University of Zurich[UZH] | ETH zürich

SCOOPED

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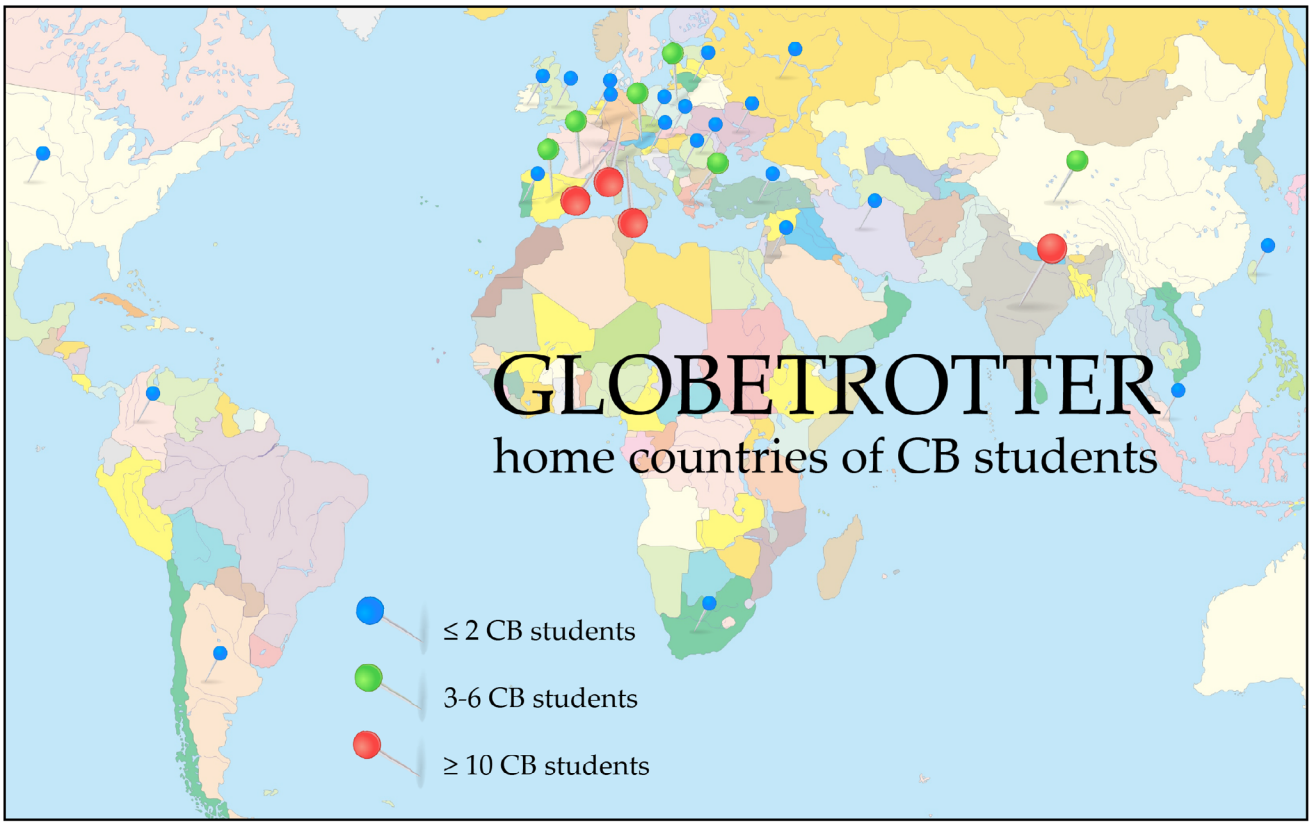
The Cancer Biology PhD Program Newsletter



Dear Readers,

This is the third issue of SCOOPED, the biannual Cancer Biology PhD program newsletter.

So far, contribution to the newsletter has been fantastic and we would like to thank everybody involved for making the effort. However, the success of this newsletter will always depend on your assistance, ideas and feedback. We therefore encourage you to contact us when:

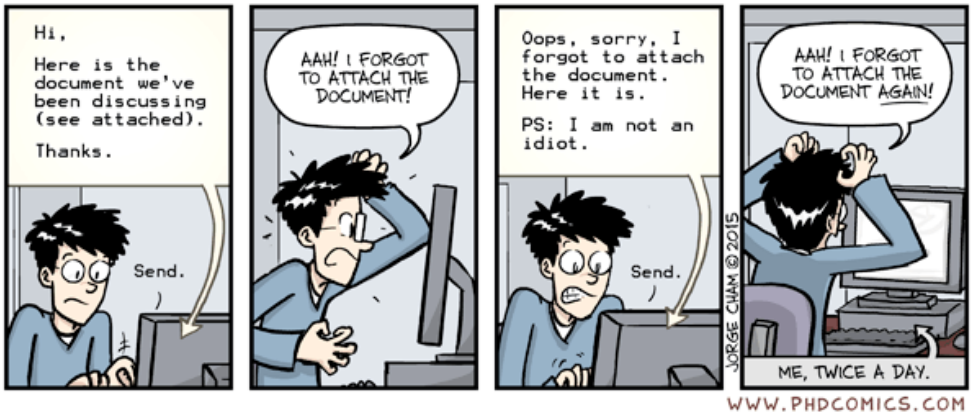
- **you publish a paper you would like to share with the cancer research community in our «Research Highlights» section**
- **you develop an exceptional technique other labs could profit from, which you would like to explain in more detail**
- **you go to a conference and would like to write a brief report about the highlights of the meeting**
- **you have some other type of information you would like to communicate**
- **you want to give us some general feedback**

