ties of solidarity, making people part of our scientific achievements by walking side by side in this promising and necessary journey.”

In the picture: Mercedes Antona.
CNIO Offices

Dean's Office
CNIO Women in Science Office
One of the elements contributing to the CNIO’s international projection is the commitment of our established investigators to foster new generations of scientists. In fact, over 60% of the workforce at our institution are personnel in training, involving undergraduate students, postdoctoral and postdoctoral fellows, medical residents and a broad spectrum of visiting scientists supported by competitive grants through various funding agencies. Also very successful are our diverse exchange and visitor programmes. In this context, we are also most grateful to the Fundación Jesús Serra, for its continuous support to our researchers. Other multiple volunteers participated in the ’Semana de la Ciencia’ and in scientific tours the CNIO offers to interested parties.

The awardee was Ángel Rivera Calzada, for the crystal structure of a nanomachine involved in the pathogenesis of tuberculosis. The recipient was María J Alcamí, for her tireless efforts and dedication to the CNIO’s Women in Science Office (WISE). The award was presented by María Luisa Villafranca from the ‘Asociación ROSAE’, a non-profit organisation in support of breast cancer patients that belongs to our growing community of ‘CNIO Friends’.

A main highlight of the Lab Day was the announcement of the recipients of our ’Director’s List Awards’. These recognise outstanding contributions made by our personnel in 3 categories: (1) predoctoral fellows with publications of the highest scientific impact; (2) excellence in research by postdoctoral and staff investigators; and (3) altruistic volunteering to further the mission of the Centre related to training, scientific divulgation and outreach.

The award was presented by María Luisa Villafranca from the ‘Asociación ROSAE’, a non-profit organisation in support of breast cancer patients that belongs to our growing community of ‘CNIO Friends’.

We are grateful to the Agüera-Nieto family for a generous donation in the name of their mother Antonia Nieto, to support an award acknowledging the PhD student authoring the article with the highest impact in a scientific journal. This year, the ‘Antonia Nieto Award’ went to Almudena Chaves-Pérez, for impressive work published in Science on new discoveries in the field of secondary effects of radiation therapy. Additional awards in the PhD category went to Marla T Blasco (Cancer Cell), Catarina P Santos (Nature Communications), Miguel Ángel Muñoz (Nature Communications) and Laura Remacha (American Journal of Human Genetics).

The lab day proceeded with 6 additional Awards from the Dean’s Office to the Best Oral Presentations and to the Best Posters. The closing included yet an additional Award for T-Shirt Design, which was particularly moving. The most voted entry was the ‘Give us a Hand’ design that illustrates the concept that to make progress, scientists need the help of multiple hands - their supervisors, academic and clinical institutions, grantees, foundations, and patients and their families. This was a beautiful allegory of our commitment to and for the society.

In summary, we are as proud as ever of the achievements of our young investigators at the CNIO. We thank all those public and private contributors who help fuel their efforts, and we will strive in our commitment to be useful to other investigators and to society at large.

“At the CNIO we aim high: to carry out the most innovative basic and translational research, and to prepare our trainees ‘to think outside the box’ so that they can best fulfil their potential as influential leaders.”
The CNIO Women in Science Office (WISE) was established in 2012. Our main objectives are to give visibility to women, to raise awareness regarding the importance of gender equality, to help correct imbalances in the career ladder at the CNIO community especially in the leadership positions, to try to promote and support women in their professional careers, as well as to come up with ideas and policies to improve the life/work balance at the CNIO. The WISE Office is composed of CNIO volunteers from across all the areas present in the Centre, including the Director.

In 2019, the WISE Office was involved in making the CNIO a better place to work and to reconcile work and private life. Thanks to the joint efforts of the CNIO Direction and Management, the WISE Office, and the Works Council, we have approved a very innovative Equality Plan, a remote working pilot programme, as well as measures to ensure digital disconnection.

In addition, we continued organising the WISE seminar series, in which we invite several top female leaders from different areas. Some of the talks given during 2019 include:

- Consuelo Madrigal, jurist. Title: 'La mujer profesional: el largo camino a la igualdad'. 15/01/2019.
- Rosa Montero, journalist and writer. Title: 'Pala brada de mujer'. 12/02/2019.
- Luz Casal, singer and songwriter, was interviewed by the journalist Virginia Díaz. Title: 'Aproximaciones a una biografía'. 05/03/2019.
- Ruth Vera, President of the Spanish Society of Medical Oncology (SEOM). Title: 'Mujeres en la Oncología'. 09/04/2019.
- Maria Luisa de Contes, General Secretary and Board Member of the subsidiaries of the Renault Group in Spain. Title: 'Un proyecto para la igualdad de Género en las Empresas'. 07/05/2019.
- María Hervás, actress. Title: 'La alquimia de un cuerpo que actúa'. 20/06/2019.
- Susana Makorra, Minister of Foreign Affairs of the Argentine Government with President Macri and Chef de Cabinet of the Secretary-General Ban Ki-moon in the United Nations. Title: 'The leadership in times of change'. 18/10/2019.
- Mª Pilar Allué, General Deputy Director of Human Resources and Training of the National Police Corps. Title: '40 años de la incorporación de la mujer a la Policía Nacional'. 26/11/2019.
- Mª José San Román, chef and restaurateur. Title: 'Mujeres en Gastronomía'. 03/12/2019.

We also organised and hosted the 1st Gender Equality Event of the SOMMa Research Centres of Excellence (held October 29, 2019). This event aimed to share best practices in the SOMMa (the Alliance of the “Severo Ochoa” Centres and Maria de Maeztu Units) to promote a change of culture in a coordinated and institutional manner, and support female talent and gender equality in science and strategic decision-making. The event was organised in collaboration with the British Embassy and different SOMMa Directors, and with the participation of gender officers.

We continued to hold Master classes from the STEM Talent Girl programme (as part of an agreement signed with the ASTI Foundation in 2018). The goal of this project is to promote STEM careers among 13 to 14-year-old students. Eight Master classes given by top professional women from the STEM field were held in the CNIO Auditorium. The last 6 took place in 2019 and were given by Carmen García Matea, Professor in the TSC Department at the University of Vigo (January, 2019); Pilar López Álvarez, President of Microsoft Spain (February, 2019); María Martín-Torres, Director of CENIEH (March, 2019); Helena Herrero, President and CEO of HP for Spain and Portugal (April, 2019); Verónica Pascual Be, CEO of AITI TechGroup (May, 2019); and Yaiza Canosa, CEO and Founder of Goi (June, 2019).

We also participated in other educational initiatives, through the Indebescribo.org platform, to promote scientific careers among students from the Comunidad de Madrid. This initiative was done in collaboration with the ‘CNIO and The City’ project, which was funded by the Spanish Foundation for Science and Technology (FECYT) – Ministry of Science, Innovation and Universities – with the aim of creating closer links between society and the education system.
Facts & Figures

Scientific Management
- Competitive Funding
- Education and Training Programmes
- Scientific Events

Administration
- Board of Trustees
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Private Sponsors
The Scientific Management Department at the CNIO is committed to assisting with the facilitation of all those key areas that help our scientists to better focus their efforts on their research. The Department encompasses various Offices: Projects and Consortia, Education and Training Programmes, Scientific Events, Scientific Publishing, and Library and Archives. It also manages agreements with different institutions, mainly with Universities.

The mission of the Projects’ Office is to guide the CNIO scientists through all stages related to the application and management processes of externally-funded projects, whether they be financed through either public and/or private institutions, or stem from either national or international funding bodies. The Office coordinates the internal call alerts, gives advice about the ethical certification for projects involving animal experimentation or human samples together with the Biobank and the IACUC, supports scientists with the preparation of the project proposals, manages the ongoing projects, and contacts the funding agencies to resolve any issues or deal with questions.

The Training Office is the central point for training at the CNIO; it aids the recruitment process, serves as an advocate for all fellows, provides administrative support, and creates educational and learning opportunities. It is responsible for helping PhD students, Postdoctoral scientists and post-resident MDs by announcing call alerts and providing the relevant key information; helping foreign students with their paperwork at the foreign office; organising the summer training call; and, in general, in collaboration with the Personnel Department, managing student’s grants.

CNIO’s events are a reference in the scientific field. The quality of our lectures as well as the topics we deal with, make our Centre an extraordinary place to achieve interaction with scientists and exchange knowledge on scientific achievements. The Events Office organises CNIO meetings, such as the CNIO-“la Caixa” Foundation Frontiers Meetings, the Distinguished Seminars series, the external Scientific Advisory Board (SAB) meeting, CNIO Progress Reports, as well as Faculty retreats, among others. The Office also helps scientists by providing advice for the organisation of specific events, including science outreach events.

The Library administers the electronic subscriptions of over 300 scientific journals at the CNIO and manages journal article requests for journals that the CNIO is not subscribed to. The Library also provides information regarding reference management software and organises the CNIO guided visits.

The Scientific Publications Office is responsible for the preparation of institutional scientific publications, including the CNIO Annual Report, booklets of the Scientific Advisory Board meeting and those of other symposia, as well as scientific dissemination books and leaflets. The Office also provides support for the scientific editing of other publications of scientific divulgation to a non-specialised audience.

“All our efforts are dedicated towards building a strong and flexible framework to support our scientists and to help them achieve excellence.”
COMPETITIVE FUNDING

The CNIO attracts a substantial proportion of its funding from external sources. Most of this funding comes from national and international funding bodies and is used not only to finance the Centre’s outstanding R&D activities, but also strategic actions in innovation together with Industry partners. The funding is also used to support other relevant activities related to dissemination and scientific outreach; these activities are aimed at promoting public awareness. In 2019, researchers at the CNIO were involved in 136 projects that received extramural funding.

CNIO actively participates in a total of 53 collaborative projects: 18 were international collaborative projects (4 of which are coordinated by the CNIO) and 35 were collaborative projects at the national level (13 of them are coordinated by the CNIO). The international collaborative projects were funded by institutions such as the European Commission through the 7th Framework Programme and Horizon 2020, the Interreg SUDOE Programme, the US National Institutes of Health (NIH), the US Department of Defense (DoD), the International Human Frontier Science Program Organization, the Melanoma Research Alliance, the Paradifference Foundation, the Worldwide Cancer Research, and the Lustgarten Foundation - Stand-up 2 Cancer Initiative. At national level, collaborative projects received important public funding through grants from the Strategic Research Action, managed by the Institute of Health Carlos III (ISCIII) and the State Research Agency, Spanish Ministry of Science and Innovation (AEI/MCI) and the R&D Activities Programmes of the Community of Madrid; most of the projects were co-funded by European Structural and Investment Funds (European Regional Development Fund and European Social Fund). Private funders and charities also recognised the excellence of our scientific projects, among them, the Scientific Foundation of the Spanish Association Against Cancer (Fundación AECC), the Ramón Areces Foundation and “La Caixa” Banking Foundation.

In addition to these collaborative projects, researchers at the CNIO attracted funding for projects carried out by individual groups. In 2019, 15 of these projects received international funds while 68 of them received national funding (mainly from the AEI/MCI, the ISCIII and private foundations). The international individual projects are funded by the European Commission (5 ERC grants and 5 Marie Curie Actions), the Worldwide Cancer Research, the Cancer Research Institute, the Prostate Cancer Foundation, the US DoD the Prostate Cancer Foundation, the European Foundation for the Study of Diabetes and the Melanoma Research Alliance.

