N. 3 February 2024

AICC NEWSLETTER

ITALIAN ASSOCIATION OF CELL CULTURES

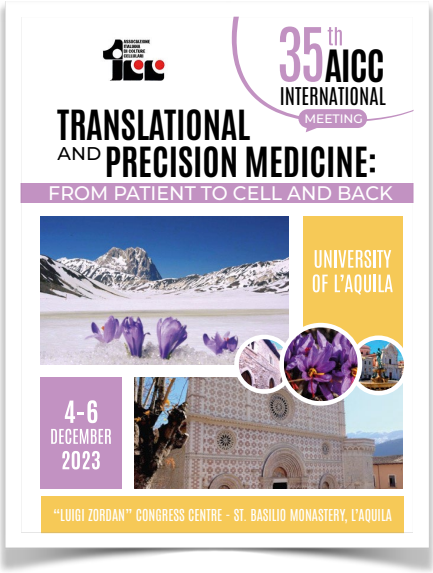
Latest AICC News

Report on the 35° AICC Annual Meeting

Translational and Precision Medicine:

from patient to cell and back

The 35th AICC Annual meeting, held in L'Aquila on 4-6 December 2023, was an incredible journey in the exiting world of precision medicine. The meeting was opened by **Prof. Antonio Iavarone from University of Miami**, who talked about the next-generation multi-omics classification and therapeutic stratification of tumor subtypes. Through the **four sessions**, we discussed about novel models to profile cancer and uncover predictive and prognostic biomarkers **(I)**, the emerging molecular therapeutic targets in cancer and beyond **(II)**, the contribute of the microenvironment to disease progression **(III)** and the possibility to translate cell findings into drug discovery pipeline **(IV)**. The keynote lecture on the the role of p53 family in the neuroblastoma was held by **Prof. Gerry Melino, from University of Rome "Tor Vergata"**, while **Prof. Guido Franzoso from Imperial College London** gave the closing talk about the cancer-selective targeting of the NF-κB signalling pathway in human cancers.



AICC Annual Meeting in Numbers

130 Registered Attendees

14 Faculty Presenters

18 Oral Communications

5 Technical Talks

16 Sponsor Exhibitors

43 Poster Presentations

10 Awards for best Oral Communications & Posters

Funding Opportunities

✓ **Partenariato Esteso INF-ACT**

Deadline: 21/12/2024

✓ **Global Health EDCTP3**

Deadline: 24/04/2024

✓ **AIRC Individual Grants**

Deadline: March 2024

✓ **EP PerMed JTC2024**

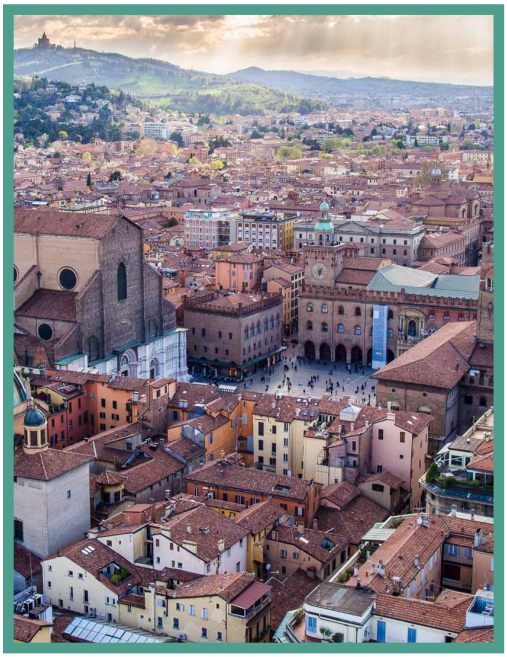
Deadline: 05/03/2024

THANK YOU ALL

FOR JOINING US

Upcoming Events

TARGETED PROTEIN DEGRADATION: from biology to pharmacology



Date: 4th June 2024

Location: IRCCS Istituto Ortopedico Rizzoli, Centro di Ricerca Codivilla Putti, Aula Anfiteatro, Via di Barbiano 1/10, Bologna

Targeted protein degradation is an emerging therapeutic modality based on the use of small molecules called degraders with the potential to tackle "undruggable targets". Join a small but multidisciplinary group of academic and pharma discovery scientists with specific expertise in drug development and experimental modeling to dive into the biggest challenges in early discovery and preclinical stages of targeted protein degradation!

SAVE THE DATE!!!

Open Positions

✓ **4-year PhD position**

Department of Oncology Interdepartmental Center ATLANTIS, University of Torino

Supervisor: Chiara Riganti

Start Date: November 2024

Studying the metabolome of non-small cell lung cancer to identify biomarkers predictive of response to chemo-immuno-therapy

Let us know if you are recruiting and we will spread the word!!!