In addition, we are looking for motivated people who are interested in joining the newsletter team. Please contact us if you would like to contribute to the next issue of SCOOPED by collecting information, conducting interviews or writing articles:

CancerBioNews@gmail.com

We hope you enjoy reading this issue :)

Corina Schmid, Michael Flori, Hannah Parker, Ana Antunes and Karthiga Kumar



"Piled Higher and Deeper" by Jorge Cham www.phdcomics.com

Recent Publications by CB PhD Students

Anna Rinaldi - Group PD Dr. Jean-Pierre Bourquin

We identified vulnerable genetic targets and novel potent agents for a rare, but incurable subtype of acute lymphoblastic leukemia. Thanks to a joint international project, it was possible to combine genomic and functional data generated by using the drug screening platform and xenograft model established in our lab.

Genomics and drug profiling of fatal TCF3-HLF-positive acute lymphoblastic leukemia identifies recurrent mutation patterns and novel therapeutic options

Ute Fischer§, Michael Forster§, Anna Rinaldi§, Thomas Risch§, Stéphanie Sungalee§, Hans-Jörg Warnatz§, Beat Bornhauser, Michael Gombert, Christina Kratsch, Adrian Stütz, et al.,
§ equal contributions to this work – listing in alphabetical order

Abstract:
TCF3-HLF–positive acute lymphoblastic leukemia (ALL) is currently incurable. Using an integrated approach, we uncovered distinct mutation, gene expression and drug response profiles in TCF3-HLF–positive and treatment-responsive TCF3-PBX1–positive ALL. We identified recurrent intragenic deletions of PAX5 or VPREB1 in constellation with the fusion of TCF3 and HLF. Moreover somatic mutations in the non-translocated allele of TCF3 and a reduction of PAX5 gene dosage in TCF3-HLF ALL suggest cooperation within a restricted genetic context. The enrichment for stem cell and myeloid features in the TCF3-HLF signature may reflect reprogramming by TCF3-HLF of a lymphoid-committed cell of origin toward a hybrid, drug-resistant hematopoietic state. Drug response profiling of matched patient-derived xenografts revealed a distinct profile for TCF3-HLF ALL with resistance to conventional chemotherapeutics but sensitivity to glucocorticoids, anthracyclines and agents in clinical development. Striking on-target sensitivity was achieved with the BCL2-specific inhibitor venetoclax (ABT-199). This integrated approach thus provides alternative treatment options for this deadly disease.

Read full article here
Nat Genetics. 2015 Sep;47(9):1020-9

Julia Pizzolato - Group Prof. Dr. Josef Jiricny

Here we studied how three endo/exonucleases with similar biochemical properties, EXO1, FAN1, and FEN1, process synthetic substrates resembling replication forks blocked by DNA interstrand cross-links (ICLs). We found that FAN1 is the only one of the three nucleases to be able to unhook ICLs in this setting, meaning that it can degrade the DNA 5'-3' even in the presence of an ICL. Cell-based assays further confirmed the functional importance of this unusual activity in vivo.

FANCD2-associated Nuclease 1, but Not Exonuclease 1 or Flap Endonuclease 1, Is Able to Unhook DNA Interstrand Cross-links in Vitro

Julia Pizzolato, Shivam Mukherjee, Orlando D. Schärer and Josef Jiricny

Abstract:
Cisplatin and its derivatives, nitrogen mustards and mitomycin C, are used widely in cancer chemotherapy. Their efficacy is linked primarily to their ability to generate DNA interstrand cross-links (ICLs), which effectively block the progression of transcription and replication machineries. Release of this block, referred to as unhooking, has been postulated to require endonucleases that incise one strand of the duplex on either side of the ICL. Here we investigated how the 5' flap nucleases FANCD2-associated nuclease 1 (FAN1), exonuclease 1 (EXO1), and flap endonuclease 1 (FEN1) process a substrate reminiscent of a replication fork arrested at an ICL. We now show that EXO1 and FEN1 cleaved the substrate at the boundary between the single-stranded 5' flap and the duplex, whereas FAN1 incised it three to four nucleotides in the double-stranded region. This affected the outcome of processing of a substrate containing a nitrogen mustard-like ICL two nucleotides in the duplex region because FAN1, unlike EXO1 and FEN1, incised the substrate predominantly beyond the ICL and, therefore, failed to release the 5' flap. We also show that FAN1 was able to degrade a linear ICL substrate. This ability of FAN1 to traverse ICLs in DNA could help to elucidate its biological function, which is currently unknown.

Read full article here
J Biol Chem. 2015 Sep 11;290(37):22602-11

Recent Publications by CB PhD Students

Karthiga Kumar - Group Dr. Martin Baumgartner

We have developed an Automated Cell Dissemination Counter (aCDc) to precisely quantify cell migration and dissemination in 2D and 3D environments. aCDC is a platform consisting of cell-based assays (in 2D and 3D), imaging devices for aquisition and software solutions for the quantification of the imaging data. aCDc is versatile and can be downloaded on any PC or Mac computers via the following link:
http://www.infozentrum.ethz.ch/uploads/user_upload/Software/
Using this new approach, we have studied the effect of various growth factors and cytokines on medulloblastoma cell dissemination. aCDc also enables detection of sensitivities to growth factors or inhibitors directly in primary tumour cells from patients or patient-derived xenografts.

