"The IGC places very strong emphases on education, independence, personal development, interaction, sharing, collaboration, generosity, criticism, breadth of scientific knowledge and understanding, and the place of science and scientists in society."

Jonathan Howard, Director of Instituto Gulbenkian de Ciência

Cover Image:
Mouse fibroblasts infected with Toxoplasma gondii
Host-Pathogen Co-evolution group and Electron Microscopy Facility, IGC
(Image captured at the FEI NanoPort on a FEI Talos in STEM mode)
the director’s introduction

A MANIFESTO FOR THE IGC

The Instituto Gulbenkian de Ciência is a rare institution on the world stage. It is scientifically eminent at an international level in several fields of biology, it is actively and creatively engaged in educational initiatives that continue to have global resonance, it has a strong and mutually supportive relationship with the larger community in which it is embedded, and it sustains, and is sustained by, its members through an unparalleled sense of belonging to something rare and valuable. Finally it is supported by a large and generous philanthropic foundation, the Fundação Calouste Gulbenkian, whose humane character allows us to develop our work within a corresponding idiom.

The largest factor responsible for generating the high international esteem the IGC has achieved was the success of the brilliant PhD programme introduced by António Coutinho in 1993. This visionary initiative was widely praised and indeed it once more. But there is the same sort of tension between the science of asking questions and the science devoted to applying the answers to these questions in the interests of mankind. Both are essential, but in our institute there are two large general dichotomies that must be taken seriously.

(1) Specialisation versus breadth: There is a strong modern tendency towards research specialisation. Research challenges are complex and need focused effort. Contemporary publishing practices are dominated by the hunt for impact and force scientists to do much more experimentation around a specific finding than earlier, in order to publish a single paper in a reputable journal. To meet these demands, group leaders feel the need to increase the size of their labs so that the research problem can be surrounded quickly. The knowledge that other groups are tackling the same problem adds to the pressure. Taken together these forces push individual research groups, and the institutions that contain them, into bidding for continuous growth. In some cases they also contribute to inappropriate competitive behaviour, to professional stress and to fraudulent work. There are, however, other pressures that push in the opposite direction and deserve much more attention. Science, and biology with it, is advancing at a tremendous rate. Areas for major progress change all the time, problems are solved or are reduced to minutiae. To stay successful a young scientist must be adequately equipped to evolve intellectually with a whole field, not just to solve the problem at hand. This demand clearly opposes specialisation. Breadth of knowledge and understanding are also essential tools in the solution of specific problems. Large group sizes and intense competition oppose this healthy process. So there is a tension between the fulfilment of short-term goals, favouring specialisation, and long-term productivity, favouring breadth. Both are essential, so a balance must be found. The analogy, if one is needed, is to be found in the evolution of life: hyperspecialisation is the precursor to extinction. The dinosaurs died out while the nimble little mammals scurrying around at their feet were the inheritors. Of course they too had to be good at something, and they chose thinking!

(2) The application of discovery: Before application there must be discovery. Translation is possible only when there is something to translate. This old ground that has been worked over so often that it should not be necessary to rehearse it once more. But there is the same sort of tension between the science of asking and answering questions and the science devoted to applying the answers to these questions in the interests of mankind. Both are essential, but in our institute a balance should be found.

The growth of the IGC into a primary research institute in its own right was completed just when António announced his intention to stand down. I inherited something that had not existed since 1993, namely a mature research institute, young in its maturity but mature nevertheless. To nurture this young mature institute was the task that I took on when I became Director and the task that I intend to continue working on.

Two important dichotomies

Because of the impulses that created the IGC as a research institute, it is a most unusual place, the small-group policy, the breadth of science conducted, the sense of community, all these are hard to find elsewhere in institutes of comparable quality. However, research institutes, no matter how special, cannot rely on their distinctive features to stay alive. It is the quality and dynamism of the science that guarantees their real and continuing value. This consideration dominates a director’s decision-making, and how to achieve and maintain it in the modern environment is the key issue. There are two large general dichotomies that must be taken seriously:

...there is a tension between the fulfilment of short-term goals, favouring specialisation, and long-term productivity, favouring breadth. Both are essential, so a balance must be found."
The IGC for the future

The IGC is a research institute that, because of its humane origins, is in a position to balance these major tensions inherent in the progress of science. In doing so the IGC will be seen as an institute aiming for human as well as scientific goals. If only scientific goals are set the IGC runs the risk of losing sight of the underlying humane philosophy of the Gulbenkian Foundation.

This vision is based on the assumption that the Gulbenkian Foundation supports science not for the practical deliverables that scientific activity generates, but for the same reason that it supports the arts, as a cultural activity that enriches the human condition. There is colossal support worldwide for science in the service of application, from national governments and supranational entities like the EU, and in biomedical science also from health oriented charities and foundations like the Wellcome Trust, the Howard Hughes Medical Institute, the Gates Foundation, Cancer Research UK and so on. For science as a humane cultural activity there is very little. Widely in Europe, indeed, the cultural role of the Universities in promoting scientific thinking and generating scientific knowledge has been systematically dismantled. I believe that exactly this should be the role of the IGC, and that it is perfectly equipped to fill it.

What does this role entail? Above all it shifts the questions normally asked about a scientific institution away from “what does it do?” to “how does it do it?” The IGC already has a name, Ciência, that rejects any special answer to the “what” question, very different from other institutes that declare their specialization in their names. Of course we can tell you in detail what we do if you ask, but there is no unifying scientific goal. On the other hand, there are some very characteristic answers to the “how” question which unify the IGC: the IGC places very strong emphasis on education, independence, personal development, interaction, sharing, collaboration, generosity, criticism, breadth of scientific knowledge and understanding, and the place of science and scientists in society. This is not just vaporous piety, but systematically integrated into the programme and into the budget. We make no parallel claim that this distinctive vision of the IGC enables better or more important science than other research organisations with clearly defined scientific priorities. But it is an intrinsic element of our vision that we conduct our science within a more humane framework in direct opposition to the de-humanising forces at work within the modern science business.

Surely there must be a penalty in swimming against the current that now flows strongly towards huge budgets, large hierarchical groups, focused assemblages with clearly-defined goals and intense competition. However we subject our publications and ourselves to the same international peer review process that other institutes do worldwide and we usually do well. The recent evaluation of the IGC as “exceptional” in the national competition for Unidades de Investigação also announces that the IGC vision is compatible with research excellence.

If there is a penalty it is not in the quality of the work we do but in its character. We are unlikely to be the lead authors (though may well have a stake) in the large-scale, multi-author studies characteristic of much modern human clinical research and human genetics, because we don’t command the resources or have the access necessary. Some of these studies are heroic and truly prominent, but they do not fit our spectrum of activity. Scale alone, however, is not the only secret of success in modern biological research, as was emphasized to me a few months ago by Ronald DePinho, the President of the MD Anderson Cancer Center in Houston, Texas, the largest cancer center in the world, with thousands of fine scientists and physicians and nearly a billion annually in research dollars. I asked him whether, in the face of such tremendous constellations of excellence he felt there was any role left for the kind of, unfocused, small-group-based research institute that we have at the IGC. He started by warmly congratulating us for having the IGC, and went on to say he believed such small structures are key ingredients in the research field they are, he said, “where the Nobel Prizes start” and are “the geese that lay the golden eggs”. I add, that he said this out loud in a public meeting.