Drop us an email by clicking on the icon below

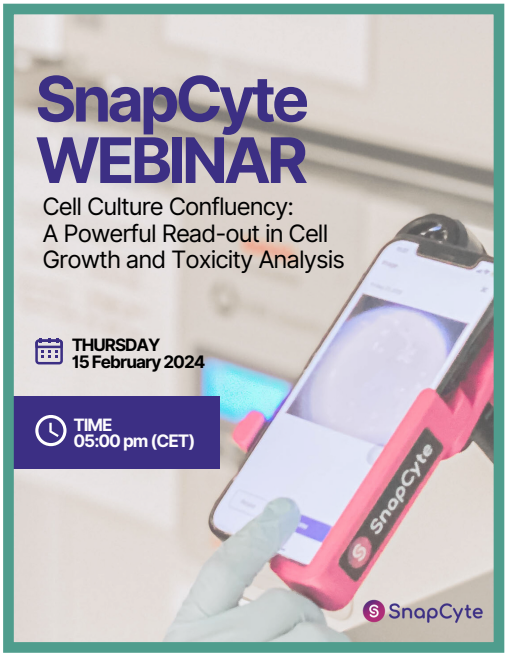
Cutting-Edge Technologies

SnapCyte Solutions Inc

We have entered a partnership with **SnapCyte Solutions Inc**, a new startup from the academic lab of Dr. Mads Daugaard at UBC, Vancouver Canada.

Exclusive to AICC members, they offer:

■ **WEBINAR** on **February 15, 2024 at 17.00** - Sign up here. Duration: ~30 minutes.



AGENDA

✓**Cell Culture Confluency: A Powerful Read-out in Cell Growth and Toxicity Analysis** - Dr. Nader Al-Nakouzi

✓**How can Confluency Measurements be Used in the Lab?** - Dr. Negin Farivar

✓**Q&A** on the use of cell confluency in your research

SUPPORT: **Any questions about cell confluency, cell counting or SnapCyte™ products** will be answered by cell biology scientist, Dr. Janny Marie L Peterslund, Denmark (jannymarie@snapcyte.com). Please email her directly.

We have secured a **50% DISCOUNT** on SnapCyte™ Apps purchased this year! Please contact SnapCyte directly about this offer.

Sign up for the free webinar now!

Featured Articles

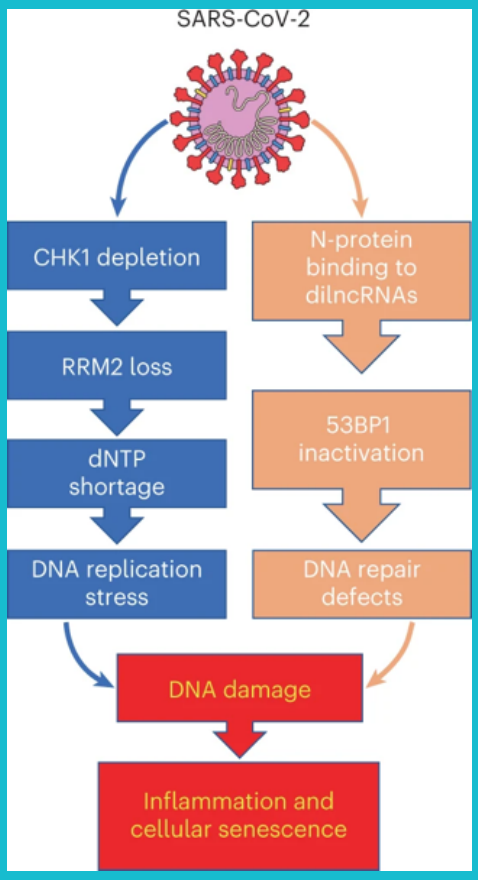
1

SARS-CoV-2 infection induces DNA damage, through CHK1 degradation and impaired 53BP1 recruitment, and cellular senescence

Ubaldo Gioia, Sara Tavella,, *et al.*

Nature Cell Biology 2023

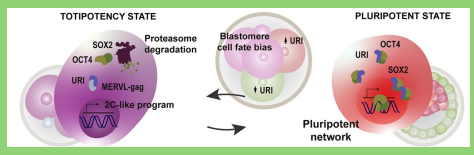
SARS-CoV-2 – the virus responsible for the COVID-19 pandemic – has a greater impact on human health than other respiratory viruses, although the mechanisms of this are not fully understood. In this recent paper, a team of researchers – coordinated by professor Fabrizio d'Adda di Fagagna – first demonstrated that SARS-CoV-2 causes DNA damage and elicits an altered DNA damage response in cells. Mechanistically, the researchers discovered that SARS-CoV-2 expresses proteins able to hijack cell nucleotide metabolism. Specifically, the viral factors ORF6 and NSP13 have been found to promote the degradation of DNA damage response checkpoint kinase 1 (CHK1) through proteasome and autophagy, respectively. CHK1 loss leads to deoxynucleotide triphosphate (dNTP) shortage, causing impaired S-phase progression, DNA damage, pro-inflammatory pathways activation and cellular senescence. In addition, the research group evidenced that DNA breaks accumulate due to an impairment in the repair mechanisms. Indeed, the author demonstrated that SARS-Cov-2 nucleocapsid protein impair the recruitment of the binding protein 53BP1 and decrease DNA repair by competing with 53BP1 for association with damage-induced long non-coding RNAs. Notably, the data first obtained in *in vitro* cell models were then confirmed also *in vivo* both in SARS-CoV-2-infected mice and in patients with COVID-19. Altogether, the obtained findings indicate that SARS-CoV-2 both induces DNA damage and impairs its repair, ultimately causing cells to age and spread inflammation.