Computer-assisted quantification of motile and invasive capabilities of cancer cells
Karthiga Santhana Kumar, Max Pillong, Jens Kunze, Isabel Burghardt, Michael Weller, Michael A. Grotzer, Gisbert Schneider and Martin Baumgartner

Abstract:
High-throughput analysis of tumour cell dissemination and its control by extrinsic and intrinsic cellular factors is hampered by the lack of adequate and efficient analytical tools for quantifying cell motility. Oncology research would greatly benefit from such a methodology that allows to rapidly determine the motile behaviour of cancer cells under different environmental conditions, including inside three-dimensional matrices. We combined automated microscopy imaging of two- and three-dimensional cell cultures with computational image analysis into a single assay platform for studying cell dissemination in high-throughput. We have validated this new approach for medulloblastoma, a metastatic peadiatric brain tumor, in combination with the activation of growth factor signalling pathways with established pro-migratory functions. The platform enabled the detection of primary tumour and patient-derived xenograft cell sensitivity to growth factor-dependent dissemination and identified tumour subgroup-specific responses to selected growth factors of excellent diagnostic value.

Read full article here
Sci Rep. 2015 Oct 21;5:15338

Call for Papers

We would like to continue the section «Research Highlights» in the next issue of SCOOPED. The idea is to briefly highlight work that you have published as first author during your PhD in order to provide others with an overview of the research topics of the PhD program.

If you would like to share your recent publication with the cancer research community using this platform, please send the abstract and concise summary/significance (no more than 300 characters) of your work to:

CancerBioNews@gmail.com

Live-Cell Cancer Biobanking in Zürich

«All science is either physics or stamp collecting» Ernest Rutherford

by Prof. Dr. Mitchell Levesque

The famous physicist and Nobel Laureate Ernest Rutherford supposedly made this remark to describe the difference between physics and all the other sciences. Should we, as biologists, be insulted? Did he suggest that physics is the only true science because it alone involves theory, deduction, mathematical modelling, and hypothesis testing?

Ernest Rutherford died in 1937, which is about when the era of modern experimental biology was born. So, to his credit, up until the 20th century there had been a long tradition of, essentially, stamp collecting in biology. During the Victorian period, Wunderkammer or cabinets of curiosities were used to display collections of natural oddities, and the world's natural history museums today are filled with the vast plant and animal collections of Renaissance philatelists or stamp collectors.

But the collecting expeditions of famous naturalists also had a legitimate scientific purpose. The breadth of these collections and the diversity of natural variation observed across the globe by Linnaeus, Humboldt, Darwin, and Wallace allowed them to better understand and classify living organisms, place them in a historical context, and develop the theory of natural selection.

So what about cancer? Certainly, biobanking is as close to stamp collecting as you can get. The systematic collection of tumor material is usually not hypothesis-driven and most of the samples have not historically even been used for experimentation. But that is changing.

Molecular profiling experiments (i.e. the use of various pan-omics assays) are now revealing the diversity of cancer types and sub-types that had been previously grouped together. For instance, a recent paper published in Cell by The Cancer Genome Atlas (TCGA) identified 4 major molecular subtypes of cutaneous melanoma from 318 patients. The further analysis of epigenetic marks, miRNAs, transcriptomes, or combinations of subsets of these features will undoubtedly reveal many more subgroups that may be relevant for tumor progression or therapeutic outcome, once they are better understood. However, because these analyses were all done on frozen patient samples they are only useful as descriptive classification tools (similar to the botanical collections of Linnaeus) and hypothesis generation. And that is why we collect cell lines: to better represent the natural diversity of cancer subtypes, and as functional tools for hypothesis testing.

A large collection of well-characterized and diverse cell lines is the essential basic research tool for the next era of precision medicine. That is, if the unique features of a patient's disease are to play a role in treatment decisions, then we need to have a much better functional understanding of what consequences those features have on disease progression. Moreover, we need a panel of cell lines that can recapitulate the actual heterogeneity present within and between patients.

Thus, as part of the University Research Priority Program in Translational Cancer Research (URPP), we have a mandate to build a live-cell biobank in Zürich that will provide the basic and translational research tools that are required for this endeavor.

Together, the Departments of Dermatology and Pathology at the University of Zurich Hospital (USZ) have spent the last two years optimizing protocols to more efficiently generate early passage cultures from many cancer types from consenting patients at the USZ. Currently, we have about 1000 early passage melanoma cultures including cells from primary tumors, various distant metastatic sites, and from multiple time-points of targeted therapy. A smaller subset of these lines is being fully profiled at the genomic, transcriptomic, and epigenetic level, and are available to the research community upon request. In addition, the Department of Pathology has available 75 authenticated cell lines and 50 early passage cultures from a variety of cancer types. More information can be found on the URPP website:
http://www.cancer.uzh.ch/research/Three.html

Thus, while the era of taxonomic collection and classification may be tapering off for Natural Historians, Cancer Biologists are just beginning to understand that each cancer type may also require similar large-scale collection efforts to establish more sophisticated cancer subtype nomenclatures. Technological developments will continue providing more accurate tools to generate high-dimensional datasets for new molecular features, but translating these data into the clinic will require in vitro reagents that reflect the actual diversity of cancer sub-types that are present in and between patients.