INTERNATIONAL GRANTS

EUROPEAN COMMISSION

7TH FRAMEWORK PROGRAMME (2007-2013)

PRINCIPAL INVESTIGATOR PROJECT TITLE

Malumbres, Marcos MicroKin: Deciphering the multifaceted pathways underlying MCPH pathogenesis in the mouse and human (financed by MEIC, Ref.: PCIN-2015-007)

HORIZON 2020 (2014-2020)

SOCIAL CHALLENGE 1: HEALTH, DEMOGRAPHIC CHANGE AND WELLBEING

PRINCIPAL INVESTIGATOR PROJECT TITLE

Benítez, Javier BRIDGES: Breast cancer risk after diagnostic gene sequencing (Ref.: 634835)

FET OPEN – NOVEL IDEAS FOR RADICALLY NEW TECHNOLOGIES

PRINCIPAL INVESTIGATOR PROJECT TITLE

Valente, Manuel NanoBRIGHT: BRInGing nano-photonics into the brain (Ref.: 628972)

INTEGRATING AND OPENING RESEARCH INFRASTRUCTURES OF EUROPEAN INTEREST

PRINCIPAL INVESTIGATOR PROJECT TITLE

Muñoz, Javier EPIC-XS: European Proteomics Infrastructure Consortium providing Access (Ref.: 823839)

MARIE SKŁODOWSKA-CURIE ACTIONS (MSCA)

PRINCIPAL INVESTIGATOR PROJECT TITLE

Peinado, Héctor ITN proEVLifeCycle: The life cycle of extracellular vesicles in prostate cancer: from biogenesis and homing, to functional relevance (Ref.: 860303)

Real, Francisco X. ITN TranSYS: Translational SYStemics: Personalised Medicine at the Interface of Translational Research and Systems Medicine (Ref.: 860895)

Soengar, Marla S. ITN IMMTRAIN: Training Network for the Immunotherapy of Cancer (Ref.: 840549)
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<td>Al-Shahrour, Fátima</td>
<td>ONCONET: European Network for Translational Research and Innovation in Oncology (Réseau Européen de Recherche transňtionnelle et d’innovation en oncologie (Ref.: SOE1/F0082))</td>
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<td>Muñoz, Inés</td>
<td>Targeting Mdm2-MdmX E3 ligases for treatment of drug-resistant lymphoma (Ref.: R01CA204852)</td>
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<td>Peinado, Héctor</td>
<td>Exosome-mediated transfer of c-MET to bone marrow progenitors promotes metastasis (Ref.: R01CA19646)</td>
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<td>Tress, Michael</td>
<td>GENCODE 2: Integrated human genome annotation: generation of a reference gene set (Ref.: U54HG007634)</td>
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<td>Olmos, David</td>
<td>Clinical qualification of DNA repair defects as prognostic and predictive biomarker in metastatic prostate cancer using genomics and tissue-based functional assays (Ref.: WIBX0H1-0770)</td>
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<td>Soengas, María S. (Coordinator)</td>
<td>Imaging and targeting dormant and pre-metastatic melanoma lesions in vivo (Ref.: 40181)</td>
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<td>Al-Shahrour, Fátima</td>
<td>SDHβ-related metastatic paraganglioma: search for the cure</td>
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<td>Valiente, Manuel (Coordinator)</td>
<td>ST80A9-dependent radiation resistance in brain metastasis (Ref.: 19-0377)</td>
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<td>Llorca, Óscar (Coordinator)</td>
<td>Photochemical trap and high-resolution imaging of transient chromatin complexes from living cells (Ref.: RGP0031/2017)</td>
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<td>Malats, Núria</td>
<td>Pancreatic Cancer Collective - Computational Approaches To Identifying High-Risk Pancreatic Cancer Populations: High Risk Cohorts Through Molecular and Genetic Data (Ref.: SU2C #6179)</td>
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<td>Soengas, María S. (Coordinator)</td>
<td>Heterogeneity in melanoma metastasis and resistance to immune checkpoint blockade</td>
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1 This Programme is cofunded by the European Regional Development Fund (ERDF).
### INTERNATIONAL GRANTS

#### INDIVIDUAL PROJECTS

### EUROPEAN COMMISSION

#### 7TH FRAMEWORK PROGRAMME (2007-2013)

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<tr>
<td>Fernández-Capetillo, Óscar</td>
<td>ERC Consolidator Grant RSHEALTH: Investigating the causes and consequences of replication stress in mammalian health (Ref.: 67840)</td>
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#### HORIZON 2020 (2014-2020)

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<td>Barbacid, Mariano</td>
<td>ERC Advanced Grant THERACAN: Novel therapeutic strategies to treat pancreatic and lung cancer (Ref.: 695366)</td>
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<td>Cortés, Felipo</td>
<td>ERC Consolidator Grant T0F0mics: Global dynamics of topoisomerase-induced DNA breaks (Ref.: 647359)</td>
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<tr>
<td>Efeyan, Akko</td>
<td>ERC Starting Grant NutrientSensingVivo: The Physiology of Nutrient Sensing by mTOR (Ref.: 638699)</td>
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<tr>
<td>Gaztán, Eva</td>
<td>ERC Consolidator Grant PLEID-RANK: Pleiotropic treatment of cancer: RANK inhibitors targeting cancer stem cells and immunity (Ref.: 692035)</td>
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### CANCEER RESEARCH INSTITUTE

<table>
<thead>
<tr>
<th>Principal Investigator</th>
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<tbody>
<tr>
<td>Valiente, Manuel</td>
<td>Role of exosomes and Endoglin in Neurofibromatosis Progression (Ref.: W81XWH-16-1-031)</td>
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</table>

### US CONGRESSIONALLY DIRECTED MEDICAL RESEARCH PROGRAMS (COMMP)/US DEPARTMENT OF DEFENSE

<table>
<thead>
<tr>
<th>Principal Investigator</th>
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<tbody>
<tr>
<td>Peinado, Héctor</td>
<td>Evaluation of obesity as a novel risk factor in metastasis (Ref.: 16-1244)</td>
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### COMPETITIVE FUNDING

#### WORLDWIDE CANCER RESEARCH (WCR, FORMERLY AICR)

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<tr>
<th>Principal Investigator</th>
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<tbody>
<tr>
<td>Blasco, Maria</td>
<td>Targeting telomeres in cancer (Ref.: 16-1077)</td>
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### EUROPEAN FOUNDATION FOR THE STUDY OF DIABETES/JUVENILE DIABETES RESEARCH FOUNDATION/LILLY

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<tr>
<th>Principal Investigator</th>
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<tbody>
<tr>
<td>Djouder, Nabil</td>
<td>Elucidating mechanisms of epigenetic changes in type 1 diabetes and treatment with DNA demethylating drugs</td>
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### INTERNATIONAL GRANTS

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<th>Principal Investigator</th>
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<tbody>
<tr>
<td>Soengas, María S. Frigo, Susana</td>
<td>METMEL: Long range-acting drivers of premetastatic niches in melanoma (Ref.: 753442)</td>
</tr>
<tr>
<td>Ehyan, Akko Fernández-Capetillo, Óscar Zauri, Melania</td>
<td>METLINK: Identification of links between cancer cell growth and metabolism genes (Ref.: 794177)</td>
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<tr>
<td>Valiente, Manuel</td>
<td>Blocking melanoma brain metastasis by targeting the environment (Ref.: 498103)</td>
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<tr>
<td>Castro, Elina</td>
<td>Prospective study of lethal prostate cancer clinical and genomic evolution in DNA repair deficient tumours</td>
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NATIONAL GRANTS | COLLABORATIVE PROJECTS

INSTITUTE OF HEALTH CARLOS III | INSTITUTO DE SALUD CARLOS III

3. This Programme is cofunded by the European Regional Development Fund (ERDF)

2. This Programme is cofunded by the European Regional Development Fund (ERDF)

SALUD (AES) | ACCIÓN ESTRATÉGICA EN SALUD

SALUD CARLOS III (ISCIII) | CARLOS III / INSTITUTE OF HEALTH

FACTS & FIGURES | SCIENTIFIC MANAGEMENT | COMPETITIVE FUNDING

RESEARCH PROJECTS IN HEALTH / PROYECTOS DE INVESTIGACIÓN EN SALUD

PRINCIPAL INVESTIGATOR | PROJECT TITLE
--- | ---
Blasco, Maria (Coordinator) | Translational Studies for the Development of Telomerase Gene Therapies as Treatments for Myocardial Infarction and Pulmonary Fibrosis (Ref.: DT19/00052)

Malats, Núria (Coordinator) | Study of the environmental and genetic risk profiles and clinical behaviour of the basal-like phenotype of pancreatic cancer. Comparison of predictive biomarkers (Ref.: PI16/00946) and validation of disease biomarkers (Ref.: PI18/01242)

González-Neira, Anna (Coordinator) | Role of the mitochondrial genes in cardiotoxicity: identification of predictive biomarkers (Ref.: PI18/02146)

Muñoz, Javier (Coordinator) | Platform of proteomics, genotyping and cell lines. Platform of resources biomolecular, PRB (Group Ref.: PI17/0019/0001)

Benitez, Javier | Platform of proteinomics, genotyping and cell lines. Platform of resources biomolecular, PRB (Group Ref.: PI17/0019/0004)

Artiga, Mª Jesús | OPTIMARK project: Optimization of tissue samples for the development and validation of disease biomarkers (Ref.: PI18/00946)

Al-Shahrour, Fátima | PLATFORM OF BIOINFORMATICS. INSTITUTO NACIONAL DE BIOINFORMATICA (Group Ref.: PI17/0019/0001)

Muñoz, Javier (Coordinator) | Building and validation of risk prediction models for pancreatecancer. The application of a multi-omics approach (Ref.: PI5/001537)

Djouder, Nabil (Coordinator) | THERATLAS Project: integration of early and adaptive genetic events to establish therapeutic subgroups in Castration-resistance to immunotherapy (Ref.: PI18/01057)

Real, Francisco X. | IMMOPDL2: Preclinical development of antibodies against the immunomodulator PD-L2 for the treatment of diseases caused by cellular damage. Validation of the strategy in residual tumors and fibrosis (Ref.: RTC-2017-6233-1)

Malumbres Marcos (Coordinator); Barbacid, Mariano | Programa TomoXliver-CM: Estudio de la disfunción del hepatocito desde un abordaje multidisciplinar (Ref.: B2017/BMD-3713)

Roncador, Giovanna | Programa RENIM-CM: Red Madrileña de Nanomedicina (Ref.: B2017/BMD-3848)

Djouder, Nabil NRCANCER: Desarrollo de nueva terapia anti-tumoral basada en el camostamida-ribosida (Ref.: RTC-2016-5431-1)

Muñoz, Inés | ATTACK: Cancer immunotherapy with bispecific antibodies that engage T-lymphocytes (Ref.: RTC-2017-5944-1)

Barbacid, Mariano | New approaches for treatment of lung cancer. (Ref.: RTC-2017-6576-1)

5. These Programmes are cofunded by the European Regional Development Fund (ERDF) and European Social Fund (ESF)

REDES DE EXCELENCIA | EXCELLENCE NETWORKS / REDES DE EXCELENCIA

REAL ACTIVITIES PROGRAMME IN BIOMEDICINE:

PRINCIPAL INVESTIGATOR | PROJECT TITLE
--- | ---
Al-Shahrour, Fátima; Robledo, Mercedes | Programa TIRONET2-CM: Fisiopatología Tiroidea. Mecanismos implicados en cáncer, autoinmunidad y acción de las inmunoterapia del cáncer (Ref.: B2017/BMD-3780)

Malumbres Marcos (Coordinator); Barbacid, Mariano | Programa iLUNG-CM: Terapias personalizadas y nanotecnología en cáncer de pulmón (Ref.: B2017/BMD3817)

Djouder, Nabil | Programa NANOSENSEMEDIC-1 CM: Nanosistemas destinados como agentes y vectores terapéuticos en distintas aplicaciones biomédicas (II) (Ref.: B2017/BMD-3703)

Muro, Francisco | Programa MINIMEDCM: Red Madridina de Nanomedicina en Imagen Molecular (Ref.: B2017/BMD-3867)

Quintela, Miguel Ángel | Programa IMMUNOTHERAC-M: Inmunidad tumoral e inmunoterapia del cáncer (Ref.: B2017/BMD-3733)

Robledo, Mercedes | Programa TIMONET2-CM: Tisopatología Torácica. Mecanismos implicados en cáncer, inmunológico y vinculación de las hormonas tiroideas (Ref.: B2017/BMD-3724)