Criteria for recruitment

I see the IGC as a reference institution for a way of doing science that builds rather than destroys personalities. (...) I am encouraged to believe that the IGC has already a reputation for supporting science in a special way that is attractive to the most original young scientists.
Because such students, post-docs and group leaders are rare, we must devote more effort to finding and attracting them. Our search for Group Leaders has made progress in the right direction. In previous years the IGC might receive 10 - 20 spontaneous applications for group leader. The recent call in 2014 had 129 responses. We reduced this to a short list of 20 and now after a splendid selection colloquium are looking forward to welcome two exceptional young scientists in 2015. It is especially interesting that the IGC attracted applications from several very young scientists whose trajectory as PhD students and post-docs so far has been exactly as eulogised above. I am encouraged to believe that the IGC has already a reputation for supporting science in a special way that is attractive to the most original young scientists.

The unique character of the IGC is not defined by what science is being done, or by its quality, but by the way in which it is being done. The multidisciplinarity is not a mere accident, evidence of a lack of focus, but an intentional means to avoid the destructive effects of specialisation inherent in modern research practice. The IGC rejects the classification of scientists by numerical indicators as guides for hiring or firing, preferring to judge the quality of the science by more subtle criteria. The IGC is concerned that modern trends in doctoral and post-doctoral training are stultifying to creative young minds and generally damaging to the science enterprise. The IGC strongly supports imaginative educational or cultural initiatives that bring science into the community, and by the same token bring community values and culture to the scientists.

The science of the institute is not defined a priori by name or target. Any scientist who does excellent, creative, independent work that resonates with our existing faculty, and where our resource infrastructure is appropriate, is welcome to apply to the IGC. At any time we may have ideas about what new science we would like to see at the IGC, but outstanding quality and sharing IGC values must be the overriding criterion for entry to the IGC.

Jonathan Howard
IGC Director
April 2015

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**FACTS & FIGURES IN 2014**

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**Model systems and human biology**

In the molecular genetic era of the last 75 years of biological science several species of organisms, selected for their convenience, their accessibility and for specific traits that enhanced their utility in specific research domains, have earned the title “model systems”, E. coli, two yeasts, the nematode worm C. elegans, the fruit fly, the zebrafish, the mouse, the flowering plant A. thaliana. During this interval these species have contributed in vast disproportion to everything we have learned about biology. They are experimentally accessible models for all of life, but in recent times, as the clinical imperative has increasingly been perceived as the main justification for biological research, their utility as models for man has been questioned. The organic world around us is the human environment, and it is rash to exclude any first-class research on any organism as beside the point. However the recent development of increasingly general methods for analytical research in biological systems have brought unprecedented access to human biology that the IGC is keen to take advantage of. The study of human biology will certainly bring many advantages in the future, not the least its impact in the discovery of disease mechanisms and in economic value. These are the new challenges that some of the best young scientists want to face, and many will be entering this area. Institutions are aware of this movement that will happen in our times, and the IGC should not stay out of it. This will also embody the contribution of biology to the integration of our knowledge of man, which we will need for the future of the world.

We expect to open a call directed to this end later in 2015.

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**Conclusion**

I believe the IGC is beginning to fulfil a unique vision of a high quality research institute, already judged “a world class institute of which Portugal should be extremely proud” as the UI report states as its last word.

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The Calouste Gulbenkian Foundation is a Portuguese private institution of general public utility founded by the will of Calouste Sarkis Gulbenkian, establishing its initial capital, and defining its statutory goals: “charity, art, education and science”. The Foundation’s statutes were established in 1956.

The Foundation actively pursues its statutory aims in Portugal and abroad, through a wide range of direct activities and grants supporting projects and programmes. The Foundation has an orchestra and a choir, organises solo and collective exhibitions in its museums and exhibition spaces. It also organises international conferences, meetings and workshops, awards scholarships and subsidies for specialist studies in Portugal and abroad, and supports programmes of scientific, artistic and social natures.

Established by the Board of Trustees of the Calouste Gulbenkian Foundation in the context of the decision to provide a higher degree of autonomy to the IGC, facilitating and expediting administrative and financial operations, thus ensuring more flexibility to the Institute’s operation. The Management Committee received ample delegation from the Board over a wide range of areas, meets regularly with the Director and oversees all activities of the Institute.

The Scientific Advisory Board of the IGC oversees the scientific progress, graduate programmes, recruitment and overall performance of staff and research groups. The Scientific Advisory Board also advises the Director of the IGC and the Board of the Calouste Gulbenkian Foundation on all matters of relevance to the mission of the Institute.

The Ethics Committee of the IGC has as mission to consider all ethical issues that may arise during the course of the research projects developed by the groups or units of the IGC, reviewing the research projects that entail human studies and/or the use of vertebrate animals. The Ethics Committee is an interdisciplinary body made up of nine members, three of whom are laypersons and four are external to the IGC. In 2014, the Ethics Committee approved 2 projects.
The Instituto Gulbenkian de Ciência (IGC) is a private institute devoted to basic biological and biomedical research, and to graduate training. The IGC is free from hierarchical structure, with small independent research groups working in an environment designed to foster interaction and cooperation.

The scientific programme of the IGC is multidisciplinary, including Cell and Developmental Biology, Evolutionary Biology, Immunology, Host-Pathogen Interactions, Disease Genetics, Plant Biology, Neurosciences, Theoretical and Computational Biology.

The IGC missions are thus:
- To promote multidisciplinary science of excellence in basic biological and biomedical research;
- To identify, educate and incubate new research leaders, providing state-of-the-art facilities and full financial and intellectual autonomy to pursue research projects;
- To improve the transfer of research expertise into developments that are of potential interest beyond basic science;
- To provide international graduate teaching and structured training programmes that respond to present-day imperatives;
- To promote the values of science in society, scientific literacy, and the active participation of citizens in scientific research, through engagement with different communities and stakeholders.

The IGC was set up by the Calouste Gulbenkian Foundation, a Portuguese private institution of general public utility, in 1961. In 1998, the IGC was majorly restructured to form the institute that runs nowadays.

Since 1998, the IGC has hosted 87 research groups; 41 of these have moved on to other research institutes, 27 to research centres in Portugal. 29 research groups in Portugal are IGC-associated groups, with access to IGC facilities and services.

A worldwide network of over 350 Gulbenkian alumni hold regular meetings.