Thus, stamp collections can be curiosities like the Victorian Wunderkammer, but they can also be a reference set for an encompassing formal classification system. Thanks to efforts like the TCGA and ICGC, the "genomic landscape" papers are providing this new taxonomy for many cancers types.

Now the next challenge will be to test the hypotheses generated by these classifications into functional experiments using an equally well characterized set of cell lines and in vivo models. Then, although we may never convince Ernest Rutherford that what we do is something other than stamp collecting, we will at least be able to reduce the information present in our collections to a set of causal relationships and actionable targets that may someday save lives.

Mass cytometry - Instant discovery tool for biology and medicine?

by Dr. Vinko Tosevski, Group of Prof. Dr. Becher

Today's modern biomedical science critically depends on advanced analytical instrumentation to support the new discoveries. If we stopped for a moment and thought about the "perfect" analytical platform, what would it be? For the sake of discussion, I guess we could all agree it needs to have a single cell resolution. Being able to analyze cells in a living tissue or as close to that as possible would be advantageous too. It would also need to be sensitive and quantitative enough to pick up differences in cellular physiological states (signaling, protein production) and have sufficient capacity to capture multitude of different readouts for each cell simultaneously. Being able to do this in high-throughput manner would also be great… To the best of my knowledge, such an "ideal" analytical platform does not exist and I personally don't expect to see one in the coming years either. That means we still have to be combing an array of methodologies to "get the job done", taking into account their different advantages and limitations. To the toolbox of existing and well known methods (flow cytometry, microscopy, gene expression analysis, mass spectroscopy, to name a few) I am adding a new one – mass cytometry!

Mass cytometry is an analytical platform that takes the sample preparation workflow typical of flow cytometry (or microscopy, in case of newly developed imaging mass cytometers) and combines it with the detection capacity of atomic mass spectroscopy. This is made possible through usage of antibodies labelled with purified metal isotopes. In short, after introduction into the instrument, the sample is vaporized, broken down, atomized and ionized. The resulting ion cloud is processed in a way that gets rid of the biological elements (carbon, nitrogen, etc) and leaves only the metal isotopes above a certain mass (ones used for labeling the antibodies). The composition of the ion cloud is analyzed by time-of-flight mass analyzer, from which the information about the presence of a particular epitope is inferred (Figure 1).

The first instrument prototype was described in 2009 (1), with the first high-impact work performed with the new platform published by Science in 2011 (2). Since then, a number of other, high impact publications based on mass cytometry have been published, additionally fueling the great excitement about this technology in the field of biomedical sciences (3).

Looking at (2), the authors have managed to quantitate, at the single cell level, 13 „core" lineage markers, 18 subset-specific surface markers and 18 intracellular epitopes across 13 different ex-vivo stimulation conditions! They were able to reliably delineate 29 different cell subsets and examine their response to various stimuli. The power of such an approach was exemplified by their notion that a small population of cells (plasmacytoid dendritic cells) did not respond to the drug treatment in the same way as all the other cell types in that experimental system have. To gain such a fine grained insight would have taken much longer with any other technique (if at all).

The capacity to measure great number of parameters simultaneously prompted for the development of new tools for data analysis and started shifting focus away from hypothesis-driven towards exploratory analysis approaches, which definitely facilitates new discoveries. New algorithms for mining and visualization of mass cytometry data are constantly being developed and currently represent a very active field of work.

Moving away from fluorochrome-labelled antibodies typical for flow cytometry was a neat solution that allowed for the increase in the number of simultaneously measured parameters without the issues of spectral overlap and associated loss of sensitivity. However, the price of such a transition was paid elsewhere, as the design requirements for implementing an atomic mass spectrometer as a detection module imposed some restrictions on the overall instrument performance. Owing to this, a mass cytometer will have slightly lower per-channel sensitivity, lower sample transmission efficiency and also lower sample acquisition speed compared to a classical flow cytometer (4). These differences (together with a current almost exclusive requirement for an antibody-based detection) do not allow a directing porting of just any flow cytometry experiment to a mass cytometry platform. Instead, the differences need to be factored in and possibly a new experiment design worked out. However, once passed that hurdle, mass cytometry becomes truly powerful tool for biological discovery. At the moment, the capacity for multiplexed measurement is limited by the availability of sufficiently purified metal isotopes and currently stands at around 50 parameters.

The University of Zurich made a strategic decision to invest in mass cytometry in 2012 and currently supports three such instruments on the Irchel campus. One of them is located in the shared resource laboratory (Mass Cytometry Facility) and every researcher is welcome to inquire about further possibilities or even perform a test experiment practically free of charge.

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3. Cheung RK, Utz PJ. SCREENING: CyTOF—the next generation of cell detection. Nat Rev Rheumatol. 2011 Jul 26;7(9):502–3.