Soengas, María S. | Programa NANODENDMEDII-CM: Nanosistemas dendríticos (II) (Ref.: B2017/BMD-3724)

Fernández-Capetillo, Óscar (Coordinator) | UBLred: Ubiquitin-like proteins in signaling, proliferation and cancer (Ref.: SAF2017-90900-REDT)

Efeyan, Aljos (Coordinator) | METABOCANCER: Crosstalk between systemic and cellular metabolism in cancer (Ref.: SAF2016-80927-REDT)

Barbacid, Mariano | New approaches for treatment of lung cancer. (Ref.: RTC-2017-6576-1)

Djouder, Nabil | NRCANCER: Desarrollo de nueva terapia anti-tumoral basada en el camostamida-ribosida (Ref.: RTC-2016-5431-1)

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Real, Francisco X. | IMMOPDL2: Preclinical development of antibodies against the immunomodulator PD-L2 for the treatment of diseases caused by cellular damage. Validation of the strategy in residual tumors and fibrosis (Ref.: RTC-2017-6233-1)
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<td>Llorca, Óscar</td>
<td>Programa TecBioCM: Tecnología Aplicada al Estudio de Nanomáquinas Biológicas (Ref: PY2018/NMT4443)</td>
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<tr>
<td>Llorca, Óscar</td>
<td>Programa NanBioCancer-CM: Nanobiotecnología Estructural y Molecular de Procesos de Reparación de ADN relacionados con Cáncer (Ref: Y2018/SBO4347)</td>
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### SCIENTIFIC FOUNDATION OF THE SPANISH ASSOCIATION AGAINST CANCER / FUNDACIÓN CIENTÍFICA DE LA ASOCIACIÓN ESPAÑOLA CONTRA EL CÁNCER (AECC)

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<tr>
<td>Dean’s Office for Academic Affairs</td>
<td>European Researchers’ Night 2018-2019, organized by Madri+d Foundation and founded by EU-H2020 Programme.</td>
</tr>
<tr>
<td>Soengas, María S.</td>
<td>Exploiting post-transcriptional regulation to uncover novel vulnerabilities of metastatic cells (Ref: HR17-00232)</td>
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<tbody>
<tr>
<td>Peinado, Héctor</td>
<td>Defining The Role of Exosome-Secreted Microparticles in Pancreatic Cancer (Ref: HR18-00256)</td>
</tr>
<tr>
<td>Soengas, María S.</td>
<td>Distinct routes of metastatic dissemination in different melanoma subtypes. Implications in the validation of new tumor biomarkers and therapeutic targets (Ref: GCB15152978SOEN)</td>
</tr>
<tr>
<td>Valiente, Manuel</td>
<td>Study of the molecular mechanisms involved in primary (glioblastoma) and secondary (metastasis) brain tumors to identify novel therapeutic targets and anti-cancer agents, biomarkers to select treatments and novel non-invasive methods for molecular diagnosis (Ref: GCTR18005530EA)</td>
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<tbody>
<tr>
<td>Berríno, Javier</td>
<td>Massive sequencing contributes to decipher the genetic bases of families with rare tumors (Ref: P18/00440)</td>
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<tr>
<td>Casón, Alberto</td>
<td>Molecular, OMIC and functional characterisation of mutations in the gene DLST in patients with phaeochromocytoma/paraganglioma (Ref: P18/00454)</td>
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<tr>
<td>Ortega, Ana</td>
<td>Targeting deregulated nutrient-sensing pathway in follicular lymphoma (Ref: P18/00816)</td>
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<tr>
<td>Quintela, Miguel Ángel</td>
<td>Tumor-tolerant immune reprogramming secondary to hypoxia-inducing antiangiogenics in breast cancer: physiopathogenic mechanisms and therapeutic utility (Ref: P18/00354)</td>
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<tr>
<td>Robledo, Mercedes</td>
<td>Progression related mechanisms in endocrine and neuroendocrine tumours (Ref: P17/07096)</td>
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<tr>
<td>Rodríguez, Sandra</td>
<td>Study of the role of epigenetic modifications in the development of Ewing sarcoma: High-throughput screening of epigenetic genes using CRISPR libraries in human (II; 22) + t cells (Ref: P18/02303)</td>
</tr>
<tr>
<td>Urioste, Miguel</td>
<td>PTEN-hamartoma tumour syndrome research: Phenotypic spectrum, associated cancers, molecular basis and search of new gene (Ref: P14/00459)</td>
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#### RAD EXCELLENCE PROJECTS/PROYECTOS DE I+D EXCELENCIA

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<tbody>
<tr>
<td>Fernández-Leiro, Rafael</td>
<td>Macromolecular complexes in the mitochondrial DNA replication and repair pathways: structural and molecular mechanisms by cryo-EM (Ref: BFU2017-87316-P)</td>
</tr>
<tr>
<td>Llorca, Óscar</td>
<td>Structural and molecular mechanisms regulating the PI3K family of kinases, including DNA-PKcs, SNK and mTOR (Ref: SAF2017-82652-P)</td>
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<tbody>
<tr>
<td>Al-Shahrour, Fatima</td>
<td>CANTHERHET: Computational targeting of cancer heterogeneity: in silico drug prescription for tumor clonal populations (Ref.: RTI2018-097706-B-100)</td>
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<tr>
<td>Babak, Song</td>
<td>RAFTING: a RAF, a key mediator of K-RAS driven cancers: Therapeutic approaches (Ref.: RTI2018-094644-B-100)</td>
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<tr>
<td>Blasco, Maria</td>
<td>TELOHEALTH: Telomeres and Disease (Ref.: SAF2017-82623-R)</td>
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<tr>
<td>Djouder, Nabil</td>
<td>URIPAT: URI loss in intestinal pathologies (Ref.: SAF2016-76598-R)</td>
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<td>Djouder, Nabil</td>
<td>HEPATOCAR: Studying the Role and Function of MCRS1 in Hepatocellular Carcinoma Development (Ref.: RTI2018-094854-B-100)</td>
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<tr>
<td>Eyhan, Alejo</td>
<td>NUTRITENTOR: Physiology of nutrient sensing and signaling by the mTOR complex I (Ref.: SAF2015-67538-R)</td>
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<td>Fernández-Capetillo, Oscar</td>
<td>RESCATE: Mechanisms of resistance to anticancer therapies (Ref.: RTI2018-102204-B-100)</td>
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<tr>
<td>Llorca, Oscar</td>
<td>RUNKLI-RubRI2-ATPases in DNA/RNA surveillance and human diseases: molecular and structural mechanisms (Ref.: SAF2014-52301-R)</td>
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<td>Losada, Ana</td>
<td>COHESIN2: Molecular mechanisms of variant cohesin function (Ref.: BFU2016-79641-R)</td>
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<td>Malumbres, Marcos</td>
<td>Cyclexit: Physiological and therapeutic relevance of mitotic kinases and phosphatases (Ref.: SAF2015-69920-R)</td>
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<td>Malumbres, Marcos</td>
<td>NewC DixTarget: Validation of a New Subfamily of Cyclin-dependent Kinases as Cancer Targets (Ref.: RTI2018-095582-B-100)</td>
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<tr>
<td>Méndez, Juan</td>
<td>REP/ICON2: Control of eukaryotic DNA replication (Ref.: BFU2016-80402-R)</td>
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<tr>
<td>Muñoz, Javier</td>
<td>EPI-PASS: Epigenetic modifiers in pluripotency: a proteomic analysis of non-histone protein methylation (Ref.: SAF2016-74962-R)</td>
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<td>Ortega, Sagario</td>
<td>ESSENCE: Extrinsic control of the skin stem cell niche in homeostasis and cancer (Ref.: BFU2015-71736-R)</td>
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<tr>
<td>Peinado, Héctor</td>
<td>EXO-NGFR: Analyzing the relevance exosome-derived NGFR during pre-metastatic niche formation (Ref.: SAF2017-82924-R)</td>
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<td>Plaza, Ivan</td>
<td>ESFORET: Structure-function studies of oncogenic RET kinase fusions in human cancers: from mechanism of action to targeted therapy (Ref.: BFU2017-86710-R)</td>
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<td>Real, Francisco X.</td>
<td>TRANS-PDAC: Transcriptional control of pancreatic cancer development (Ref.: SAF2015-70553-R)</td>
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<tr>
<td>Real, Francisco X.</td>
<td>TF-PDAC: Transcription factors in pancreatic cancer: from biology to therapy (Ref.: RTI2018-100271-B-100)</td>
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<td>Rodríguez, Cristina</td>
<td>PREDICT: Identification of genetic markers and physiopathologic factors predictive of the peripheral neuropathy of paclitaxel and of other oncologic drugs: massive sequencing of candidate genes (Ref.: SAF2016-64650-R)</td>
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<td>Rodríguez, Cristina</td>
<td>RCC MARKER: Improving the clinical management of advanced renal cell carcinoma through genomic technologies (Ref.: RTI2018-095039-B-100)</td>
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<tr>
<td>Squarrito, Massimo</td>
<td>GLO-TRK: TRKing down oncogenic rearrangements in gliomas (Ref.: RTI2018-102035-B-100)</td>
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<tr>
<td>Sosangas, María S.</td>
<td>MEL-STOP: Whole-body imaging of melanoma metastasis as a platform for gene discovery and pharmacological testing (Ref.: SAF2017-89533-R)</td>
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<tr>
<td>Valente, Manuel</td>
<td>Stat3 REACTIVE: Biology of Stat3 reactive astrocytes in brain metastasis (Ref.: SAF2017-89643-R)</td>
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8. This Programme is cofunded by the European Regional Development Fund (ERDF)

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**FACTS & FIGURES SCIENTIFIC MANAGEMENT**

**COMPETITIVE FUNDING**

**GRANTS FOR EMERGING GROUPS:**

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<td>Efeyan, Alejo</td>
<td>Nutrient signaling in the pathogenesis and treatment of B cell Lymphoma (Ref.: LABAE16001EFEY)</td>
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<td>Peinado, Héctor</td>
<td>Defining the mutational landscape in plasma and lymphatic fluid-derived exosomes in melanoma patients (Ref.: LABAE19027PEIN)</td>
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<tr>
<td>Squatrito, Massimo</td>
<td>Novel therapeutic approaches for therapy-resistant malignant brain tumors (Ref.: LABAE16055SQUA)</td>
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<tr>
<td>Valiente, Manuel</td>
<td>New treatments for brain metastasis based on the study of their biology (Ref.: LABAE19002VALU)</td>
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<td>Olmos, David</td>
<td>Genomic epidemiology and clinical implications of DNA-repair genes and other oncogenic drivers in metastatic hormone-sensitive prostate cancer (Ref.: PROYE19054OLMO)</td>
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<td>&quot;IDEAS SEMILLA&quot; GRANTS (SEED FUNDING):</td>
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<tr>
<td>Squatrito, Massimo</td>
<td>Identification of biomarkers of tumor treating fields (TTFields) in glioblastoma (Ref.: IDEAS185SQUA)</td>
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<td>Guerra, Carmen</td>
<td>Desarrollo de estrategias terapéuticas dirigidas contra el estroma del cáncer de páncreas</td>
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<td>Malats, Núria</td>
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<td>Blasco, Maria</td>
<td>Validation of the TRF1 telomere protective protein as a novel anticancer target in pediatric glioma and ependymoma</td>
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**health research programme**

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<td>Blasco, Maria</td>
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<td>Blasco, Maria</td>
<td>TRF1 inhibitors as a first-in-class therapy for glioblastoma and lung cancer (Ref: C18-00017)</td>
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<td>Rodrigo, Sandra</td>
<td>Gene therapy for human cancers driven by fusion genes (Ref: C18-00017)</td>
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<td>Salazar, María</td>
<td>mRNA-based strategy to expand cell therapy potential for treating diabetes (Ref: C19-00001)</td>
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<td>Blasco, Maria</td>
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**INOCENTE**