FACTS & FIGURES IN 2014*

398 People work at the IGC (including 8 visitors)
- 153 Males
- 245 Females

318 Researchers (including 8 Visitors)
- 143 PhD holders in research

41 Group leaders
- 25 Portuguese
- 16 Rest of the world
- 18 Females
- 23 Males

91 Post-docs
96 PhD students
32 Masters students
35 Research groups’ Technicians
15 Trainees

10 Core facilities
- 42 Core facility staff

9 Services
- 41 Service staff

38 Nationalities
- 294 Portuguese
- 104 Rest of the world

3 New research groups
2 New visiting groups

3 PhD programmes

The IGC pioneered graduate training in Portugal. Since 1993, 8 PhD Programmes have been set up, with approximately 80 speakers/year/programme.

* As of December 31st, 2014
In 2014:

184 Peer-reviewed publications
   162 from In-house groups
   22 from Associated groups

4 Proceedings

2 Book chapters

In the last 5 years:

865 Scientific Publications
659 from in-house groups
206 from associated groups

In 2014:

17 PhD theses
14 MSc theses

164 International presentations by IGC researchers
65 National presentations by IGC researchers

203 Seminars at IGC
120 External speakers
17 Conferences, Meetings, Workshops at IGC

22 New research grants that started in 2014:

3 European Commission Framework Programme 7 (FP7)
1 European Research Council (ERC) grant
1 Association for International Cancer Research (AICR-UK)
1 EMBO Installation Grant
1 European Crohn’s and Colitis Organisation (ECCO) Grant
1 University Cologne: UoC Cooperation
14 Fundação para a Ciência e a Tecnologia, Portugal

In-House Publications
Associated groups Publications
In-House Citations
Associated groups Citations

In-House Publications: 2014
Associated groups Publications: 2014
In-House Citations: 2014
Associated groups Citations: 2014

In-House Publications:

In-House Citations:

Associated groups Publications:

Associated groups Citations:

Total
Fundação para a Ciência e a Tecnologia, Portugal
European Commission Public
Other Private
Other Public
Other Public-Private Partnership

In-House Publications: 2004 - 2014
Associated groups Publications: 2004 - 2014
In-House Citations: 2004 - 2014
Associated groups Citations: 2004 - 2014

Total
Fundação para a Ciência e a Tecnologia, Portugal
European Commission Public
Other Private
Other Public
Other Public-Private Partnership

2004 - 2014: New research grants breakdown by source of funding
Total grant number is 350
(Source: IGC Research Funding Affairs)

2004 - 2014: Proportion of research grants breakdown by funding source
Total grant number is 350
(Source: IGC Research Funding Affairs)

45 Prizes and honours, including:
1 ERC Consolidator Grant
1 ERC Starting Grant
9 FCT investigators
1 EMBO Installation grant
1 Melo e Castro SCML Award
1 Nikon Small World in Motion Competition 2013 – 1st Place
1 Best PhD student talk
1 Best PhD student poster

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Fundação para a Ciência e a Tecnologia, Portugal
European Commission Public
Other Private
Other Public
Other Public-Private Partnership

**Budget Overview**

**Sources of Funding 2014**

- Total Budget 2014: €17.4M
- 59% External Funding
- 41% Internal Funding

**Breakdown of IGC Expenditure 2014**

- Total Budget 2014: €17.4M
- 25% Personnel (Staff and Researchers)
- 27% Equipment
- 26% Fellowships
- 14% Infrastructure (Building maintenance, Refurbishments)
- 8% Operations (Facility costs, others)
IGC scientist won top prize in “Nikon Small World in Motion Competition 2013”

Gabriel Martins, head of the Advanced Imaging Unit at IGC, won the first prize of $3000 in this competition with a video showing a 3D reconstruction of a quail embryo with 10 days of gestation (when still inside the egg).

IGS launched a new blog

Written by Thiago Carvalho, Investigator at IGC, “The Opposing Thumb” blog provides new insights through the biological literature.

IGC PhD students retreat

IGC doctoral students organized another edition of the Annual Meeting for Gulbenkian Students (AMdoGCS), this time opened to the participation of students from the Champalimaud Neuroscience Programme (CNP) and from the Centro de Estudos de Doenças Crónicas (CEDOC) located in the Oeiras campus.

Lars Jansen awarded with an ERC Consolidator Grant

Lars Jansen, group leader at IGC, was awarded with a Consolidator Grant from the European Research Council (ERC) of 1.6 million Euros. This funding will support Jansen’s research on epigenetic mechanisms.

Graduate Programme Science for Development (PGCD) launched

The academic year of the first edition of PGCD started in Praia, Cape Verde. The opening ceremony counted with the presence of senior representatives of Portugal, Cape Verde and Brazil.

Crowdfunding football game: Scientists vs. Veterans of Benfica

IGC scientists participated in a football game aiming to raise funds for cancer research. This initiative was promoted by Maristano da Silva.

Call for the 2015 PhD Programme (BB)

A call was opened to recruit students for the 2015 edition of the IGC PhD Programme in Integrative Biology and Biomedicine – BB.

Symposium of Labescolas

Twenty-five high-school students came to the IGC to discuss their scientific proposals with the IGC scientists. Students presenting the top 3 proposals were invited for a one-week internship at the IGC.

Symposium of Occam’s Beard

Researchers from the IGC and the Champalimaud Neuroscience Programme organized the first Symposium of Occam’s Beard, aiming to show the importance of critical thinking in science in an entertaining way. The event took place at the Champalimaud Centre for the Unknown.

António Coutinho awarded Doctor Honoris Causa by Universidade Federal de Minas Gerais

The award granted by this Brazilian University to António Coutinho, member of the Management Committee and former Director of the IGC, acknowledged the work done for the progress of science and training of scientists.
IGC annual report ’14 • a walk through the year

CALL FOR NEW GROUP LEADERS
For the first time, the IGC opened a public call for group leaders. The call raised wide discussion within the scientific community for announcing that numerical indicators would not be taken in consideration throughout the selection procedure. Instead, applicants were invited to propose up to three of their papers that they considered of special merit. Over hundred and twenty one scientists answered the call, 88 were from outside Portugal.

SUMMER INTERNSHIP PROGRAMME WITH OXFORD UNIVERSITY
Six undergraduate students from Oxford University initiated an 8-week internship at the IGC.

EMBO CONFERENCE: CENTROSOMES AND SPINDLE POLE BODIES
Three hundred scientists from around the world gathered at the Calouste Gulbenkian Foundation to attend the EMBO Conference organized by Monica Bettencourt-Dias, group leader at IGC.

POSTDOC RETREAT
The scientific retreat of the IGC Postdoctoral fellows took place in Sintra. Post-docs from Instituto de Medicina Molecular and from Chronic Diseases Research Centre were invited to participate.

EU-LIFE MEETING AT IGC
The strategy meeting of EU-LIFE alliance took place at the IGC, gathering the Directors of all 13 European institutes.

CALL FOR THE 2015 PGCD
Applications to the 2015 edition of the Graduate Programme Science for Development (PGCD) were opened.