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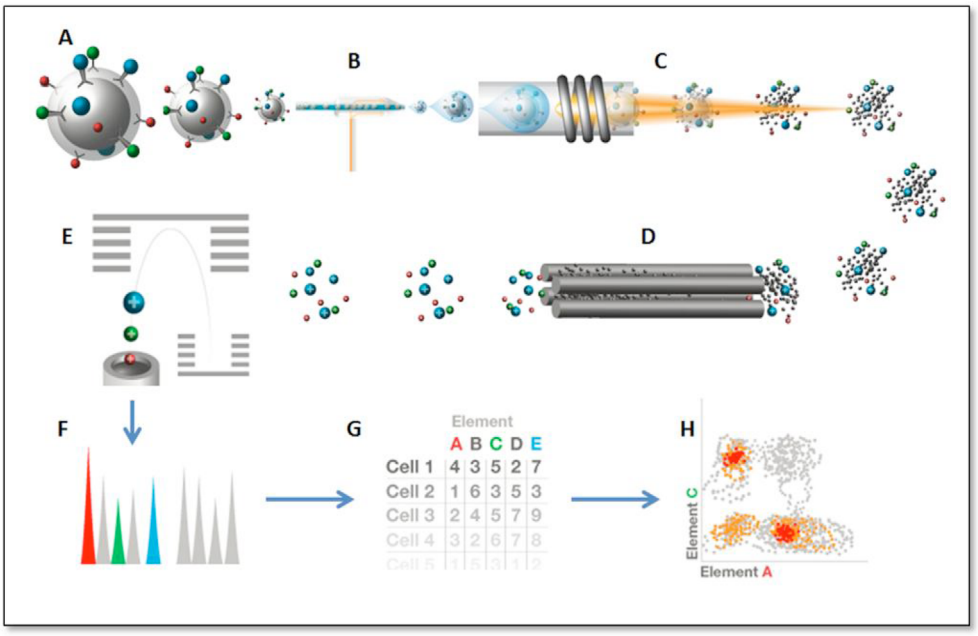


Figure 1: Mass Cytometry Workflow
A liquid sample containing cells labeled with heavy metal isotope conjugated probes (A) is introduced into the nebulizer (B) where it is aerosolized. The aerosol droplets are directed into the ICP torch (C) where the cells are vaporized, atomized and ionized. Low mass ions are removed in the RF Quadrupole Ion Guide (D), resulting in a cloud of ions enriched for the probe isotopes. The ion cloud then enters the Time-of-Flight (TOF) chamber (E) where the probes are separated on the basis of their mass to charge ratio as they accelerate towards the detector. The time-resolved detector thus measures a mass spectrum (F) that represents the identity and quantity of each isotopic probe on a per-cell basis. Data is generated in .fcs format (G) and analyzed in third-party software programs (H) (5).

aCDc - an automated cell counting tool

by Karthiga Kumar - Group Dr. Martin Baumgartner

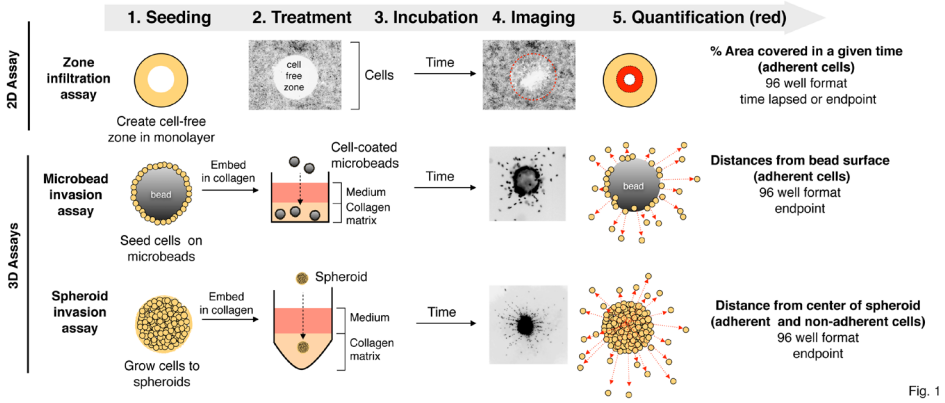


Figure 1: Schematic overview of 2D and 3D cell base motility and invasion assay

Metastatic dissemination of tumour cells is the leading cause of death in cancer patients, and understanding of the causative events of cancer metastasis will be essential for developing effective targeted therapies (1, 2). The identification of the relevant cell migratory processes remains a formidable challenge because of the difficulties to reproducibly track altered cell motility at high spatial and temporal resolution (3). Oncology research and oncologists would greatly benefit from a technique that allows rapid determination and quantification of motile behaviour of cancer cells under different environmental conditions, including inside three-dimensional matrices.

To overcome the aforementioned challenges in cell motility studies, our laboratory has established automated cell dissemination counter (aCDc). aCDc combines automated microscopy imaging of two- and three-dimensional cell cultures with computational image analysis in a single assay platform for studying cell dissemination in high-throughput. aCDc consists of two parts: a) 2D and 3D cell motility / invasion assays and b) software solutions to effectively quantify the 2D and 3D assays.

A) 2D and 3D cell motility / invasion assays:

To explore extrinsic and cell intrinsic factors controlling collective cancer cell migration in 2D, we have optimized the zone exclusion assay, which provides circular cell free surfaces of identical area and allows the quantification of area covered by cells over time (Figure 1).

To quantify cell dissemination and invasion in 3D, we established the microbeads invasion and the spheroid cell invasion assays, that measure how far cells have disseminated from a defined reference point into a matrix (Figure 1). The reference points are the surface of the microbeads and the centre of the spheroid, respectively.

Figure 1: Schematic overview of 2D and 3D cell based motility and invasion assay.

B) Software:

In addition to the wet lab assays, aCDc consists of three unique software tools (4), which we developed in collabration with Prof. Schneider's group of the Institute of Pharmaceutical Science of the ETH and which we named according to their working principles: aZEcs (automated Zone Exclusion counter software), aMDIcs (automated Microbead Dissemination/Invasion counter software) and aSDIcs (automated Spheroid Dissemination/Invasion counter software). In brief, the workflow of aCDc includes providing the microscopic images obtained from the 2D and 3D assays to the software and the software, that automatically quantifies the images and generates numerical values that quantitatively represent cell migration and invasion in 2D and 3D environments.