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**ASOCIACIÓN DE CANCER DE PANCREAS/ASOCIACIÓN ESPAÑOLA DE PANCREATOLOGÍA**

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<tr>
<td>Peinado, Héctor</td>
<td>Liquid biopsy by nanoplasmonic detection of exosomes: predicting response to (immuno- and radio-)therapy</td>
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<td>Valiente, Manuel</td>
<td>Predictive biomarkers for brain metastasis in small cell lung cancer</td>
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<td>Peinado, Héctor</td>
<td>Developing a targeted therapy to promote melanoma immune-recognition and suppress metastasis</td>
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<tr>
<td>Valiente, Manuel</td>
<td>Reactive astrocytes as a therapeutic target in brain metastasis</td>
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<tr>
<td>Peinado, Héctor</td>
<td>Tumour exosome integrins determine organotropic metastasis</td>
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<tr>
<td>Djouder, Nabil; Teijeiro, Ana I.</td>
<td>Metabolic Inflammation-Associated IL-17A Causes Non-alcoholic Steatohepatitis and Hepatocellular Carcinoma</td>
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<tr>
<td>Ortega, Ana</td>
<td>Estudio de la implicación de ruta de señalización de mTORC1 en la patología del Linfoma Folicular y autoinmunidad</td>
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<tr>
<td>Molina, Esther</td>
<td>Radiomics en cáncer de páncreas para una medicina estratificada y de precisión: un estudio piloto.</td>
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<tr>
<td>Squarrito, Massimo</td>
<td>Leonardo Grant: Precision glioma mouse models by somatic genome editing with the RCAS-CRISPR-Cas9 system (Ref.: IN17_BBM_TRA_0366)</td>
</tr>
</tbody>
</table>
EDUCATION AND TRAINING PROGRAMMES

One of the principal goals of the CNIO is to increase its training capacity in order to give students and professionals the opportunity to advance their careers in the healthcare sector. During 2019, the CNIO signed several new agreements with Spanish Universities and other institutions, namely with the Universidad de Alcalá de Henares, Universidad San Pablo CEU, Universidad de Barcelona, Universidad Oporta de Cataluña, Universidad Castilla La Mancha, Universidad de Oviedo, IES Félix Rodríguez de la Fuent, IES Villaverde, IES Príncipe Felipe, Rocas Educación SL, Centro Profesional Europeo de Madrid, Escuela Técnica de Enseñanzas Especializadas, Colegio Virgen de Mirasierra and Ministerio de Ciencia, Innovación y Universidades.

TRAINING OF BSC/MSC STUDENTS

The CNIO is committed to training junior scientists at the onset of their careers. To this end, the Centre has established a Programme that offers BSc and MSc students the opportunity to obtain hands-on practical laboratory experience by working on ongoing research projects in one of the CNIO groups. The CNIO offers 2 types of short-term laboratory training:

→ An annual Summer Training Programme for undergraduate students, from any country, who are in their last years of study in the biomedical field. The Programme encompasses 8 weeks of full-time laboratory training (292.5 hours). During this time, the students actively participate in research projects in one of the CNIO groups. During 2019, 6 students from 3 different countries participated in this programme.

→ Additionally, students can apply for laboratory training throughout the academic year by directly contacting the Heads of CNIO individual Research Groups or Units. This year, 150 students participated in these programmes, of whom 7 ended up joining the CNIO as pre-doctoral students.

TRAINING OF PHD STUDENTS

The training of PhD students in cutting-edge cancer research is of key importance to the CNIO. The Centre offers many opportunities for bright and dynamic university graduates, of all nationalities, to pursue an ambitious PhD project. Attesting to this, 14 students obtained their PhD degrees in 2019 and 21 others joined the CNIO in the same year. Over 15% of the 100 students working at the CNIO in 2019 were graduates from foreign universities, thus contributing to the internationalisation of the Centre.

Since 2008, the Fundación “la Caixa” offers international fellowships to PhD students to enable them to carry out their thesis projects in biomedical research in Spanish centres of excellence, such as the CNIO. In 2018, a new call for the doctoral fellowship programme of the “la Caixa” Foundation, named INPhINIT, was launched to recruit talented Early-Stage Researchers of any nationality, who wish to pursue doctoral studies in Spanish or Portuguese territory, offering them an attractive and competitive environment for conducting research of excellence. The CNIO was chosen as a host institution. During 2019, 2 pre-doctoral students received this fellowship to join the CNIO.

<table>
<thead>
<tr>
<th>TRAINING PROGRAMMES</th>
<th>PARTICIPANTS IN EDUCATION AND TRAINING PROGRAMMES</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>2015</td>
</tr>
<tr>
<td>Training of PhD students</td>
<td>105</td>
</tr>
<tr>
<td>Post-doctoral training</td>
<td>48</td>
</tr>
<tr>
<td>Training for MDs</td>
<td>25</td>
</tr>
<tr>
<td>Laboratory training for MSc/BSc students</td>
<td>80</td>
</tr>
<tr>
<td>Laboratory training for technicians</td>
<td>27</td>
</tr>
</tbody>
</table>
The distribution of students across the CNIO’s Research Programmes in 2019 was as follows: 67% of students worked in the Molecular Oncology Programme, 13% in the Structural Biology Programme, 11% in the Human Cancer Genetics Programme, 1% in the Experimental Therapeutics Programme, 3% in the Biotechnology Programme, and 9% in the Clinical Research Programme.

Thanks to an individual donation received through the ‘CNIO Friends’ platform, CNIO created the Predoctoral Carmen Gloria Bonnet Moreno Contract Programme that offered 1 position to carry out a thesis at the CNIO. This call is expected to have only this one single edition.

**POST-DOCTORAL TRAINING**

One of the CNIO’s prime objectives is to attract young researchers who have recently obtained their PhD or MD degrees, and to offer them highly attractive research projects at the forefront of cancer research.

In 2019, 49 postdoctoral fellows worked at the CNIO. Notably, about one third of these fellows were from outside of Spain, many coming from very prestigious international institutions.

In 2019, the Fundación Banco Santander renewed the agreement with the CNIO to continue the highly competitive fellowship programme aimed at supporting outstanding young scientists who have been trained in the UK or in the USA, and who wish to start or continue their postdoctoral training at the CNIO. This call will be closed in 2020.

Thanks to the donations received through the ‘CNIO Friends’ platform launched in 2016, the fourth call of the ‘CNIO Friends’ Postdoctoral Contract Programme, launched in 2019, resulted in the recruitment of 4 scientists for a 2-year period each. Also, thanks to a single donation to ‘CNIO Friends’, CNIO launched the Postdoctoral ‘Eva Plaza/CNIO Friends’ Programme that offered a postdoctoral researcher the opportunity to carry out a 2-year postdoctoral stay at the CNIO, to accomplish a research project on triple negative breast cancer. This call is expected to have only this single edition. Additionally, thanks to a ‘Juganteriori-CNIO Friends’ Postdoctoral Contract, in 2019, 1 scientist was able to start a project related to paediatric oncology.

**FACTS & FIGURES**

<table>
<thead>
<tr>
<th>SPANISH ORGANISATIONS</th>
<th>NO.</th>
</tr>
</thead>
<tbody>
<tr>
<td>State Research Agency / Agencia Estatal de Investigación (AEI), Ministry of Science, Innovation and Universities / Ministerio de Ciencia, Innovación and Universidades (I+D Projects)</td>
<td>48</td>
</tr>
<tr>
<td>State Research Agency / Agencia Estatal de Investigación (AEI), Ministry of Science, Innovation and Universities / Ministerio de Ciencia, Innovación y Universidades (Predoctoral fellowships)</td>
<td>6</td>
</tr>
<tr>
<td>Spanish Association Against Cancer (AEEC) / Fundación Científica de la AECC (I+D Projects)</td>
<td>4</td>
</tr>
<tr>
<td>Institute of Health Carlos III / Instituto de Salud Carlos III (ISCIII)</td>
<td>2</td>
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<tr>
<td>Cris Foundation / Fundación Cris</td>
<td>2</td>
</tr>
<tr>
<td>Community of Madrid / Comunidad de Madrid</td>
<td>3</td>
</tr>
<tr>
<td>CNIO</td>
<td>4</td>
</tr>
<tr>
<td>Banco Santander Foundation / Fundación Banco Santander</td>
<td>2</td>
</tr>
<tr>
<td>“la Caixa” Banking Foundation/ Fundación Bancaria “la Caixa” (I+D Projects)</td>
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<tr>
<td>“la Caixa” Banking Foundation/ Fundación Bancaria “la Caixa” (Predoctoral fellowships)</td>
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**INTERNATIONAL ORGANISATIONS**

<table>
<thead>
<tr>
<th>NO.</th>
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</thead>
<tbody>
<tr>
<td>17</td>
</tr>
</tbody>
</table>

| Fundación Lilly | 1 |
| European Society for Clinical Nutrition and Metabolism (ESPEN) | 1 |
| European Society for Clinical Nutrition and Metabolism (ESPN) | 1 |
| European Commission Framework Programme / H2020 | 1 |
| European Research Council | 2 |
| GENCODE | 2 |
| Human Frontier Science Program Foundation | 1 |
| Lilly Foundation / Fundación Lilly | 1 |
| Marie Sklodowska-Curie actions of the European Commission | 3 |
| Portuguese Foundation for Science and Technology (FCT) | 1 |

| TOTAL | 100 |

<table>
<thead>
<tr>
<th>SPANISH SOURCES OF POST-DOCTORAL RESEARCHERS</th>
<th>NO.</th>
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<tbody>
<tr>
<td>State Research Agency / Agencia Estatal de Investigación (AEI), Ministry of Science, Innovation and Universities / Ministerio de Ciencia, Innovación y Universidades (Postdoctoral fellowships)</td>
<td>6</td>
</tr>
<tr>
<td>State Research Agency / Agencia Estatal de Investigación (AEI), Ministry of Science, Innovation and Universities / Ministerio de Ciencia, Innovación y Universidades (Postdoctoral fellowships)</td>
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</tr>
<tr>
<td>Spanish Association Against Cancer (AEEC) / Fundación Científica de la AECC (Fellowships)</td>
<td>5</td>
</tr>
<tr>
<td>Community of Madrid / Comunidad de Madrid</td>
<td>4</td>
</tr>
<tr>
<td>CNIO</td>
<td>17</td>
</tr>
<tr>
<td>Banco Santander Foundation / Fundación Banco Santander</td>
<td>2</td>
</tr>
<tr>
<td>“la Caixa” Banking Foundation/ Fundación Bancaria “la Caixa” (Postdoctoral fellowships)</td>
<td>1</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>INTERNATIONAL ORGANISATIONS</th>
<th>NO.</th>
</tr>
</thead>
<tbody>
<tr>
<td>10</td>
<td></td>
</tr>
</tbody>
</table>

| Daiichi Sankyo | 1 |
| European Commission Framework Programme / H2020 | 1 |
| European Research Council | 1 |
| European Society for Medical Oncology / Sociedad Europea de Oncología Médica | 1 |
| Marie Sklodowska-Curie actions of the European Commission | 1 |
| Worldwide Cancer Research UK | 2 |

| TOTAL | 49 |
POSTGRADUATE PROGRAMMES

In addition, the CNIO – in collaboration with academic institutions across Spain – provides access to a variety of postgraduate programmes that cover the areas of Cellular & Molecular Biology, Molecular Biomedicine, Biotechnology, Biocomputing, Clinical & Applied Cancer Research, and Therapeutic Targets.

Official Postgraduate Programmes in Molecular Biosciences

The majority of the international postgraduate trainings offered at the CNIO are developed in collaboration with the Faculty of Medicine and Faculty of Sciences at the Autonomous University of Madrid (UAM). These trainings fall under 4 official Postgraduate Programmes, namely, the Doctorate in Molecular Biosciences, Master's in Biomolecules & Cell Dynamics, Master's in Molecular Biomedicine, and Master's in Biotechnology. CNIO also collaborates with the UAM as a partner institution of UAM's Doctoral School (EDUAM) and is a member of the Management Committee.

