decrease of p-mTOR expression after everolimus treatment. Due to the higher prevalence of p-mTOR in basal-like tumors, we treated three basal-like cell lines with Everolimus to assess the effects on cell invasion and aggregation. Cell invasion was significantly inhibited in response to Everolimus. Conslusion: The results revealed that there is a significant higher frequency of p-mTOR in basal-like tumors, compared with the other subtypes. In addition, Everolimus is able to significantly decrease mTOR expression and activity, inhibiting invasion capacity of basal-like breast cancer cells emphasizing the antitumour activity of mTOR inhibitors in breast cancer models.

***In vivo models in cancer research***

Madalena Costa[1,2], Filipa Quintela, Vilela [1,3] and Regina A. Silva[1]

[1]Department of of Pathological, Cytological and Thanatological Anatomy, School of Allied Health Technologies, Polytechnic Institute of Porto, Vila Nova de Gaia, Portugal
[2]Abel Salazar Biomedical Sciences Institute, University of Porto, Porto, Portugal
[3]Cancer Biology and Epigenetics Group –Research Center, Portuguese Oncology Institute – Porto, Porto, Portugal

Cancers figure among the leading causes of morbidity and mortality worldwide. Over the last decade there has been an extraordinary increase in our knowledge of the fundamental molecular processes that are involved in the development of cancer and its response to treatment. Studies in tissue culture have multiplied our acquaintance of cancer cell pathophysiology, mechanisms of transformation and strategies of survival of cancer cell lines, revealing therapeutically exploitable differences to normal cells. However, tumors are heterogeneous, structurally complex and result from an evolving crosstalk between different cell types and its surrounding tissue. A full elucidation of events occurring inside the cancer microenvironment is fundamental more effective therapies. Experiment in vivo models remains essential to understand the fundamental mechanisms underpinning malignancy and to discover improved methods to prevent, diagnose and treat cancer. This presentation will summarize currently available in vivo models of cancer, define the limitations and advantages of each modeling option and suggest the basis with which particular models should be used to answer a specific scientific question.