The working principle of each of the software is as follows:

aZEcs: For automatic evaluation of zone exclusion, the algorithm determines the percentage of a cell-free area at time point T1. The algorithm then compares the T1 image (image taken at time point T1 – before the cell have begun to migrate) with the corresponding T2 image (image taken at time point T2 – after the cells have migrated) and determines the area that remains uncovered by cells at time point T2. The remaining cell-free area at time point T2 is expressed as the percentage of area covered by the cells, i.e. percentage of cells migrated at a given time period (Figure 2). aZEcs takes into account pipetting artefacts and eliminates the defects before quantification, a feature not found in any other available software.

aMDIcs: For automatic evaluation of cell invasion using the microbeads invasion assay, aMDIcs converts the acquired images to black and white. The algorithm then systematically scans the whole image for circular, white structures (beads). After scanning the image, the algorithm recursively selects the beads with the highest coverage and extracts them from the original image for analysis (Figure 2). From the selected beads, the distance of each cell disseminated from the bead surface is calculated. A histogram depicting the cumulated means is generated and a log-file, containing the average of the distance disseminated by the cells and standard deviations is produced.

aSDIcs: For automatic evaluation of cell invasion using the spheroid invasion assay, the images are also converted into a black and white image. In contrast to the microbeads invasion assay, in the spheroid invasion assay no bead surface is available as a reference point. The spheroid is therefore converted into a single cluster of white pixels and the centre of this cluster defines the reference point for distance quantification (Figure 2). A histogram and a log file containing the average of the distance disseminated by the cells are generated similarly to aMDIcs.

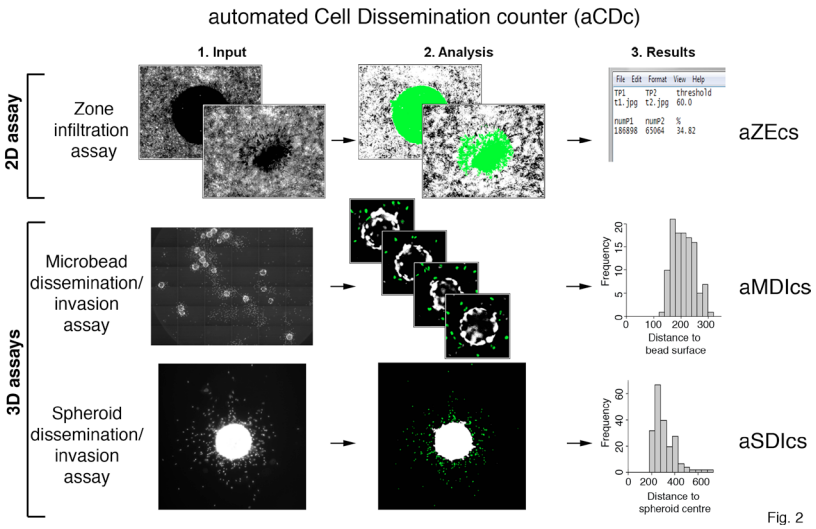


Figure 2: Schematic overview of the working principle of aCDc software tools – aZEcs, aMDIcs and aSDIcs

What have we accomplished with aCDc?

- We determined the differential impact of growth factors and cytokines present in the tumour microenvironment on medulloblastoma (MB) cell migration and invasiveness.
- We used the differential impact of growth factors and cytokines on MB patient derived xenografts (Med PDX) cells and MB primary tumour cells for motility based profiling (sub-grouping).
- In addition, we are investigating the cross-talk between various growth factor induced signalling pathways in MB.

Potential applications of aCDc:

- aCDc is versatile. It can be used to quantitatively and qualitatively describe the cell migration and invasiveness of any solid tumour.
- Effects of growth factors, cytokines and/or inhibitors on the migratory and invasive behaviour of any solid tumour can be studied.
- aCDc is an excellent tool to identify the downstream effectors of signalling pathways that induce cell invasiveness in cancer cells. These downstream effectors are attractive druggable targets for an effective anti-metastatic therapy.
- aCDc can arbitrate the cross-talk among various invasiveness related signalling pathways.
- aCDc can be used to elucidate the additive, synergistic or antagonistic effects of anti-metastatic drug combinations, which is very critical in cancer therapy.

Advantages of aCDc:

- aCDc is easy to use. Minimal knowledge in bioinformatics is required to use this tool.
- aCDc is readily available and can be downloaded from the following weblink: http://www.infozentrum.ethz.ch/uploads/user_upload/Software/.

aCDc is compatible on any operating system and can be run on any Mac, Windows or Linux systems.

- Quantification using aCDc is fully automatic, fast and precise. Approximately 100 images can be quantified in less than 5 minutes!!!
- aCDc saves the original and the processed images as log files, which can always be traced back to confirm appropriate quantification.
- aZECs, aMDIcs and aSDIcs comes with an additional file called the "parameters file". This file has a set of parameters like the threshold, which users can modify according to their image quality. This aids a more accurate quantification of the images.