10TH ANNIVERSARY OF GRIPENET
The online flu surveillance platform – Gripenet – celebrated its 10th anniversary and started an official collaboration with the Portuguese National Health Institute (Instituto Nacional de Saúde Doutor Ricardo Jorge).

IGC AT NOS ALIVE MUSIC FESTIVAL
IGC scientists brought science to this music festival, within the scope of a partnership established with the festival promoter, Everything is New. This partnership also results in two fellowships for young people aiming to start a career in science.

EMBO PRACTICAL COURSE ON “3D DEVELOPMENTAL IMAGING”
IGC organised and hosted the 2014 EMBO Practical course on “3D Developmental Imaging”. The course aimed to provide new tools of imaging techniques to young developmental biologists.

IGC OPEN DAY
The IGC invited the public to come and participate on a journey to the day-to-day research at IGC. Over 100 scientists and staff organised different activities, including hands-on activities and talks. One thousand five hundred citizens accepted the invitation.

THE EUROPEAN COMMISSIONER FOR SCIENCE AND RESEARCH VISITED THE IGC
Carlos Moedas, European Commissioner for Science and Research, came to the IGC during his first official business visit to Portugal.

RAQUEL OLIVEIRA AWARDED WITH AN ERC STARTING GRANT
Raquel Oliveira, group leader at the IGC, received a Starting Grant from the European Research Council (ERC) of approximately 1.5 million Euros. This funding will support Oliveira’s research on how chromosome morphology influences cell division.

ANA DOMINGOS AWARDED WITH AN EMBO INSTALLATION GRANT
Ana Domingos, group leader at the IGC, received one of the two EMBO installation grants in Portugal to pursue her studies in the identification of the reward pathways associated with sugar sensing.

MOISÉS MALLO AWARDED WITH MELO E CASTRO AWARD
Moisés Mallo, group leader at the IGC, was awarded with the Melo e Castro Award from Santa Casa da Misericórdia de Lisboa on Spinal Cord Injury Research.

IGC RATED IN THE HIGHEST CATEGORY OF THE EVALUATION OF PORTUGUESE RESEARCH UNITS
The results of the evaluation of Research Units, conducted by the national funding agency Fundação para a Ciência e a Tecnologia, were known and the IGC was rated in the highest category “Exceptional”, one of only 11 Research Units in all academic fields in the country.

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in-house collaborations

**RESEARCH AREA:**
- Cell and Developmental Biology
- Immunobiology
- Plant Biology
- Quantitative and Computational Biology
- Evolutionary Biology
- Neurobiology

**RESEARCH GROUPS:**
- ADY: Actin Dynamics
- BAS: Bacterial Signalling
- BGM: Biophysics and Genetics of Morphogenesis
- CBV: Cell Biology of Viral Infection
- CCR: Cell Cycle Regulation
- CSN: Cellular and Systems Neurobiology
- CHR: Chromosome Dynamics
- CDY: Collective Dynamics
- CAS: Complex Adaptive Systems and Computational Biology
- CGN: Computational Genomics
- DEE: Development, Evolution and the Environment
- DGT: Disease Genetics
- EEG: Eco-evolutionary Genetics
- EAS: Epigenetics and Soma
- EPM: Epigenetics Mechanisms
- EVB: Evolutionary Biology
- EVO: Evolution and Development
- EGS: Evolution and Genome Structure
- HMI: Host-Microorganism Interactions
- HPC: Host-Pathogen Co-evolution
- IAM: Infections & Immunity
- INF: Inflammation
- III: Innate Immunity and Inflammation
- INB: Integrative Behavioural Biology
- LAI: Lupus and Autoactive Immune Repertoires
- LYP: Lymphocyte Physiology
- MBT: Membrane Traffic
- MNB: Molecular Neurobiology
- NMD: Network Modelling
- OBE: Obesity
- PAM: Patterning and Morphogenesis
- PND: Physical Principles of Nuclear Division
- PLG: Plant Genomics
- PRM: Plant Molecular Biology
- PSS: Plant Stress Signalling
- PCG: Population and Conservation Genetics
- PNA: Protein-Nucleic Acid Interactions
- QOB: Quantitative Organism Biology
- SCP: Science and Policy
- TEL: Telomeres and Genome Stability
- VDS: Variation Development and Selection
In 2014, Freeman, M. (2014) Regulation of receptor tyrosine trafficking. Membrane biology and biochemistry. Combination of mouse genetics, disease models, cell over signalling in the projects indicated below, using a stability. We elaborate this theme of trafficking control post-translational modifications or regulation of protein by additional influences, including trafficking partners, trafficking, especially of membrane proteins, is controlled rate that they are produced. However, it is now clear that proteins are packaged into trafficking vesicles at the mechanism called ‘bulk flow’ whereby newly synthesized that secretory traffic was accomplished by a default reticulum (ER) and traffic to the plasma membrane, where signalling occurs. Until recently, it was believed in eukaryotes, one third of translated proteins are secretory proteins. These fold in the endoplasmic the secretory pathway better.

1. Genetic screens to identify novel trafficking factors for the major inflammatory cytokine receptors. In collaboration with Prof. Paul Lehner, University of Cambridge, we have initiated a series of genetic screens in haploid cells to identify trafficking factors for IL1RAP, a co-receptor required for signalling through the inflammatory receptors IL-1, IL-33 and IL-36. We are currently examining a number of candidate cofactors identified in the screen, which we will eventually test in cellular and mouse models.

2. Role of quality control in the secretory pathway during development and disease. In conjunction with the transgenics facility, we have generated two novel mutant mice lines in genes that have emerged as potentially important regulators of ER-associated degradation (ERAD), a quality control process whereby proteins in the ER lumen are retrotranslocated into the cytoplasm for proteasomal degradation. ERAD is important for preventing the accumulation of misfolded proteins in the ER, which risks stressing secretory cells to the point that they undergo cell death. We will proceed to examine the phenotype of these mutant animals, focusing on professional secretory tissues/organisms.

3. How membrane trafficking regulates signalling controlled by metalloproteases. IIRoms are catalytically inactive members of the rhomboid superfamily. Although they are related to rhomboid proteases, IIRoms lack the hallmark catalytic serine residue and thus cannot function as proteases. They are however conserved amongst metazoans, implying that they fulfill important functions. We recently showed that mammalian IIRoms are essential for the trafficking of the metalloprotease TACE/ADAM17 within the early secretory pathway. ADAM17 plays a key role in shedding important signalling molecules, such as TNFa and growth factors, from the cell surface. In IIRom null mice, ADAM17 is defective because it fails to traffic from the endoplasmic reticulum into the Golgi apparatus, where it would normally undergo an essential activation step. We are now dissecting how regulation of IIRom by inflammatory and growth-promoting signals controls the sheddase activity of ADAM17. We have also conducted screens to identifying new interactors of IIRoms, whose biology, we will examine in our IIRom mutant animals. Finally, using the genetic screens described above, we have identified some potentially novel trafficking factors for the related ADAM metalloprotease, ADAM10, which itself is essential for notch signalling in flies and mammals.