Master's Degree in Biocomputing Applied to Personalised Medicine and Health

The Master's in Bioinformática Aplicada a la Medicina Personalizada y la Salud is organised together with the National School of Health of the National Institute of Health Carlos III (Escuela Nacional de Sanidad del Instituto de Salud Carlos III, ENS-ISCHII).

Official Master's Degree in Clinical and Applied Cancer Research

The CNIO and the CEU-San Pablo University in Madrid (USP-CEU) co-organise a Postgraduate Training Programme in Clinical and Applied Cancer Research: the Máster Universitario en Investigación Clínica y Aplicada en Oncología.

Official Master's Degree in Therapeutic Targets of Cell Signalling: Research and Development

The CNIO collaborates with the Biochemistry and Molecular Biology Department at the University of Alcalá de Henares (UAH) for the Máster Oficial en Dianas Terapéuticas en Señalización Celular: Investigación y Desarrollo.

LABORATORY TRAINING FOR TECHNICIANS

This training programme has been developed for students in Anatomical Pathology, Clinical Diagnostic Laboratory, and Archiving/Recording. It is organised through agreements with 19 institutions that provide secondary education for laboratory technicians in Spain. It provides students with hands-on knowledge in cellular and molecular biology techniques. The programme consists of 14 weeks (370-400 hours) of laboratory training for students. Of the 18 students who participated in this programme in 2019, 2 were hired by the CNIO.

TRAINING FOR MDS

In line with CNIO's commitment to bridge the 'bench to bedside' gap, the Centre offers 3 training opportunity programmes to MDS and other health care professionals. Training usually consists of a 3-month period during residency. In 2019, 20 medical residents from 10 different hospitals enjoyed the benefits of rotations within the different Groups and Units at the CNIO.

ADVANCED TRAINING OF SCIENTISTS THROUGH EXTRAMURAL PROGRAMMES

During 2019, the Ramón y Cajal Programme supported 7 scientists. This special initiative, established in 2001 by the former Spanish Ministry of Science and Technology (currently the State Research Agency of the Spanish Ministry of Science, Innovation and Universities) aims to encourage Spanish or foreign scientists working abroad to return to or relocate to Spain. Successful candidates are selected on the basis of their potential capacity to lead independent projects and groups, or to contribute successfully to the ongoing research in the existing groups. Seven other scientists were funded by similar programmes, including the Juan de la Cierva programme (Spanish Ministry of Science, Innovation and Universities, 3 contracts), Miguel Servet programme (1 contract) of the Institute of Health Carlos III, and the Spanish Association Against Cancer (ABCC, 3 contracts).

VISITING RESEARCHER PROGRAMME

The Jesús Serra Foundation, part of the Catalana Occidente Group, aims to help eminent international specialists work together with CNIO researchers for a few months in order for them to expand their knowledge in areas of common interest. During 2019, Scott Lowe, from the Memorial Sloan Kettering Cancer Centre in New York (USA) and Sonia Lain, from the Karolinska Institute in Stockholm (Sweden), were beneficiaries of the Jesús Serra Foundation’s Visiting Researcher Programme.

‘SCIENCE BY WOMEN’ PROGRAMME

Thanks to the ‘Science by Women’ Programme, launched by the Spanish Fundación Mujeres por África, the CNIO selected Mai Tolba from Ain Shams University (Egypt), to carry out a 6-month stay at the CNIO during 2020.

During 2019, thanks to this Programme, we had the pleasure of hosting Hayet Rafa from the University of Science and Technology Houari Boumediene, Algiers, for a 6-month stay as a visiting scientist in the CNIO’s Melanoma Group.
**SCIENTIFIC EVENTS**

### CNIO-“LA CAIXA” BANKING FOUNDATION FRONTIERS MEETINGS

The CNIO-“La Caixa” Foundation Frontiers Meetings (CFMs) are the main international conferences co-organised by the CNIO and “La Caixa” Foundation. They focus on specific, cutting-edge aspects of cancer research, thus providing a unique platform for an intensive and dynamic exchange and debate on scientific ideas. The invited speakers – 20 internationally renowned leaders in oncology – present their latest findings during 2 and a half days. The provided learning environment encourages delegates to exchange experiences, ideas and practices and their companies; network and create connections with researchers with similar interests; listen to and meet the keynote speakers; enjoy the extra-curricular conference programme; and hear about the latest developments in the research field. Up to 100 additional participants are selected – via a widely publicised call for applications – based on their potential to make relevant contributions to the conference by presenting hot topics as posters or short talks. In 2019 we arranged 2 CFMs: ‘Structural and Molecular Biology of the DNA Damage Response’, during which the potential use of novel approaches was analysed for studying DNA damage and naturally-occurring DNA-repair failures – a cross-cutting theme in cancer research – and ‘Heterogeneity and Evolution in Cancer’. These brought together more than 130 cancer experts and computational, physical and mathematical biologists from the world’s most active groups in the area.

### STRUCTURAL AND MOLECULAR BIOLOGY OF THE DNA DAMAGE RESPONSE

20-22 MAY 2019

**ORGANISERS**
- Óscar Llorca, Spanish National Cancer Research Centre (CNIO), Madrid, Spain
- Rafael Fernández Leiro, Spanish National Cancer Research Centre (CNIO), Madrid, Spain
- Laurence H. Pearl, University of Sussex, Brighton, UK
- Tiitia Siimna, Netherlands Cancer Institute, Amsterdam, Netherlands

**SESSIONS**
- Chromatin and chromatin complexes
- DNA Replication and replication stress
- DNA transcription
- DNA damage and repair

**SPEAKERS**
- James Berger, Johns Hopkins School of Medicine, Baltimore, US
- Maria Blasco, Spanish National Cancer Research Centre, Madrid, Spain
- Alessandro Costa, The Francis Crick Institute, London, UK
- Patrick Cramer, Max Planck Institute for Biophysical Chemistry, Göttingen, Germany
- Aidan Doherty, Genome Damage and Stability Centre, Univ. of Sussex, Brighton UK
- Daniel Durocher, The Lunenfeld-Tanenbaum Research Institute, Toronto, Canada
- Karl-Peter Hopfner, Gene Center Munich, Munich, Germany
- Meindert Lamers, Leiden University, The Netherlands
- Óscar Llorca, Spanish National Cancer Research Centre, Madrid, Spain
- Juan Méndez, Spanish National Cancer Research Centre, Madrid, Spain
- Eva Nogales, EHMC/University of California at Berkeley, US
- Lori Passmore, MBC Laboratory of Molecular Biology, Cambridge, UK
- Xiaodong Zhang, Imperial College London, UK

In addition, 9 short talks were selected among participants’ contributions and 42 posters were presented.

**HETEROGENEITY AND EVOLUTION IN CANCER**

23-25 SEPTEMBER 2019

**ORGANISERS**
- Fátima Al-Shahrour, Spanish National Cancer Research Centre, CNIO, Madrid, Spain
- Solip Park, Spanish National Cancer Research Centre, CNIO, Madrid, Spain
- Basíl Babadín, Columbia Systems Biology, Columbia University, New York, US

**SPEAKERS**
- Alexander R. A. Anderson, Moffitt Cancer Center and Research Institute, Tampa, US
- Niko Beerenwinkel, ETH Zürich, Switzerland
- Ivana Bozic, University of Washington, US
- Curtis G. Callan, Princeton University, US
- Neal G. Copeland, University of Texas MD Anderson Cancer Center, Houston, US
- Christina Curtis, Stanford University, School of Medicine, Stanford, US
- Adolfo Ferrando, Institute for Cancer Genetics, Columbia University Medical Center, New York, US
- Trevor Graham, Barts Cancer Institute, London, UK
- Benjamin D. Greenbaum, Icahn School of Medicine at Mount Sinai, New York, US
- Holger Heyn, National Centre for Genomic Analysis, Barcelona, Spain
- Nancy Jenkins, University of Texas MD Anderson Cancer Center, Houston, US
- Laurence H. Pearl, Genome Damage and Stability Centre, University of Sussex, Brighton, UK
- Luca Pellegrini, Cambridge University, Cambridge, UK
- Song Tan, Penn State University, Pennsylvania, US
- Nicolas Thomà, Friedrich Miescher Institute, Basel, Switzerland
- Alessandro Vannini, Institute of Cancer Research, ICR, London, UK
- Roger Williams, MRC Laboratory of Molecular Biology, Cambridge, UK
- Wei Yang, National Institutes of Health, NIH, Bethesda, US
- Xiaodong Zhang, Imperial College London, UK

**APPLICATION DEADLINE**
- 6 May
- 22 April

For further information and to apply please go to www.cnio.es/events
· Tal Korem, Columbia University Irving Medical Center, New York, US
· Christina Leslie, Memorial Sloan Kettering Cancer Center, New York, US
· Arnold Levine, The Simons Center for Systems Biology, Institute for Advanced Study, Princeton, US
· Nuria Lopez-Ribas, Institute for Research in Biomedicine, Barcelona, Spain
· Scott W. Lowe, Memorial Sloan Kettering Cancer Center, New York, US
· Guillermo Lozano, University of Texas Anderson Cancer Centre, Houston, US
· Marta Llorente, Icahn School of Medicine, Mount Sinai, New York, US
· David Posada, School of Biology, University of Vigo, Spain
· Carol Prives, Columbia University, New York, US
· Benjamin J. Raphael, Lewis-Sigler Institute for Integrative Genomics, Princeton University, US
· Darryl Shibata, Keck School of Medicine of USC, Los Angeles, US
· Andrea Sottoriva, The Institute of Cancer Research, London, UK
· Doug Winton, Cancer Research UK Cambridge Institute, Cambridge, UK

In addition, 11 short talks were selected among participants’ contributions and 22 posters were presented.

OTHER MEETINGS & CONFERENCES

The CNIO annually hosts various international meetings and conferences.

IV TRANSLATIONAL MEETING
17 JANUARY 2019

ORGANISERS:
· María González Cao, Quiron Dexeus University Hospital, Barcelona, Spain
· Susanna Puig, Clinic Hospital, Barcelona, Spain
· Marisol Soengas, Spanish National Cancer Research Centre, Madrid, Spain

ADVANCES IN CANCER RESEARCH
JOINT MICC - SPANISH NATIONAL CANCER RESEARCH CENTRE (CNIO) SYMPOSIUM
4-5 SEPTEMBER 2019

ORGANISERS:
· Weizmann Institute of Sciences - Moross Integrated Cancer Center (MICC)
· Spanish National Cancer Research Centre, CNIO

VI JORNADAS DE JÓVENES INVESTIGADORES EN PROTEÓMICA
4-5 MARCH 2019

ORGANISERS:
· Centro Nacional de Investigaciones Oncológicas, CNIO Proteomics Unit
· SEProt, Sociedad Española de Proteómica

METABOCANCER I
CLOSING MEETING
27-28 MAY 2019

NETWORK MEMBERS:
· Alejo Efeyan, CNIO
· Anna Rivas, IMIM
· Arkaitz Carracedo, bioGUNE
· Guadalupe Sabio, CNIC
· José Cuezva, CBMSO
· Marc Claret, IDIBAPS
· María Mittelbrunn, CBMSO
· Mariona Graupera, IDIBELL
· Ruben Nogueiras, CIMUS
· Xosé Bustelo, CIC-USAL

PROGRESS AND CHALLENGES IN CANCER IMMUNE THERAPY
EUROPEAN TRAINING NETWORK IMMUTRAIN
23-26 JULY 2019

ORGANISERS:
· María Soengas, CNIO, Madrid, Spain
· Sebastian Kobold, LMU, Munich, Germany
· Stefan Endres, LMU, Munich, Germany

CNIO-CNIO JOINT MEETING
19 SEPTEMBER 2019

ORGANISER:
· Spanish National Cancer Research Centre, (CNIO)
FIRST GENDER EQUALITY EVENT OF THE SOMMA RESEARCH CENTRES OF EXCELLENCE
29 OCTOBER 2019

ORGANISERS:
· British Embassy in Madrid
· Spanish National Cancer Research Centre, CNIO

Whilst most research centres are committed to gender equality, activities are still mostly taken forward by individuals. In addition, the absence of dedicated resources, the lack of the required critical mass that leads to transformation or stability over time, and the absence of a coordinated strategy with other centres, prevent the gender agenda from being embedded into the institution’s spirit.