References:

1. Wells, A., et al., Targeting tumor cell motility as a strategy against invasion and metastasis. Trends Pharmacol Sci, 2013. 34(5): p. 283-9.
2. Palmer, T.D., et al., Targeting tumor cell motility to prevent metastasis. Adv Drug Deliv Rev, 2011. 63(8): p. 568-81.
3. Zimmermann, M., C. Box, and S.A. Eccles, Two-dimensional vs. three-dimensional in vitro tumor migration and invasion assays. Methods Mol Biol, 2013. 986: p. 227-52.
4. Kumar, K.S., et al., Computer-assisted quantification of motile and invasive capabilities of cancer cells. Sci Rep, 2015. 5: p. 15338.

Whatever became of...

...Nitin Kumar - Quantitative Data Scientist at Quantum Business Intelligence Services, Zurich, CH

Could you tell us in which group of the CNZ you graduated, and how you proceeded after obtaining your PhD?
I did my PhD with Dr. Michael Baudis at the Institute of Molecular Life Sciences, University of Zurich. After completing my PhD, I stayed in the same lab for a post-doc for 9 months. Afterwards, I did a postdoc at UKBB Basel in the field of mathematical and statistical medical biology in the group of Urs Frey and under the supervision of Dr. Edgar Delgado-Eckert.
Could you give us a short description of your current position, including daily responsibilities?
I am currently working as a Quantitative Data Scientist (Consultant) at Quantum Business Intelligence Services, Technoparkstrasse – 1, Zurich. My work involves development and testing of models to answer data analysis related questions for various clients.
Why did you choose this position? Because I love number crunching and what better profession than being a data analyst to crunch numbers.
Where did you apply for your current position and what was the application process?
I applied directly through the company website. The application process consisted of 3 rounds of interview including a presentation of a small data analysis project which I had to do.
Are you happy with your current position and to whom would you recommend it?
I am quite happy as I really like my work. I would recommend my position to people who know programming (or like it), maths, stats, IT, behavior sciences and data analysis.
What are your plans for the future? I want to grow in what I do, it can involve being a project manager, to director, to any high level position anyone can think of.

New CNZ Members 2016

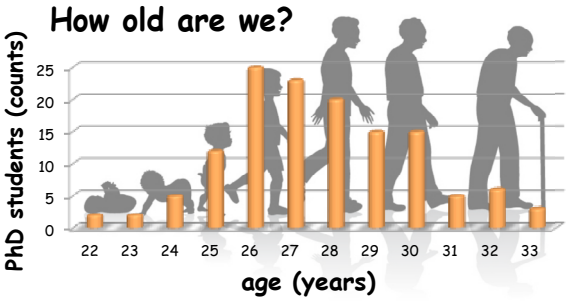
Prof. Dr. Lorenza Penengo, Institute of Molecular Cancer Research

Can you give us a brief overview of your career (where/what did you study, what were the different stages of education/work you passed until you moved to Zurich)?
I studied Biology at the University of Turin (Italy). Afterwards, I started my PhD at the University of Piemonte Orientale (Italy), and I ended up in Israel at the Weizmann Institute of Science, where I completed my PhD project. This was a terrific personal and professional experience. Then I moved back to Italy for my postdoc in the lab of Pier Paolo Di Fiore at the IFOM-IEO Campus in Milan. At the end of the postdoctoral period, I was selected for a permanent position as Assistant Professor at the University of Piemonte Orientale, where I initiated my independent lab.
When did you move to Zurich?
I moved to the University of Zurich, at the Vetsuisse Faculty, in March 2014. During the first months I was commuting back to Italy every week to accomplish my teaching duties and to lead my group that was still in Italy. At the end of 2014, I finally moved to IMCR where I launched my new lab.
When did you join the Cancer Network Zurich and why?
I joined the CNZ at the beginning of 2015. I welcomed the idea to be part of a network that brings together different points of view, expertize and experimental approaches on the same topic, i.e. cancer research.
How many people are currently working in your lab?
My lab in Zurich is currently formed by 4 people: a postdoc, a PhD student, a Master student, and me.
What is the main focus of your research?
My research is focused on the regulation of DNA damage response and DNA repair by ubiquitin and ubiquitin-like modifications. I am also interested in understanding how these mechanisms are modulated (or altered) in different pathological contexts, such as infection and chronic inflammation.
What was your most memorable lab experience?
It was during the period of transition to independence. I started working on few factors expected to play a role in endocytosis, and I ended up with the identification of a crucial factor of the DNA damage response. Although this implied landing in an extremely competitive research field, this has brought a high level of excitement in my newborn lab and has changed the profile of my research from that point on.
What is the motivation that keeps you going?
We are doing the most exciting, interesting and stimulating job I could ever imagine. Everyday we have unforeseen challenges to face; overcoming them within the team, with good ideas and with positive attitude, is an amazing experience.
Which advice would you give a fresh PhD student?
Science is for open-minded people. Don't be dogmatic; try to see your scientific problem from different perspectives. Many obstacles are on the way of your success, and you have to pass through all of them to reach your goal. So, be as positive as possible, and accept your failures because they are part of the game.
What is the last book you have read?
"Maya's notebook", Isabel Allende and "L'infinito viaggiare", Claudio Magris.