Adrain, Colin
Group Leader at IGC since 2013

PHD in Molecular & Cell Biology
Trinity College, Ireland, 2003

Previous Positions:
Postdoctoral Fellow | MRC Laboratory of Molecular Biology, Cambridge, UK
Postdoctoral Fellow | Trinity College, Dublin, Ireland

► RESEARCH INTERESTS

We are interested in how secretory trafficking coordinates cellular signalling during normal physiology, and its contribution to inflammatory disease and cancer. 60% of all current drugs target membrane proteins, illustrating the medical importance of this pathway. However the complex biogenesis and trafficking of many signalling proteins is poorly understood, providing an incentive to understand the secretory pathway better.

In eukaryotes, one third of translated proteins are secretory proteins. These fold in the endoplasmic reticulum (ER) and traffic to the plasma membrane, where signalling occurs. Until recently, it was believed that secretory traffic was accomplished by a default mechanism called ‘bulk flow’ whereby newly synthesized proteins are packaged into trafficking vesicles at the rate that they are produced. However, it is now clear that trafficking, especially of membrane proteins, is controlled by additional influences, including trafficking partners, post-translational modifications or regulation of protein stability. We elaborate this theme of trafficking control over signalling in the projects indicated below, using a combination of mouse genetics, disease models, cell biology, and biochemistry.

► PUBLICATIONS


► COLLABORATIONS

Christopher Gerner (University of Vienna, Austria)
Seamus Martin (Trinity College, Dublin, Ireland)
Kubu Strosnay (Institute of Organic Chemistry and Biochemistry, Czech Republic)

► FUNDING

Cancer Research Worldwide (formerly known as AICR)
European Commission, FP7, Marie Curie actions
European Crohn’s and Colitis Organisation (ECCO)

► PUBLIC ENGAGEMENT IN SCIENCE

IGC Open Day 14 - hands on activities, October

► LAB MEMBERS

<table>
<thead>
<tr>
<th>Name</th>
<th>Position</th>
<th>Start Date</th>
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<tbody>
<tr>
<td>Emma Bubridge</td>
<td>Postdoc</td>
<td>Started in April</td>
</tr>
<tr>
<td>Laura Corston</td>
<td>Postdoc</td>
<td>Started in July</td>
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<tr>
<td>Joanna Okonowicz</td>
<td>PhD Student (BB 2014)</td>
<td>Started in July</td>
</tr>
<tr>
<td>Tanvi Hu</td>
<td>Masters Student</td>
<td>Started in August</td>
</tr>
<tr>
<td>Catalina Marini</td>
<td>Research Assistant</td>
<td>Started in November</td>
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<tr>
<td>Luis Rodrigues</td>
<td>Research Assistant</td>
<td>Left in March</td>
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► PROJECTS RUNNING IN 2014

1. Genetic screens to identify novel trafficking factors for the major inflammatory cytokine receptors.

2. Role of quality control in the secretory pathway during development and disease.

biophysics &
genetics of
morphogenesis

Alves, Filipa
Group Leader of IGC since 2011

PhD in Physics
Universidade Técnica de Lisboa, Portugal, 2006

Previous Positions:
Post-doctoral Fellow | IGC, Portugal

RESEARCH INTERESTS

Our research focuses on the biophysical and genetic bases of pattern formation and morphogenesis. How is gene expression regulation coordinated in space and time during embryonic development? How are gene expression patterns reliably shaped in the presence of molecular fluctuations, genetic variability and environmental perturbations? We address these questions using a multilevel modelling approach, capturing key quantitative aspects of the interplay between the biophysical mechanisms underlying cell and tissue morphogenesis and the regulation of gene expression. Our theoretical models are developed in close relation with experimental data and are mainly used to formulate organised hypotheses and make testable predictions.

At the models’ validation is strongly dependent on quantifying and estimating the biological parameters involved, we also work on the development of quantitative image analysis methods, databases and parameter optimisation algorithms.

SOFTWARE DEVELOPMENT

WingPatterns - The WingPatterns knowledge base combines in the same platform the experimental image collections (with the respective associated metadata) and the quantitative analysis results of the gene expression patterns in larvae and pupae, adult pigmentation, vein patterning and wing shape; among other morphometric traits. Associated with the databases, we are developing automated image analysis algorithms and data-mining techniques.

Public website: http://wingpatterns.igc.gulbenkian.pt

FijiColor (Beta) - FijiColor is a set of Fiji plugins implementing novel methods for the quantitative analysis of color patterns in natural color images.

COLLABORATIONS

Patrícia Belkaidé (IGC, Portugal)
José Viel (University of Maryland, USA)
Jan Raaber (University of Amsterdam, The Netherlands)
Christian Mirle (IGC, Portugal)

FUNDING

Instituto Ciência e Inovação, Portugal

PROJECTS RUNNING IN 2014

1. Modelling and quantifying patterned cell fate determination in butterfly wings.
3. Modelling the biophysics of cell polarization.

HOW DO LOCAL GENE REGULATION AND TISSUE ARCHITECTURE ACT TOGETHER TO DEFINE ORGANIZED PATTERNS OF CELL DIFFERENTIATION?
The morphological changes during butterfly wing development and the associated formation of pigmentation patterns is an excellent model system to address this question. The mechanisms of cell fate determination leading to the biosynthesis of different pigments are strongly constrained by the wing morphology, mainly by the venation system and wing shape.

We are using a theoretical modelling approach to study the interaction between tissue architecture and the gene regulatory networks underlying wing patterning. We are especially interested in understanding how this interplay both generates and constrains the phenotypic variation observed within and among species.

We are testing different candidate genes and network topologies that are able to explain the gene expression patterns underlying wing morphology and pigmentation in Bicyclus anynana. Unlike Drosophila, the butterfly wings develop from nearly flat imaginal disks, and the key morphogenetic events in wing development take place approximately in the same plane. Our models take into account a two-dimensional wing tissue, where the gene regulatory networks are defined using partial differential equations and the spatial gene expression patterns are represented using finite differences methods. The parameters in the gene regulatory networks represent kinetic variables such as protein production and degradation rates, effective diffusion coefficients, and binding affinities of transcription factors to promoters. The model results predict the temporal evolution of the gene expression patterns during key stages in wing disc and pupal wing development. Furthermore, we provide testable hypotheses for how the observed variation in the pigmentation patterns may depend on subtle changes on specific biophysical parameters.

The models’ parameter values are being estimated by comparing the theoretically predicted gene expression patterns with experimental images from the Variation Development and Selection lab (IGC).

In order to have a quantitative description of the experimental images, we have been focusing on the development and implementation of image analysis methods, together with a dedicated image acquisition system and a structured database. Our algorithms for shape and colour analysis enable the quantitative characterization of phenotypes, according to their morphometric parameters and pigmentation (or gene expression) patterns. These methods are being applied to different image types, from butterfly wing disks and adult wings to Drosophila pupae and adult abdominal pigmentation patterns.