This event aims at sharing best practices in the SOMMA Alliance (‘Severo Ochoa’ Centres and María de Maeztu Units, or SOMMa) to learn and promote a change of culture, and support female talent and gender equality in science and strategic decision-making.

The gender expert Cheryl Smythe, from the Babraham Institute in Cambridge, UK, presented her work on implementing the gender equality measurements at the Babraham, as a result of which the centre received the Athena-SWAN award. Also, presentations from SOMMa Directors included examples of success stories on gender equality, scientific excellence and leadership carried out at their institutions.

TRAINING COURSES AND WORKSHOPS

ADVANCE CELL SORTING WORKSHOP
7-8 FEBRUARY 2019

ORGANISERS:
· Flow Cytometry Unit, CNIO, Madrid, Spain

SPEAKERS:
· Rui Gardner, Head of the Flow Cytometry Core Facility. Memorial Sloan Kettering Cancer Center, NY, USA
· Lola Martínez, Head of the Flow Cytometry Unit. CNIO, Madrid, Spain

This course is aimed at students and postdocs currently in the process of building and refining atomic models into cryo-EM maps. The course covered the theory and principles behind the software and procedures through a series of seminars and thorough tutorial sessions on the tools widely used by the community. During the workshop there was time to interact with all the speakers and instructors, and participants were welcome to bring their own data to solve specific issues.

ONCONET-SUDEOE
WORKSHOP ON INNOVATIVE IT FOR HEALTHCARE.
"THE PATIENT JOURNEY: INFORMATION TECHNOLOGIES FOCUSED ON THE CANCER PATIENT"
3-4 APRIL 2019

TOPICS:
→ Technical standards for information regarding cancer care throughout the disease course.
→ Ensuring patient confidentiality and privacy.
→ Patient virtual communities and social media: value in connecting with each other and in mining the online environment for information to help them cope with their disease.
→ In silico drug prescription and clinical trials design.
→ Analysing potential side effects of cancer therapies.
→ Improving continuity of care across disease stages.
→ Electronic Health Records (EHRs).
→ Development of new programmes for digital training of clinical and medical staff.
→ Challenges: data interoperability, systems interoperability, usability, adaptation to physicians’ workflows.
→ Overcoming resistance to digital change in patients and clinical personnel.
→ Financial incentives for digital transformation.
→ Transversal topics: Ethics, GDPR, patient rights, access to sensitive clinico-genomics data.
SOFTWARE CARPENTRY WORKSHOP - R FOR REPRODUCIBLE SCIENTIFIC ANALYSIS
6-7 JUNE 2019

TOPICS:
→ An introduction to scripting in R and using the language for scientific applications and data handling.
→ Effective use of the Unix command line.
→ Version control with git and GitHub.

WORKSHOP: ADVANCES IN THE R2TP/URI-PREFOLDIN COMPLEX IN CANCER
3 OCTOBER 2019

ORGANISERS:
- Nabil Djouder, Growth Factors, Nutrients and Cancer Group, Molecular Oncology Programme, CNIO
- Oscar Llorea, Macromolecular Complexes in DNA Damage Response Group, Structural Biology Programme, CNIO

CNIO WORKSHOP ON PHILOSOPHY & BIOMEDICAL SCIENCES:
“DEBATES ON CONCEPTUAL AND SOCIAL ISSUES”
19 NOVEMBER 2019

ORGANISERS:
- Maria A. Blasco (CNIO)
- Antonio Diéguez (UMA)
- Arantza Itxeburria (UPV/EHU)

WITH THE SUPPORT OF:
- Sabadell Foundation

SPEAKERS:
- Maria A. Blasco, Spanish National Cancer Research Centre, Spain
- Maria Cerezo, University of Murcia, Spain
- Iñigo de Miguel Berrain, University of the Basque Country, Spain
- Antonio Diéguez, University of Málaga, Spain
- Arantza Itxeburria, University of the Basque Country, Spain
- Michael Hauskeller, University of Liverpool, UK
- Lluís Montoliu, National Centre for Biotechnology, Spain
- Alfonso Valencia, Spanish National Bioinformatics Institute (INB-ISCIII), Spain
- Henrik Vogt, The University of Oslo, Norway

CNIO DISTINGUISHED SEMINARS

The purpose of the Distinguished Seminars Series is to invite outstanding and internationally renowned scientists to give a seminar and to meet with researchers at the CNIO. Distinguished Seminars are recurrent events that are open to the public and are held throughout the year, usually on Fridays at noon in the CNIO Auditorium. Each Distinguished Seminar series includes world-leading scientists who address topics that are of general interest to the CNIO faculty.

In total, the CNIO hosted 15 distinguished speakers in 2019.
<table>
<thead>
<tr>
<th>DATE</th>
<th>SPEAKER</th>
<th>ORGANISATION</th>
<th>TITLE</th>
</tr>
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<tbody>
<tr>
<td>JANUARY</td>
<td>Jeremy N. Rich</td>
<td>Brain Tumor Institute University of California, San Diego, US</td>
<td>Brain Tumor Stem Cells</td>
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<tr>
<td>16/01/2019</td>
<td>Jan H. J. Hoekmakers</td>
<td>Erasmus MC, Rotterdam, Netherlands</td>
<td>DNA damage-induced transcriptional stress in aging and the protective effect of nutritional interventions</td>
</tr>
<tr>
<td>FEBRUARY</td>
<td>Maite Huarte</td>
<td>Center for Applied Medical Research (CIMA), University of Navarra, Pamplona, Spain</td>
<td>Ochronin-dependent and independent functions of IncRNAs in cancer</td>
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<tr>
<td>05/02/2019</td>
<td>Rebecca Fitzgerald</td>
<td>University of Cambridge Hutchison/ MRC Research Centre, UK</td>
<td>Applying molecular characterisation of oesophageal cancer and its precursor Barrett’s to clinical practice</td>
</tr>
<tr>
<td>08/02/2019</td>
<td>Didier Stainier</td>
<td>Max Plank Institute, Bad Nauheim, Germany</td>
<td>Genetic compensation and transcriptional adaptation</td>
</tr>
<tr>
<td>15/02/2019</td>
<td>Riccardo Della Fave</td>
<td>Institute for Cancer Genetics Columbia University, New York, US</td>
<td>From genomics to targeted therapy in Diffuse Large B cell Lymphoma</td>
</tr>
<tr>
<td>MARCH</td>
<td>W. Kimryn Rathmell</td>
<td>Vanderbilt University Medical Center, Nashville, US</td>
<td>Linking epigenetics and immune response in renal cell carcinoma</td>
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<tr>
<td>08/03/2019</td>
<td>Magdalena Götz</td>
<td>German Research Center for Environmental Health, Neuherberg, Germany</td>
<td>From mechanisms of neurogenesis towards neuronal repair</td>
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<tr>
<td>29/03/2019</td>
<td>Kathrin Plath</td>
<td>UCLA School of Medicine, Los Angeles, US</td>
<td>A new framework for the function of the IncRNA XIin in X-inactivation</td>
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<tr>
<td>05/04/2019</td>
<td>Katherine L. Nathanson</td>
<td>Perelman School of Medicine, University of Pennsylvania, Philadelphia, US</td>
<td>From Soup to Nuts: Inherited Genetics and Testicular Germ Cell Tumors</td>
</tr>
<tr>
<td>12/04/2019</td>
<td>Charles M. Perou</td>
<td>UT Southwestern Medical Center, Dallas, TX</td>
<td>Quantitative Medicine for Breast Cancer Patients</td>
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<tr>
<td>26/04/2019</td>
<td>Natasha Kaur</td>
<td>University of Iowa, Iowa City, IA</td>
<td>Exploring and Therapeutically Exploiting the Tumor Microenvironment</td>
</tr>
<tr>
<td>MAY</td>
<td>Johanna Joyce</td>
<td>University of Bologna, Italy</td>
<td>Exploring and Therapeutically Exploiting the Tumor Microenvironment</td>
</tr>
<tr>
<td>17/05/2019</td>
<td>David Sancho</td>
<td>Spanish National Center for Cardiovascular Research, Madrid, Spain</td>
<td>Dendritic cells in immunity and inflammation</td>
</tr>
<tr>
<td>28/06/2019</td>
<td>Himisha Beltran</td>
<td>Dana Farber Cancer Institute, Boston, US</td>
<td>Understanding treatment resistance and the neuroendocrine phenotype in prostate cancer</td>
</tr>
<tr>
<td>SEPTEMBER</td>
<td>Susan S. Taylor</td>
<td>University of California, San Diego, US</td>
<td>PKA: from Molecules to Cells</td>
</tr>
<tr>
<td>25/09/2019</td>
<td>Borja Ibarra</td>
<td>MDOEA Nanocientia, Madrid, Spain</td>
<td>Optical tweezers to study life under tension, one molecule at a time</td>
</tr>
</tbody>
</table>
FACTS & FIGURES

University of Cambridge, UK
Factors that impair tissue regeneration in
Georg-Speyer-Haus & Frankfurt Cancer Institute
Netherlands Cancer Institute, NYC Langone Health New York, USA
Transcriptional networks governing self-
Aspect Biosystems Ltd, Vancouver, Canada
Microfluidic 3D bioprinting: Bringing
La Paz Hospital, Madrid, Spain
Optimizing CAR-T cells to kill pediatric cancer
MD Anderson Center, Houston, US
The pancreatic tumor microenvironment and the
National Institute of Genetics, Mishima-shi, Japan
Chromosome organization in living human cells
The Scripps Research Institute, La Jolla, US
Structure of the human Volume-Regulated Anion Channel
Topouridou Mazzone
Mazzone
CIB-CSIC, Madrid, Spain
Life in a crowded phase-separated world: biochemical and physiological consequences

WOMEN IN SCIENCE SEMINARS

DATE | SPEAKER | ORGANISATION | TITLE
--- | --- | --- | ---
15/01/2019 | Consuelo Madrigal | Prosecutor of the Supreme Court Chamber | La mujer profesional: al largo camino a la igualdad
12/02/2019 | Rosa Montero | Journalist and writer | Mujeres: una biografía
05/03/2019 | Luis Casal | Musician, singer, author and songwriter | Mujeres en la Oncología
09/04/2019 | Ruth Vera García | Spanish Society of Medical Oncology (SEOM), Chairman, Spain | Un proyecto para la igualdad de Género en las Empresas
07/05/2019 | María Luisa de Contes | Secretaria General y Consejera de las filiales del Grupo Renault en España, Directora (SEOM), Chairman, Spain | La mujer profesional: al largo camino a la igualdad
20/06/2019 | María Herrán | Attorney General of the Republic | La mujer en la Policía Nacional
15/10/2019 | Susana Malcorra | First Lady of Argentina | Mujeres en el liderazgo de cambio
29/10/2019 | Cheryl Smythe | Babraham Institute, Cambridge, UK | Creating an inclusive environment (what, why and how)
26/11/2019 | María Pilar Albiat | Deputy Director General of Human Resources and Training of the National Police Corps, Madrid, Spain | 40 años de la incorporación de la mujer a la Policía Nacional
03/12/2019 | María José San Román | Chef and restaurateur | Mujeres en Gastronomía
The CNIO also dedicates considerable efforts to bringing science and society closer together; one of these endeavours is its collaboration with the madri+d research network for the organisation of the Madrid Science Week (XIX Semana de la Ciencia y de la Innovación, 4-17 November 2019). In 2019, 53 people participated in the guided visit.