2

Endogenous retroviruses shape pluripotency specification in mouse embryos

Sergio de la Rosa, María Del Mar Rigual, *et al.*



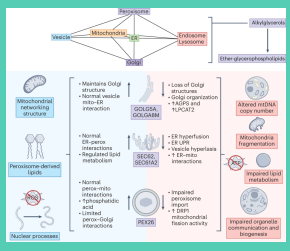
Science Advances 2024

All animals have evolved thanks to viruses that, hundreds of millions of years ago, infected the first multi-cellular beings. The viral genetic material, integrated into the genome of these primitive organisms, is still in our DNA. Researchers from the CNIO (Spanish National Cancer Research Centre) describe the role played by these viruses in a process that is absolutely vital for our development, and which occurs a few hours after fertilization: the transition to pluripotency, when the oocyte goes from having two to four cells. Using cutting-edge genetic and biochemical techniques in mice, the research group identified MERVL-gag, a retroviral protein, as a crucial modulator of pluripotent factors OCT4 and SOX2 during lineage specification. MERVL-gag tightly operates with URI, a prefoldin protein that concurs with pluripotency bias in mouse blastomeres, and which is indeed required for totipotency-to-pluripotency transition. Accordingly, URI loss promotes a stable totipotent-like state and embryo arrest at 2C stage. Mechanistically, URI binds and shields OCT4 and SOX2 from proteasome degradation, while MERVL-gag displaces URI from pluripotent factor interaction, causing their degradation. The obtained findings first reveal a symbiotic coevolution of endogenous retroviruses with their host cells to ensure the smooth and timely progression of early embryo development.

3

Quantitative subcellular reconstruction reveals a lipid mediated inter-organelle biogenesis network

Richard G. Lee, Danielle L, *et al.*



Nature Cell Biology 2024

Mitochondria have been shown to interact with multiple organelles and even if literature data suggest a marked inter-organelle dependency, the nature of these interconnections and their implications have yet to be elucidated. In this study, the research group of Aleksandra Filipovska used a whole-genome CRISPR screening to identify regulators of mitochondrial biogenesis using the expression of a known mitochondrial biogenesis impairment marker (MRPL12) as a readout for mitochondrial stress. Genes enriched in the nucleus, peroxisome, Golgi and ER were identified, with regulators of organelle biogenesis eliciting the highest mitochondrial stress. Focusing on genes that induced high reporter signal, stable knockout cell lines were created to examine the effects of peroxisomal, ER and Golgi biogenic stress on mitochondrial dynamics. In addition, the author developed an accessible focused ion beam scanning electron microscopy (FIB-SEM) analysis method to generate unbiased, quantitative and fully visualizable profiles of organelle morphologies, including the alterations in organelle membranes and interactions between organelles when their biogenesis is perturbed. Finally, they established a comprehensive multi-omics pipeline (transcriptomics, proteomics, lipidomics and glycomics) and showed how the dysfunction of a single organelle induces a cell-wide network of organelle dysfunctions. These results indicated a commonality in mechanisms by which alteration of biogenesis of other organelles can cause mitochondrial dysfunction, highlighting the need to consider the cellular system as an interconnectome with high connectivity and interdependence.

4

Antibodies targeting the fusion peptide on the HIV envelope provide protection to rhesus macaques against mucosal SHIV challenge

Amarendra Pegu, Sarah E, *et al.*

Science Translational Medicine 2024

As known, the fusion peptide (FP) on the HIV-1 envelope (Env) trimer is a conserved site of vulnerability that can be targeted by broadly neutralizing antibodies (bNAbs). Despite this, the extent of protection conferred by FP-directed antibodies in the context of mucosal infection is still unclear. I this study published in Science Translational Medicine, Dr. Pegu and colleagues demonstrate that such fusion peptide–directed antibodies can protect primates from acquisition of simian-HIV (SHIV) by mucosal challenge. In details, macaques were intravenously infused with one of three NAbs interacting with the fusion peptide: one isolated from a person living with HIV-1 (VRC34.01) and two from macaques immunized with fusion peptide and soluble Env trimer (DFPH-a.15 and DF1W-a.01). After the infusion, the monkeys were challenged intrarectally with a SHIV, carrying Env derived from the isolate BG505 of clade A and engineered to interact well with simian receptors, a virus that vigorously infects macaques at the chosen dose. All control monkeys, which received no antibody, became infected. In contrast, animals infused with VRC34.01or highest DF1W-a.01 doses were protected, whereas those infused with DFPH-a.15 were partially protected. Overall, the protective serum neutralization titers observed in these animals were similar to what has been observed for other bNAbs in similar SHIV infection models and in human clinical trials, supporting further development of both anti-FP antibody therapies and vaccines designed to elicit anti-FP humoral responses.