PATTERNED CELL FATE DETERMINATION IN BUTTERFLY WINGS. A) Examples of results from the theoretical models. B) Image analysis; colour quantification.

LAB MEMBERS

Pedro S. Lopes (Research Assistant) | Left in October
Tago Pereira da Silva (Research Assistant) | Left in February
cell biology of viral infection

Amorim, Maria João
Group Leader at IGC since 2012

PhD in Virology
University of Cambridge, UK, 2007

Previous Positions:
- Research Associate in Digard Lab | Univ of Cambridge, UK
- Research Associate | National Institute of Medical Research, London, UK

Research Interests:
Influenza A virus is a major human pathogen that causes yearly epidemics and occasional pandemic outbreaks. Despite a tight surveillance and a yearly vaccination scheme, the pathogen is responsible for high mortality, morbidity and economic damage. Development of antivirals is therefore necessary. The elucidation of cellular pathways used by the virus, can contribute to identify novel therapeutic targets. The virus genome consists of 8 segments of negative sense, single stranded RNA (vRNAs) that encodes 10-12 identified proteins. Each vRNA is separately encapsidated into ribonucleoprotein (RNP) particles by the trimeric viral RNA polymerase (PB1, PB2 and PA) and RNA-binding protein NP. Unusually for an RNA virus, the genome is transcribed and replicated in the host cell nucleus. After exiting this compartment, new vRNPs reach the apical side of the PM using at least a two-step mechanism in the cytoplasm: first they accumulate around the microtubule organizing centre where they are loaded onto Rab11-vesicles and are then transported using both microtubules and actin to the cell periphery. Understanding the mechanisms that govern vesicular trafficking (and therapeutic methods to inhibit them) is the main focus the research plan of the lab. The factors involved in the biogenesis of vesicles carrying viral genome, or in the anchoring and fusion to target membranes will be investigated, as well as molecular motors involved in this transport. As the virion is composed not only of vRNAs but also 5 other viral proteins, the cellular pathways involved in their trafficking to the budzone will be addressed. Ultimately we are interested in understanding the process of viral assembly and budding from the cells.

Projects Running in 2014

1. The role of ARFGEFs in influenza A virus infection.
2. Membrane regulators of complement activation modulate immune response to influenza A virus infection.
3. The role of mitochondria during infection.
4. The role of ARLs in influenza A virus infection.
5. Molecular motors important for trafficking of influenza A virus genome.

Collaborations
- Paul Digard (University of Edinburgh, UK)
- Michael Laessig (University of Cologne, Germany)
- John McCauley (MRC National Institute for Medical Research, London, UK)
- Luca Scorrano (Venetian Institute of Molecular Medicine, Italy)
- Wenchao Song (Institute for Translational Medicine and Therapeutics, University of Pennsylvania, USA)
- Elizabeth Sztul (University of Alabama at Birmingham, USA)

Funding
Fundação para a Ciência e a Tecnologia, Portugal

Public Engagement in Science
- Radio interview on “Science in Portugal”, organised by the University of Trás-os-Montes e Alto Douro, January
- Gripenet newsletter – weekly column “In the Lab”, IGC Open Day 14 – hands on activities, October

Main Research in 2014

My lab main interests are to identify and characterise host cell processes that contribute to influenza A virus assembly and budding. Building on our previously identified requirement for the recycling endosome in mediating this process, we have been characterising structural alterations to this organelle during infection. Such data has provided valuable clues on what is being deregulated at the molecular level. Using correlative light and electron microscopy and super-resolution microscopy we have now acquired sufficient data to prepare a manuscript for publication. We have also identified a novel ARL involved in the transport of progeny RNA towards the surface of the cell, place of viral assembly and budding. At the moment we are exploring its role in infection. Furthermore, we are expanding our interests by investigating regulatory processes of complement in vivo during IAV challenge.
Sequence is not fate. Proteins demonstrate an impressive ability not only to recognize and bind to particular pieces of nucleic acids code but also to alter its information content by catalysing reactions that rearrange its sequence or specifically change one nucleotide for another. Organisms have found in such mechanisms the means for creating sequence diversity as it is gloriously exemplified in the diversification of immunoglobulin genes. The recent realization that multicellular organisms achieve phenotypic complexity without the two viral inhibitors of interferon response antiviral pathway.

In vertebrate species the innate immune system down-regulates protein translation in response to viral infection through the action of the dsRNA activated protein kinase PKR. Not surprisingly viruses have evolved proteins that inhibit such host responses. Pox viruses encode for that purpose E3L, a potent inhibitor of PKR and interferon response. In some teleost species another protein kinase, PKZ, plays a similar role but instead of dsRNA binding domains, PKZ has Za domains. Za domains recognize the left-handed conformer of dsDNA and dsRNA known as Z-DNA/Z-RNA. Cypriphebusitis 3 (CyHV-3) which infects common carp and koi carp, that have PKZ, encodes the ORF112 protein which we previously demonstrated encodes a Za domain and suggested that it is a competitive inhibitor of PKZ. This would be the first evidence that Hepes viruses use a similar strategy to inhibit interferon response as Pox viruses through E3L.

We determined the crystal structure of ORF112-Za in complex with an 18 bp Cpg DNA repeat, at 1.5 Å. We demonstrated that the bound DNA is in the left-handed conformation and we identified key protein nucleic-acids interactions accounting for the specificty of ORF112. In collaboration with the Veterinary Medicine lab of Alain Vanderplaschen at the University of Liege we demonstrated that ORF112 protein localises in stress granules of CyHV-3 infected fish cells suggesting a not only structural but also functional behaviour similar to that of host Za domains.

## PROJECTS RUNNING IN 2014

1. Implication of A to I RNA editing in circular RNA biogenesis.

## RESEARCH INTERESTS

- Protein-Nucleic acids interactions
- Recognition of Foreign Nucleic Acids in Innate Immunity.