Throughout the year, the CNIO provides tailor-made opportunities to visit its installations and to learn about the essentials of cancer research. During 2019, more than 907 people participated in such guided visits; most of them were ESO and Bachillerato student groups, but also professionals in the health sector.
ADMINISTRATION

BOARD OF TRUSTEES

→ Honorary President

- Pedro Francisco Duque Duque
  Minister of Science, Innovation and Universities
  Ministro de Ciencia, Innovación y Universidades

→ President

- Rafael Rodrigo Montero
  Secretary General for Scientific Policy Coordination of the Spanish Ministry of Science, Innovation and Universities
  Secretario General de Coordinación de Política Científica del Ministerio de Ciencia, Innovación y Universidades

→ Vice-President

- Raquel Yotti Álvarez
  Director of the National Institute of Health Carlos III
  Directora del Instituto de Salud Carlos III

→ Appointed Members

- Faustino Blanco González
  Secretary General for Health and Consumer Affairs of the Spanish Ministry of Health, Consumer Affairs and Social Welfare
  Secretario General de Sanidad y Consumo del Ministerio de Sanidad, Consumo y Bienestar Social

- Rosa Menéndez López
  President of the Spanish National Research Council (CSIC)
  Presidenta del Consejo Superior de Investigaciones Científicas (CSIC)
  Director of the Department of National Affairs of the Cabinet of the Presidency of the Government (appointment pending)
  Director del Departamento de Asuntos Nacionales del Gabinete de la Presidencia del Gobierno (pendiente de nombramiento)

- Margarita Blázquez Herranz
  Deputy Director General for Networks and Cooperative Research Centres of the National Institute of Health Carlos III
  Subdirectora General de Redes y Centros de Investigación Cooperativa del Instituto de Salud Carlos III

- Juan Cruz Cigudosa García
  Advisor of University, Innovation and Digital Transformation of the Government of Navarre
  Consejero de Universidad, Innovación y Transformación Digital del Gobierno de Navarra

- Carlos Pesquera González
  Head of Cabinet of the Healthcare Counsellor of the Government of Cantabria
  Jefe de Gabinete de la Consejera de Sanidad del Gobierno de Cantabria

→ Elected Members

- BBVA Foundation
  Representative: Rafael Pardo Avellaneda, General Director

- la Caixa Banking Foundation Caixa d’Estalvis i Pensions de Barcelona
  Representative: Antonio Vila Bertrán, General Director
  Alternate Representative: Angel Pont Vidal, Corporate Director of Research and Strategy

- Grupo PRISA
  Representative: Ignacio Polanco Moreno, Chairman

→ Secretary

- Margarita Blázquez Herranz
  Deputy Director General for Networks and Cooperative Research Centres of the National Institute of Health Carlos III
  Subdirectora General de Redes y Centros de Investigación Cooperativa, Instituto de Salud Carlos III

→ Legal Advisor

- Fernando Arenas Escrúbano
  Chief State’s Attorney of the Spanish Ministry of Health, Consumer Affairs and Social Welfare
  Abogado del Estado-Jefe en el Ministerio de Sanidad, Consumo y Bienestar Social

* In accordance with the Spanish Transparency Legislation (Spanish Royal Decree 451/2012, of March 5), the following information is hereby provided:
  - The amount received by the Top Management of the Foundation – the CNIO’s Director plus the Managing Director – at the end of the financial year amounted to 359,124 euros in 2019 (272,471 euros in 2018). To this amount, the variable remuneration for directors amounting to 135,954 euros accrued during 2016, 2017 and 2018, must be added. Like every year, there is a provisional amount of 55,605 euros for the variable accrued in 2019.
  - Members of the CNIO Board of Trustees are not remunerated.
SCIENTIFIC ADVISORY BOARD

- **Mariann Bienz, PhD, FRS, FMedSci (Chair)**
  Joint Divisional Head
  Division of Protein and Nucleic Acid Chemistry
  Medical Research Council Laboratory of Molecular Biology
  Cambridge, United Kingdom

- **Genevieve Almouzni, PhD**
  Director, Institut Curie Research Centre
  Head of Nuclear Dynamics & Genome Plasticity Unit
  Institut Curie, Paris, France

- **José Costa, MD, FACP**
  Professor of Pathology and of Orthopaedics and Rehabilitation
  Director of the Translational Diagnostics and the Musculoskeletal Tumor Programs
  Yale University School of Medicine
  New Haven, USA

- **Sara Courtneidge, PhD, DSc (hc)**
  Associate Director for Translational Sciences, Knight Cancer Institute
  Professor, Departments of Cell, Developmental and Cancer Biology and Biomedical Engineering
  Oregon Health & Science University
  Portland, USA

- **John F.X. Diffley, PhD**
  Associate Research Director
  The Francis Crick Institute
  London, United Kingdom

- **Rosalind Eeles, PhD, FRCP, FRCR, FMedSci**
  Honorary Consultant in Clinical Oncology and Oncogenetics
  The Royal Marsden NHS Foundation Trust
  London, United Kingdom

- **Denise Galloway, PhD**
  Associate Division Director, Human Biology Division at Fred Hutchinson Cancer Research Center
  Research Professor of Microbiology at the University of Washington
  Seattle, USA

- **Edith Yvonne Jones, FRS, FMedSci**
  Joint Head Division of Structural Biology, Wellcome Centre for Human Genetics, University of Oxford
  Oxford, United Kingdom

- **Scott W. Lowe, PhD**
  Chair, Cancer Biology and Genetics Program, SKI
  Chair, Geoffrey Beene Cancer Research Center
  Memorial Sloan-Kettering Cancer Center
  New York, USA

- **Ángela Nieto, PhD**
  Full Professor and Head of the Developmental Neurobiology Unit
  Neuroscience Institute of Alicante (CSIC-UMH)
  Alicante, Spain

- **Andre Nussenzweig, PhD**
  NIH Distinguished Investigator, Head of the Molecular Recombination Section
  Laboratory of Genome Integrity
  Center for Cancer Research, National Cancer Institute
  Bethesda, USA

- **Daniela Rhodes, PhD, FRS**
  Professor, School of Biological Sciences and School of Chemical and Biomedical Engineering
  Director Emeritus, NTU Institute of Structural Biology
  Nanyang Technological University
  Singapore

- **Josep Tabernero, MD PhD**
  Director, Vall d’Hebron Institute of Oncology (VHIO)
  Head, Medical Oncology Department of Vall d’Hebron University Hospital
  Barcelona, Spain
# Management

## Director

**Blasco, María A.**

**Vice-Director**

**Fernández-Capetillo, Óscar**

**Executive Management**

- **Director**
  - Managing Director: Arroyo, Juan
  - Infrastructure Manager: de Dios, Luis Javier

- **Management Office**
  - Secretary: de Dios, Luis Javier

- **Finance & Administration**
  - Director: Fontaneda, Manuela

- **Human Resources**
  - Director: Pérez, José Lorenzo

- **Economic Management**
  - Director: Salido, M. Isabel

- **Purchasing**
  - Director: Álamo, Pedro

- **Economic Management**
  - Director: García-Risco, Silvia

- **Audit**
  - Director: García-Bielsa, Silvia

- **Infrastructure Management**
  - Director: de Dios, Luis Javier

- **Science Communication and Social Media**
  - Director: Herrera, Irene

- **Technology Transfer and Valorisation Office**
  - Director: Martín, M. Cruz

- **Technology Transfer and Valorisation Office**
  - Director: Mendoza, Julia

- **Education and Training Programmes**
  - Director: Zamora, Helena

- **Scientific Management**
  - Director: Barthelemy, Isabel

- **Scientific Events**
  - Director: Cerdá, Sonia

- **Library and Archives**
  - Director: López, Victoria

- **Scientific Publishing**
  - Director: Cerdá, Sonia

- **Secretariat**
  - Coordinator: Camacho, Pablo

- **Communication**
  - Director: Noriega, Nuria

- **Extramural Clinical Research**
  - Director: López, Antonio

- **Institutional Image and Outreach to Society**
  - Coordinator: Garrido, Amparo

- **International Affairs**
  - Director: Pola, Carolina

- **Development and Philanthropy**
  - Director: Rose, Jessica

- **Research**
  - Coordinator: Camacho, Pablo

- **Science Communication and Social Media**
  - Director: Noriega, Nuria

- **Technology Transfer and Valorisation Office**
  - Director: Martín, M. Cruz

- **Secretariat**
  - Coordinator: Camacho, Pablo

- **Secretariat (Communication, Innovation, Scientific Management, Development and Philanthropy)**
  - Coordinator: Rodríguez, M. Carmen

*Plan de Empleo Joven (Youth Employment Plan) (since October)*
# CNIO Personnel 2019

## Distribution by Programmes

<table>
<thead>
<tr>
<th>Programme</th>
<th>Percentage</th>
<th>Personnel</th>
</tr>
</thead>
<tbody>
<tr>
<td>Molecular Oncology</td>
<td>32%</td>
<td>150</td>
</tr>
<tr>
<td>Structural Biology</td>
<td>11%</td>
<td>51</td>
</tr>
<tr>
<td>Human Cancer Genetics</td>
<td>10%</td>
<td>46</td>
</tr>
<tr>
<td>Clinical Research</td>
<td>18%</td>
<td>84</td>
</tr>
<tr>
<td>Biotechnology</td>
<td>20%</td>
<td>89</td>
</tr>
<tr>
<td>Experimental Therapeutics</td>
<td>7%</td>
<td>32</td>
</tr>
<tr>
<td>Biobank</td>
<td>1%</td>
<td>5</td>
</tr>
</tbody>
</table>

## Distribution by Professional Category

<table>
<thead>
<tr>
<th>Category</th>
<th>Percentage</th>
<th>Personnel</th>
</tr>
</thead>
<tbody>
<tr>
<td>Principal Investigators</td>
<td>11%</td>
<td>49</td>
</tr>
<tr>
<td>Staff Scientists</td>
<td>16%</td>
<td>74</td>
</tr>
<tr>
<td>Post-doctoral fellows</td>
<td>10%</td>
<td>45</td>
</tr>
<tr>
<td>Graduate Students</td>
<td>21%</td>
<td>98</td>
</tr>
<tr>
<td>Technicians</td>
<td>42%</td>
<td>191</td>
</tr>
</tbody>
</table>

## Gender Distribution

- **Total CNIO Personnel**: 547
  - **Research**: 457 (84%)
  - **Administration**: 90 (16%)

- **Gender Distribution**: 356 Female (65%), 191 Male (35%)

- **Age Distribution**: 158 41-50 (29%), 148 31-40 (27%), 165 31-40 (30%), 76 < 50 (14%)
### Total Scientific Personnel

<table>
<thead>
<tr>
<th>National Origin</th>
<th>Percentage</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>Spain</td>
<td>92%</td>
<td>419</td>
</tr>
<tr>
<td>Rest of Europe</td>
<td>5.03%</td>
<td>23</td>
</tr>
<tr>
<td>America</td>
<td>1.53%</td>
<td>7</td>
</tr>
<tr>
<td>Asia</td>
<td>1.53%</td>
<td>7</td>
</tr>
<tr>
<td>Total</td>
<td>100%</td>
<td>457</td>
</tr>
</tbody>
</table>

### Distribution of Scientific Personnel by National Origin

#### Basic Research

- **Principal Investigators**: 24 (12%)
- **Staff Scientists**: 31 (15%)
- **Post-Doctoral Fellows**: 29 (14%)
- **Graduate Students**: 65 (32%)
- **Technicians**: 52 (26%)
- **Total**: 201 (100%)

#### Translational Research

- **Principal Investigators**: 11 (9%)
- **Staff Scientists**: 32 (25%)
- **Post-Doctoral Fellows**: 14 (11%)
- **Graduate Students**: 31 (24%)
- **Technicians**: 42 (31%)
- **Total**: 130 (100%)

#### Innovation

- **Principal Investigators**: 13 (11%)
- **Staff Scientists**: 11 (9%)
- **Post-Doctoral Fellows**: 2 (2%)
- **Graduate Students**: 2 (2%)
- **Principal Investigators**: 13 (11%)
- **Total**: 121 (100%)

#### BioBank

- **Principal Investigators**: 1 (20%)
- **Technicians**: 4 (80%)
- **Total**: 5 (100%)

---

**Scientific Personnel: National Origin**

- **Total Scientific Personnel**: 457
- **Spanish**: 419 (92%)
- **Non-Spanish**: 38 (8%)

**Foreign Scientific Personnel: Distribution by Professional Category**

- **Principal Investigators**: 6 (12%)
- **Staff Scientists**: 6 (12%)
- **Post-Doctoral Fellows**: 9 (18%)
- **Graduate Students**: 8 (16%)
- **Technicians**: 9 (18%)

Total foreign scientific personnel 38

Percent values represent percentages of foreign employees of the total CNIO personnel in each category.
PRIVATE SPONSORS

“We take this opportunity to express our thanks and appreciation to all our sponsors and donors for the generous support that we received from them in 2019. They play an inherent role in our present and future successes.”