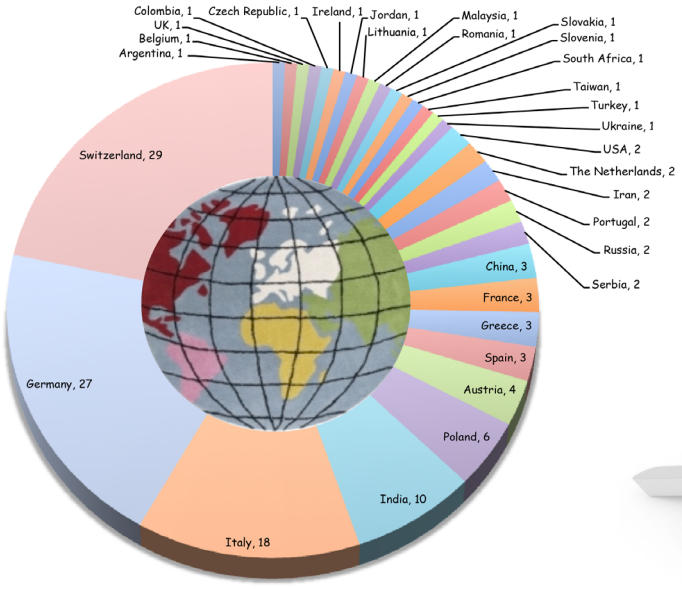
Richard Lutz

Institute of Molecular Cancer Research

Where do you come from and how long have you been in Switzerland? Did you come to Switzerland for your PhD?
I am from Atlanta, GA USA. After studying for my Masters in Germany, I moved to Switzerland for my PhD.
What do you like about Zürich and miss most about your home country?
I really like the fact that Zürich is in close proximity to the wonderful nature of Switzerland where one can enjoy many outdoor activities. What I miss most about home is my family and friends.
What is your favourite place and/or activity in Zürich?
My favorite place in Zürich would be anywhere near the lake or river, which coincides with
my favorite things like cycling and swimming.
Would you like to continue living in Switzerland after you finish your PhD or move (where?)?
When I first came to Switzerland for the interviews, I was not sure that I could live here because I was afraid of the difference between Germany, which I had grown accustomed to.
However, after living here for two years, I really do hope I will have the opportunity to stay in Switzerland after my studies.



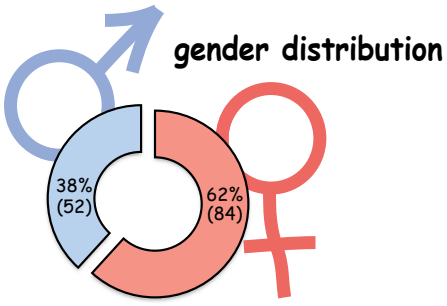
Where are we from?

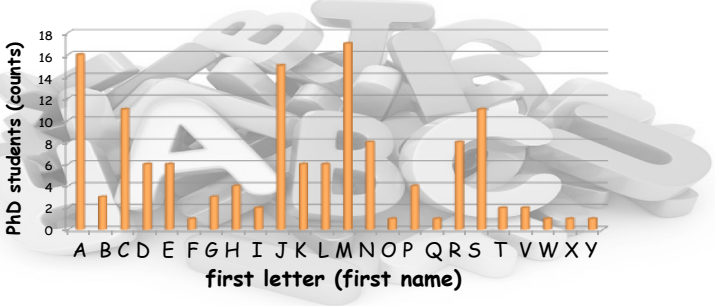


Hind Hashwah

Institute of Molecular Cancer Research

Where do you come from and how long have you been in Switzerland? Did you come to Switzerland for your PhD?
I am Palestinian; I was born and raised in East Jerusalem where my family currently still resides. I have been in Switzerland since 2011. I first came to Basel for my MSc degree in Biotechnology at the department of Biosystems Science and Engineering (D-BSSE) of the ETH Zürich, and subsequently decided to stay in Switzerland for my PhD.
What do you like about Zürich and miss most about your home country?
I find Zürich to be a very diverse city, especially in terms of its natural landscape and its people. It is also very international, thus offering a unique advantage to foreigners who wish to experience Swiss culture in a multicultural city. Despite the numerous things I like about Zürich, I mostly miss the sea and the warm weather of my home country. Our summers are dry and last for around 6 months; hence one can enjoy the hot weather for long periods of time. I also miss the delicious (non-cheese-dominated) food.
What is your favourite place and/or activity in Zürich?
I think my favorite place in Zürich is the lake, because it is always lively no matter the season or the time of day. I enjoy it most on hot days when people bathe and tan on its shores while enjoying a cold drink and a chat.
Would you like to continue living in Switzerland after you finish your PhD or move (where?)?
I have still not decided where I would like to live after my PhD, but staying in Switzerland is a
viable and attractive option. On the other hand, my plan was always to go back to my home country and apply the knowledge I have gained abroad to help strengthen the Palestinian education system and economy, perhaps as a modest and non-violent way of contributing to the resistance against occupation in our continuing struggle for independence.





CB PhD Program Christmas event

Every year the Cancer Biology PhD program organizes a Christmas event for all its PhD students. This traditional social event is a great way to meet, chat and get to know each other and new PhD students. And so this year, despite the cold, almost 90 PhD students joined. The starting point was at the Weihnachtsdorf at Bellevue, where the lights, Christmas trees and the smell of fondue and Glühwein welcomed us with a perfect Christmas atmosphere.
The ice-skating rink, our first destination, was waiting for us. With a lot of fun, first skeptical rounds, spectacular pirouettes and some Glühwein to keep the athletes warm, we skated into the evening. Afterwards we moved to the Congress Halle nearby to warm up with a delicious cheese fondue. The place was very nicely set up, enabling us to enjoy the dinner and leave the place at the end of the evening fully satisfied.

Impressum

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