XV FISV CONGRESS
Sapienza University of Rome, Italy
September 18-21, 2018

Programme & Abstracts

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FISV - Federazione Italiana Scienze della Vita

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also involved in circRNA biogenesis. We performed a RNA sequencing using murine motor neurons (MNs) derived from embryonic stem cells (mESC). We analysed circRNA expression in wild type MNs as well as in MNs Knockout for FUS and we found several circRNAs affected in FUS KO condition. Among these we selected two circRNAs in order to study their function in MNs, circ31 and circ16. We decided to generating mESC KO by using CRISPR/Cas9 technology in order to identify altered pathways by performing RNA sequencing (RNAseq); we have set up and performed circ31 and circ16 pull down in MNs in order to identify protein interactors by mass-spectrometry analysis and we are studying the subcellular localization of circ-31 and circ-16 by using Fluorescent in situ hybridization both in normal and in stress condition.

P9.4 - microRNA-375 distinguishes neuroendocrine from non-neuroendocrine lung tumors in FFPE samples

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Lung cancer is one of the leading causes of death worldwide. The main challenges in treating this disease are the early diagnosis and the correct classification of the tumour. Clinical variability of lung cancer is high and frequently disentangling this complexity is demanding. In this context, correct discrimination of pulmonary neuroendocrine (NE) from non-NE tumours (squamous cell carcinomas and adenocarcinomas) may be problematic and of critical relevance. The spectrum of NE tumours is various and each type has molecular and phenotypical differences. We explored the possibility of using microRNAs in Formalin-Fixed, Paraffin Embedded (FFPE) samples in order to classify lung tumours. In this study, we analyzed a series of 82 FFPE lung tumour tissues by RT-qPCR and we found that microRNA-375 expression is able to classify low-grade NE lung tumors from non-NE lung tumors, but not large cell NE from small cell lung cancer tumours. Albeit miR-375 deregulation has been observed in several neuroendocrine tumours (intestine, thyroid etc.) this is to our knowledge the first time its upregulation is described as a potential biomarker for lung NE tumours.

P9.5 - *Charme* long noncoding RNA links up with chromatin shaping the 3D nuclear organization

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The mammalian genome contains thousands of long noncoding RNAs (lncRNA), which have been proposed to be fundamental in the regulation of many biological processes. Among them, nuclear lncRNAs are generally associated to chromatin and they can act as genome architects contributing to the formation or disassembly of 3D structures. We identified a subset of new polyadenylated and multi-exonic lncRNAs differentially expressed during murine *in vitro* myogenesis. In particular *Charme* is an abundant and highly conserved noncoding transcript specifically required for *in vitro* muscle differentation. Interestingly, its ablation *in vivo* resulted in a peculiar cardiac phenotype in which the morphology of the heart is remodelled. Mechanistically, *Charme a*cts in the nucleus as a structural RNA, contributing to the formation of chromosome territories where coordinated expression of pro-myogenic genes occurs. Our recent finding that *Charme i*nteracts with Matrin3, a major component of the nuclear matrix, also