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## RESEARCH INTERESTS

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- Recognition of Foreign Nucleic Acids in Innate Immunity.
Mounting evidence suggests that in plants, environmental information is partly conveyed through sugar signals. Accordingly, sugars have been linked to stress responses, to the regulation of growth and to specific developmental decisions such as germination, phase transition, and flowering. A sophisticated sugar signalling network has been uncovered in the last decade that translates the plant carbon status into growth and development. A central component of this network is the SNF1-related Protein Kinase1 (SnRK1), which senses declining ATP levels associated for example with situations of stress and promotes stress tolerance and survival. On the other hand, transient SnRK1 silencing results in growth arrest by yet unknown mechanisms. Despite the importance of SnRK1 virtually nothing is known about how it operates. Our goal is the dissection of this key pathway as a first step towards understanding how plants cope with adverse conditions and uncover translation, organelle function and specific TCP SnRK1 signalling (Confraria, Martinho et al. 2014). We are currently preparing a manuscript on this work and are exploring interactions with the laboratory of Paula Duque (IGC) has also revealed a role for the SR45 splicing factor in SnRK1 stability and sugar signalling. We have found that SnRK1 activity results into the SUMOylation-dependent ubiquitination of several substrits of the complex and their subsequent degradation through the proteasome. Most interestingly, mutations that render SnRK1 inactive abrogate its degradation, suggesting that SnRK1 activity and SUMOylation are tightly coupled to prevent detrimental pathway overactivation. SUMOylation of SnRK1 requires the SIZ1 E3 SUMO ligase, and accordingly, siz1-2 mutants exhibit higher SnRK1 accumulation and an overactivation of the SnRK1 pathway, as reflected by an overinduction of SnRK1 marker genes in response to stress signals. Furthermore, similarly to the SnRK1 overexpression, siz1-2 seeds display a delayed delay in germination, and normal germination is restored in a siz1-2 snrk1.1 double mutant, demonstrating the involvement of SnRK1 in the siz1-2 phenotype.

We are currently preparing a manuscript on this work and are exploring several novel aspects derived from it in addition, our collaboration with the laboratory of Paula Duque (IGC) has also revealed a role for the SR45 splicing factor in SnRK1 stability and sugar signalling. Whether or not this is related to SUMO-dependent regulation of SnRK1 is thus far unknown.

Our previous work showed that miRNAs are downstream effectors of SnRK1 signalling (Confraria, Martinho et al. 2013, Front Plant Sci.), and uncovered translation, organelle function and specific TCP
transcription factors as the most highly enriched functional clusters potentially co-regulated by SnRK1 and miRNAs. Intriguingly, our deep sequencing and Northern analyses have shown that enhanced target repression is not accompanied by mature miRNA accumulation, raising the question of how SnRK1 activity is translated into enhanced miRNA action. To tackle the molecular mechanism by which SnRK1 controls miRNA function, we have developed several approaches and tools that include a set of luciferase-based reporters to monitor the in vivo activity of several miRNAs (Martinho, Confraria et al, 2014, Mol Plant).

Some of the same targets that we see affected by the SnRK1 pathway (namely the TCP transcription factors) are important for the acquisition of age-dependent features in leaf morphology. We have recently contributed to a work showing that the interplay between miRNA-regulated SPL/CUC/TCP transcription factors is crucial for the age-dependent increase in leaf complexity (Rubio-Somoza et al, 2014, Curr. Biol).

Finally, we have carried out non-biased high-throughput screens (namely identification of novel SnRK1 interactors by Y2H and mass spectrometry as well as luciferase-based mutant screens for the SnRK1 signaling pathway) that are currently shaping into exciting novel directions of research.

► MAIN RESEARCH IN 2014 (cont.)

Lack of the SIZ E3 SUMO ligase in the siz1-2 mutant causes a constitutive defense response with a subsequent penalty on growth. Part of the siz1-2 growth and developmental phenotypes can be attributed to SnRK1 overactivation. SnRK1 activation during stress causes the SUMO-dependent ubiquitination of several subunits of the complex and their subsequent proteasomal degradation. In the absence of SUMOylation SnRK1 stability is increased resulting in an overactivation of the pathway.

WT and siz1-2 plants were grown in short-days to maximize vegetative growth. The SnRK1 complex was immunoprecipitated from WT or siz1-2 plants and analysed by immunoblotting with the indicated antibodies. Loss of SUMOylation in siz1-2 cells results into an increased stability of the SnRK1 catalytic subunit.
How the vast majority of B cells express only one of the two alleles at their immunoglobulin loci remains a biological puzzle. Here, in mice reconstituted with a single hematopoietic stem cell, we demonstrate that each of the two immunoglobulin heavy chain (Igh) alleles has a similar probability to be the first to undergo VH to DJH rearrangement. We also observe this similar probability in clones from multipotent and common lymphoid precursors. The extreme biases in the expression of the alleles that we find in more differentiated subsets are mostly due to constraints imposed by early rearrangements. Our data demonstrate that each of the two Igh alleles in a B cell behaves independently of the other, up to the moment when a successful rearrangement in one allele triggers a feedback mechanism that prevents further recombination [Pereira CF et al. (2014) Nature Communications].

**MAIN RESEARCH IN 2014**

1. **Activation-Induced Cytidine Deaminase as a guardian of the genome.**

2. **Targets and off-targets of the lymphocytes recombinase.**

We study the DNA editing of the immunoglobulin genes to understand random mono-allelic expression and the interplay of DNA repair pathways with Activation-Induced Deaminase (AID), the enzyme that triggers class switch recombination (CSR) and somatic hypermutation (SHM).

Random mono-allelic expression is the most striking example of an epigenetic phenomenon, because at the level of each cell only one of two identical molecules (the alleles) is expressed. We are studying the immunoglobulin genes as a model to dissect how a given allele undergoes rearrangement first.

In SHM, point mutations are introduced into the variable region of the Ig heavy and light chain genes in germinal centre activated B cells, generating the required diversity to fuel the affinity maturation of antibodies. In CSR, the variable region of the heavy chain gene is combined with gene segments encoding distinct constant regions, each with unique effector functions. AID is essential for SHM and CSR. However, its mutagenic ability has a pernicious side effect and AID has been implicated in B lymphomas and other neoplasias. We use classical molecular approaches and genetically engineered mice to discover AID cofactors for CSR, address the rules governing AID targeting to the immunoglobulin loci and establish murine models to evaluate the ectopic expression of AID.

**PROJECTS RUNNING IN 2014**

1. **Deterministic (left) and stochastic (right) models of allelic exclusion of the light loci.**

**RESEARCH INTERESTS**

- We study the DNA editing of the immunoglobulin genes to understand random mono-allelic expression and the interplay of DNA repair pathways with Activation-Induced Deaminase (AID), the enzyme that triggers class switch recombination (CSR) and somatic hypermutation (SHM).

- Random mono-allelic expression is the most striking example of an epigenetic phenomenon, because at the level of each cell only one of two identical molecules (the alleles) is expressed. We are studying the immunoglobulin genes as a model to dissect how a given allele undergoes rearrangement first. In SHM, point mutations are introduced into the variable region of the Ig heavy and light chain genes in germinal centre activated B cells, generating the required diversity to fuel the affinity maturation of antibodies. In CSR, the variable region of the heavy chain gene is combined with gene segments encoding distinct constant regions, each with unique effector functions. AID is essential for SHM and CSR. However, its mutagenic ability has a pernicious side effect and AID has been implicated in B lymphomas and other neoplasias. We use classical molecular approaches and genetically engineered mice to discover AID cofactors for CSR, address the rules governing AID targeting to the immunoglobulin loci and establish murine models to evaluate the ectopic expression of AID.

