Individualized PaediatricCure

MAIN ACHIEVEMENTS AND ONGOING WORK

The ultimate goal of the iPC project is to improve the care of children with cancer by developing cloud-based technologies and infrastructures that help identify effective individual therapies. Much has already been done in the first two project periods to achieve this goal and our partners are continuously working in the third project period to solve the mathematical and computational bottlenecks of data- and model-based medicine. Therefore, the fourth iPC factsheet describes the most important achievements so far and the ongoing work in the current project period.

Main Achievements

Some important goals have already been achieved within the project, so only a small part of them is listed. Further important achievements and the latest developments can be found under **Results & Downloads**.

IBM, University of Zurich (UZH), Prinses Maxima Centrum voor Kinderoncologie (PMC) and Baylor College of Medicine (BCM) have collaborated on high spectral flow cytometry and data analysis of samples from AML patients. IBM and BCM have also jointly developed an algorithm for clonal deconvolution of tumour RNA and protein profiles. Germans Trias i Pujol Research Institute (IGTP) has established an "Omics HB database" with nearly 500 samples and an "HB patient platform" with biological samples from more than 150 patients that in collaboration with Unitversita degli Studi di Napoli FREDERICO II (UNINA), Ludwig-Maximilians-Universität München (LMU) and Barcelona Supercomputing Center (BSC), has been key to validate the computational tools (MultiAffinity, Drug Sense), key prognostic biomarkers (i.e. 16- and 14q32-gene signatures, etc) and therapeutic targets (CDK9) from which to select specific anti-tumoral drugs.

Ludwig-Maximilians-Universität München (LMU) and Alacris Theranostics (AT) have found that Anaplastic lymphoma kinase and the Hedgehog signalling pathway could be potential therapeutic targets in hepatoblastoma.

LMU has established an in vitro testing platform for hepatoblastoma, and The Children's Hospital of Philadelphia (CHOP) is exploring the possibility of using NB to develop and build a computational model for immune system response and immunotherapy.

Unitversita degli Studi di Napoli FREDERICO II (UNINA) developed a computational method for predicting small molecule inhibitors of cancer cell growth. A proteomic study involving IGTP, UNINA and Universitätsklinikum Heidelberg (UKL-HD) has also led to the identification of key deregulated signalling pathways and three prognostic proteins in hepatoblastoma patients.
Universiteit Gent (UGent) has tested different deconvolution algorithms and optimised parameter settings in terms of data transformation, normalisation, and marker selection to achieve accurate deconvolution results. An array CRISPR interference screening platform was also established for high-throughput gene disruption with serial cellular and molecular phenotyping.

CURIE has identified a cluster of miRNAs that regulate a TF network in different medulloblastoma subgroups and developed a framework for analysing miRNA expression from the perspective of clustering samples. In addition, CURIE has developed a metabolic model of intratumoral heterogeneity of Ewing sarcoma tumours.

Ongoing Work

Integrating the different data modalities collected for each patient is key to accurate personalised models for diagnosis, prognosis and improved treatment of a variety of diseases, including paediatric cancers. Our plan is to link the iPC platform with established European research infrastructures (e.g. **ELIXIR**, **BBMRI-ERIC** and **EATRIS**) and centres of excellence (e.g. **BioExcel**, PerMedCoE and **CompBioMed**) to provide data and analysis results to scientists and clinicians involved in the deposit of molecular and omic data, and to analyse previously anonymised paediatric patient data using tools developed by iPC. The collection of molecular and clinical data from previous and ongoing studies is progressing, and an ongoing hepatoblastoma study is now actively testing our predictive models. Efforts have been made to develop animal models required for drug testing and to conduct genetic disruption experiments where results are evaluated by single cell RNA sequencing.