The Fundación “la Caixa” helps finance our most prominent international conferences, the CNIO-“la Caixa” Foundation Frontiers Meetings. Another main goal of the “la Caixa” Foundation is to support an innovative programme aimed at fostering international fellowships in order to attract the most outstanding students from the international arena to obtain their doctoral degrees at accredited “Severo Ochoa” Centres of Excellence. The CNIO has been participating in a new doctoral fellowship programme of the “la Caixa” Foundation, named INPhINIT, since 2017; the aim of this programme is to attract outstanding international students to carry out doctorates at top Spanish research centres.

The Fundación Banco Santander funds the Banco Santander Foundation – CNIO Fellowships for Young Researchers. These fellowships have the aim to support highly talented and motivated young scientists who have been trained in the UK or in the USA, and who wish to pursue their postdoctoral training at the CNIO. One young scientist, Luis Javier Leandro-García from the Memorial Sloan Kettering Cancer Center in New York, was the recipient of a Santander Foundation-CNIO Fellowship in 2019.

The Fundación Seve Ballesteros is a private not-for-profit institution focused on securing, financing and promoting research projects centred on brain tumours. Fundación Seve Ballesteros has been supporting the Seve Ballesteros Foundation – CNIO Brain Tumour Group, headed by Massimo Squatrito, since 2012. This Group focuses on the identification of markers for brain tumours as its principal activity.

The Fundación Jesús Serra-Catalana Occidente continues to fund the Visiting Researchers’ Programme that was established to support prestigious international professors for short stays at the CNIO. The recipients of the Jesús Serra Foundation’s Visiting Researchers’ Award in 2019 were Scott W. Lowe, Chair of the Cancer Biology and Genetics Program and the Geoffrey Beene Cancer Research Center at Memorial Sloan Kettering Cancer Center in New York (USA), and Sonia Lain, Group Leader at the Karolinska Institutet in Stockholm (Sweden).

Our activities are also supported by individual donations – citizens who wish to contribute personally to the battle against cancer – as well as via external fundraising from local associations that are equally dedicated to the battle against cancer. During 2019, our research activities and seminars were supported, among others, by Asociación Bandera Rosa, Asociación de Mujeres Afectadas de Cáncer de Mama “ROSAE”, Colectivo de afectados “El árbol de la Vida”, Freesia Group, Fundación Banco Sabadell, Fundación Inocente Inocente, Fundación Investigación Biomédica Hospital Universitario 12 de Octubre, Fundación Juegaterapia, L‘Oreal España, Petroplast, Santa Lucia Seguros, and the British Embassy.

The AXA Research Fund (ARF) – a global initiative of scientific philanthropy run by the insurance group AXA – awarded an AXA-CNIO Endowed Permanent Chair position in Molecular Oncology to Mariano Barbacid as part of its 2011 call.

Lastly, we extend our heartfelt thanks to all ‘CNIO Friends’ donors, sponsors and benefactors who, thanks to their generous donations to support cancer research at the CNIO, ensured the continuation of our research endeavours throughout 2019.
CNIO Friends

CNIO Friends
Quantum Physics and Photography, Brought Together by CNIO Arte
Meeting with Our Friends
CNIO-La Roche-Posay Agreement
Benefactor Friends/Sponsor Friends
Donations to the CNIO
‘CNIO Friends’ is celebrating its 5th birthday with nearly €1.4 million raised from 1,350 donors over five years. The initiative, which has become a bridge connecting society to cancer research, is ready for a new, more mature stage, marked by the establishment of a Philanthropy Office. This year, ‘CNIO Friends’ raised a total of €515,000 which is our most successful year yet for the programme.

Donations to ‘CNIO Friends’ enables the Centre to hire new predoctoral and postdoctoral talent from around the world via a competitive application process. In 2019, we were delighted to recruit 4 young researchers to explore new ways of diagnosing and treating cancer: Ruben Martínez joined the Kinases, Protein Phosphorylation and Cancer Group; María Moreno joined the Genome Integrity and Structural Biology Group; Neibla Priego will continue working on her projects in the Brain Metastasis Group; and Sarita Saraswati joined the Telomeres and Telomerase Group.

For the second year in a row, we organised CNIO Arte, an initiative supported by Banco Santander Foundation to connect internationally renowned artists and scientists and invite them to explore common ground together. Each year, the exploration results in a unique artwork, which is then sold to fund the hiring of scientists through the ‘CNIO Friends’ Programme. In its 2nd edition, CNIO Arte was curated by Amparo Garrido, visual artist and Coordinator of the Office of Institutional Image and Outreach to Society at CNIO. It featured quantum physicist Ignacio Cirac, winner of the Prince of Asturias Award 2006, and photographer Chema Madoz, winner of the National Photography Award 2000. Madoz created a photographic work based on Cirac’s research, which led to a series of 30 numbered and signed photo engravings. The work, presented at the ARCOmadrid Contemporary Art Fair and at the Centre de Cultura Contemporània de Barcelona (CCCB), was on display at CNIO from February to April.

In 2019, the CNIO was delighted to receive support from all over Spain. In addition, CNIO enjoyed working with a number of foundations, companies and associations to both raise awareness and raise funds for cancer research. To highlight a few examples, in February, ROSAE, an association of breast cancer patients, invited us to attend their convivial meal in Valdepeñas, Ciudad Real. In June, the Bandera Rosa association, supporting breast cancer patients and their families, held a number of activities in Campo de Gibraltar, Cádiz to raise funds for the Centre. In October, El Árbol de la Vida, an association based in Pedroñeras, Cuenca, held their 3rd Charity Race Against Cancer, drawing 3,000 participants and donating part of the funds raised to the CNIO.

To recognise World Cancer Day, CNIO and La Roche-Posay (L’Oréal Group) carried out the #InvestigacionsVida (ResearchIsLife) campaign, handing out CNIO leaflets in over 1,000 pharmacies across Spain and thus reaching more than 60,000 users.

In June, we invited all of our donors to join us for our annual ‘CNIO Friends’ Meeting Day. Over 100 Friends and their companions were welcomed by Scientific Director Maria Blasco, to hear the latest news and major developments at CNIO. Researchers Paula Martínez, María Moreno, Neibla Priego and Miguel Jiménez enjoyed the opportunity to present their research projects that were made possible thanks to donations to the CNIO. Afterwards, our visitors took a tour of our labs before sitting down to a shared meal in the late afternoon.

In September 2019, CNIO established a Development and Philanthropy Office aimed at concentrating and optimising the efforts to identify and cultivate new donor relationships and continue to recognise and thank our existing supporters. The newly established office will manage the ‘CNIO Friends’ initiative and seek to build new collaborative partnerships with corporate partners, individuals and philanthropic foundations. The legacy programme continues to grow and has received a cumulative total of €888,000 since 2015. In 2019, CNIO received charitable bequests of €284,000 with €844,000 pending to be executed.

It has been an exciting and successful year for the CNIO Friends and we look forward to a whole host of innovative opportunities to collaborate with society through our new Philanthropy Office in 2020. We would like to take this opportunity to thank our donors once again for their commitment and support. The best way of demonstrating our thanks is by continuing to maintain the quality of cancer research we have been doing for the past 20 years, whilst always striving to do more. Together, let’s stop cancer.
The 2nd CNIO Arte, a project sponsored by Banco Santander Foundation, was curated by Amparo Garrido. It featured quantum physicist Ignacio Cirac, winner of the Prince of Asturias Award 2006, and photographer Chema Madoz, winner of the National Photography Award 2000. Madoz created a photographic work based on Cirac’s research, which led to a series of 30 numbered and signed photo engravings. The funds raised from the sale go to CNIO Friends.

On June 27, 2019, we opened our doors to the community of CNIO Friends’ donors to celebrate the CNIO Friends Day and honour them for their support of cancer research.

More than 100 Friends and their companions were welcomed by María Blasco, who told them about the latest CNIO achievements. Researchers Paula Martínez, María Moreno, Neihla Priego and Miguel Jiménez described the four projects they are carrying out thanks to donations from CNIO Friends. Our supporters were given a lab tour and enjoyed a lunch with the researchers. Raquel Yotti, Director of Spanish Institute of Health Carlos III, under whose purview CNIO is ascribed, also attended the presentation.
On the occasion of World Cancer Day, CNIO and La Roche-Posay (L’Oréal Group) carried out the #InvestigaciónEsVida [ResearchIsLife] campaign.

Unfolding for 2 weeks in January and February, the campaign consisted of handing out CNIO leaflets in over 1,000 pharmacies across Spain and thus reaching more than 60,000 users, including customers and L’Oréal/La Roche-Posay staff. The campaign was advertised in mass media and in the L’Oréal website and social media.
Last but not least, we would also like to extend our heartfelt thanks to all the anonymous benefactors who have donated their legacies to support cancer research at the CNIO; in doing so they have contributed to society for generations to come.
CREATIVE TEAM

In order to pour the Annual Report into a more creative concept, the CNIO works closely with selected professionals in the artistic and creative sectors who ensure delivery of an end product that is attractive in more ways than one. We extend our thanks to the creative team, the visual artist Amparo Garrido, and the graphic design studio Underbau whose invaluable work created the images and design that illustrate this Annual Report.

AMPARO GARRIDO  PHOTOGRAPHY

A Madrid-based visual artist working with photography and video, Amparo Garrido has been represented in individual and group shows both in Spain and abroad since 1998. Her work has been honoured in several prestigious competitions. She obtained the first place in the 2001 edition of the ABC Photography Prize, and second place in the 2007 Purificación García Prize. Other honourable mentions include the Pilar Citoler and Ciudad de Palma prizes. Her work can be found in major collections, including the Museo Nacional Centro de Arte Reina Sofía in Madrid, the photographic holdings of the Madrid regional authority, the Coca-Cola Foundation, the Es Baluard Museum of Modern and Contemporary Art in Palma de Mallorca, and the Galician Centre of Contemporary Art (CGAC) in Santiago-de-Compostela, among many others. Amparo’s most recent work, feature film ‘The Silence that Remains’, was selected to be part of the Documentary Feature Film section of the Málaga Spanish Film Festival in its 22nd edition, Málaga 2019, as well as for competition in the TFFDOC/INTERNAZIONALE – Torino Film Festival – Best International Documentary section (TFFDOC/INTERNAZIONALE) – Torino, Italy 2019, among others that have not yet officially unveiled their film selection.

UNDERBAU  DESIGN

Underbau is a design studio that emerged in 2008 from professional designers with 20 years of experience in the field of corporate design, publishing and advertising. From the very beginning, the studio has sought to maintain its primary focus on art and culture, working together with Spanish and international bodies such as the Orquesta y Coro Nacionales de España, Museo Picasso Málaga, Fundación de Amigos de Museo del Prado, Instituto Cervantes and Museo Thyssen-Bornemisza. Underbau’s total-design approach puts the emphasis on coherency. To achieve that, the studio assumes full responsibility for the entire creative process, from the initial concept to the final product.