One of the next steps is downstream analysis, which includes genomic sequencing data. The Instituto per le Applicazioni del Calco M.Picone of the National Research Council (CMRI) is working on the schedules in the laboratory to provide the DNA sequence to proceed with the data analysis. Furthermore, the DAC management portal has already been developed and a first implementation is already available. The DAC-Notify module has been proposed and is currently under development. Finally, initial tests have been conducted for the integration of the EGA data access framework into the iPC computing platform. By combining expertise ranging from computational modelling to clinical patient management, iPC is developing innovative, clinical-ready software tools that meet the real needs of paediatric tumour patients.

Individualized PaediatricCure

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Budget

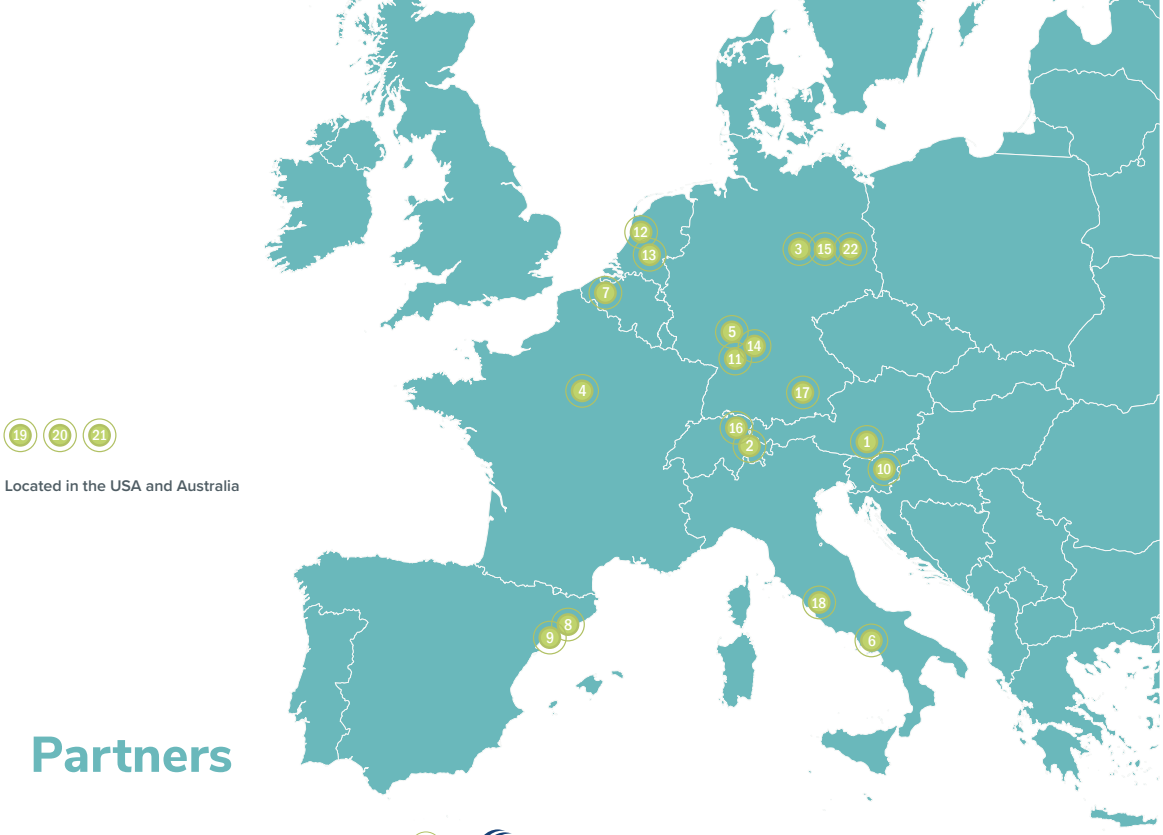
€ 15.1 Million
14.7 Million EU-funded

Consortium

22 Partners
3 Continents

Duration

53 Months
01/2019 - 05/2023



Partners

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More information about the consortium can be found on the project website.

The iPC project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No. 826121.

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