**PUBLICATIONS**


**COLLABORATIONS**

- Jocelyne Demengeot (IGC, Portugal)
- P. Hammarström (Karolinska Institute, Sweden)
- Paulo Vieira (Institut Pasteur, France)
- Y. Zhao (China Agricultural University, China)

**FUNDING**

- Fundação para a Ciência e a Tecnologia, Portugal
Our group is interested in the mechanisms underlying sexual reproduction and early embryogenesis with a particular focus on the role of the male gametes. Recent studies have shown that male gametes both in the plant and animal kingdom carry complex sets of RNA molecules, including not only mRNAs but also small RNAs. We are particularly interested in the role of these two RNA classes before, during and after fertilization. Using the angiosperm Arabidopsis thaliana and the bryophyte Physcomitrella patens as our primary experimental models we are addressing specific questions like: (1) What are the functions of small RNA and DNA methylation pathways in sperm cells? (2) Do sperm cell derived RNAs play a role in double fertilization and initiation of embryogenesis in angiosperms? (3) What are conserved core sets of genetic modules underlying the male gametes? In accordance, a subset of ovules showed transmission through the female and absence of transmission through reciprocal backcrosses with wild type confirmed a reduced self-compatibility that the conserved CCR4-NOT complex plays a major role in this regulation. We could show that the conserved CCR4-NOT complex plays a major role in this function and the last steps of gametophyte differentiation coincide with an extensive reduction of transcript diversity of the pollen transcriptome. We could show that the conserved CCR4-NOT complex plays a major role in this function and the last steps of gametophyte differentiation coincide with an extensive reduction of transcript diversity of the pollen transcriptome. We could show that the conserved CCR4-NOT complex plays a major role in this function and the last steps of gametophyte differentiation coincide with an extensive reduction of transcript diversity of the pollen transcriptome. We could show that the conserved CCR4-NOT complex plays a major role in this function and the last steps of gametophyte differentiation coincide with an extensive reduction of transcript diversity of the pollen transcriptome.
developmental defects causing abnormal seed set, while not1 pollen grains showed defects in male germ unit organization and were largely impaired in pollen tube growth. Most importantly, comparative transcriptional profiling of wild type versus not1/+ pollen revealed that missing NOT1 expression adversely affects transcriptome reprogramming. Transcripts strongly down-regulated from the bi- to tricellular to mature stage in wild type pollen were among the most up-regulated in mutant pollen, indicative of a possible failure of CCR4-NOT driven mRNA decay. In addition, a number of transcripts that ought to increase in abundance during this phase failed to do so in mutant pollen. The broad implications of this misregulation for maturation and cell fate determination of the developing male gametophyte are under further analysis.
My research in evolutionary developmental biology is focused on the mechanistic basis of phenotypic variation and adaptation. Heritable phenotypic variation is the raw material for natural selection, and a universal property of biological systems — including traits of medical importance. Understanding the mechanisms that generate this variation is a key challenge in biological research. What are the gene types (e.g. transcription factors versus enzymes), specific genes, and gene regions (e.g. regulatory versus coding sequence) that contribute to evolutionarily relevant variation? How do they affect development to account for adaptive phenotypic plasticity versus enzymes), specific genes, and gene regions (e.g. regulatory versus coding sequence) that contribute to evolutionarily relevant variation? How do they affect development to produce different adult phenotypes? How does the external environment regulate organismal development to account for adaptive phenotypic plasticity? For the dissection of variation in complex, development to account for adaptive phenotypic plasticity? How does the external environment regulate organismal development to account for adaptive phenotypic plasticity? For the dissection of variation in complex, diversified and ecologically-relevant phenotypes the lab is currently using three complementary systems: wing diversified and ecologically-relevant phenotypes the plasticity? For the dissection of variation in complex, developmental hierarchies. 1) We focused on thermal plasticity in butterflies to investigate the effects of environmental cues and of internal signals responsible for conveying information about those cues to developing tissues. We found that temperature and ecdysone affect phenotype in a manner that differs between the two, and between traits. This work, done by AR Mateus with IGC (M Marques-Pro) and international collaborators, was published in BMC Biol and Am Nat. 2) The work of E Lafuente focused on thermal plasticity in Drosophila body pigmentation and benefitted from interactions with IGC’s F Alves (phenotyping), É Sucena (co-supervision), and A Athanasiadis (RNA editing), and interactions with external labs: S M Ghabrial (FR) and R Reenan (USA). We uncovered...

**PROJECTS RUNNING IN 2014**

1. Morphological diversification through the evolution of developmental hierarchies.
2. Wound response and pigmentation pattern formation: cellular, molecular and evolutionary considerations.
5. Adaptation to new ecological niches: nutrition and Drosophila suzukii.

**RESEARCH INTERESTS**

My research in evolutionary developmental biology is focused on the mechanistic basis of phenotypic variation and adaptation. Heritable phenotypic variation is the raw material for natural selection, and a universal property of biological systems — including traits of medical importance. Understanding the mechanisms that generate this variation is a key challenge in biological research. What are the gene types (e.g. transcription factors versus enzymes), specific genes, and gene regions (e.g. regulatory versus coding sequence) that contribute to evolutionarily relevant variation? How do they affect development to account for adaptive phenotypic plasticity versus enzymes), specific genes, and gene regions (e.g. regulatory versus coding sequence) that contribute to evolutionarily relevant variation? How do they affect development to produce different adult phenotypes? How does the external environment regulate organismal development to account for adaptive phenotypic plasticity? For the dissection of variation in complex, diversified and ecologically-relevant phenotypes the lab is currently using three complementary systems: wing diversified and ecologically-relevant phenotypes the plasticity? For the dissection of variation in complex, developmental hierarchies. 1) We focused on thermal plasticity in butterflies to investigate the effects of environmental cues and of internal signals responsible for conveying information about those cues to developing tissues. We found that temperature and ecdysone affect phenotype in a manner that differs between the two, and between traits. This work, done by AR Mateus with IGC (M Marques-Pro) and international collaborators, was published in BMC Biol and Am Nat. 2) The work of E Lafuente focused on thermal plasticity in Drosophila body pigmentation and benefitted from interactions with IGC’s F Alves (phenotyping), É Sucena (co-supervision), and A Athanasiadis (RNA editing), and interactions with external labs: S M Ghabrial (FR) and R Reenan (USA). We uncovered...

**PUBLIC ENGAGEMENT IN SCIENCE**

- Media appearance in newspapers, TV and other channels, January.
- IGC Open Day ’14 – Top Model room, October.
- Public talk for primary school students, “Meet the scientist”, Paço das Artes, Lisbon, November.
- Public talk for Master’s students, FCSH-UNL, Lisbon, December.
differences between genotypes in how pigmentation is affected by temperature, and in the developmental window of thermal sensitivity. For this work, Elvira won a poster-prize at the Congress of the Portuguese Soc Evol Biol. 3) M Marialva explored the effects of an abiotic (temperature) and a biotic (Wolbachia) factors on transposable element (TE) dynamics in Drosophila oogenesis. We discovered that both factors affect TE expression, possibly mediated by a piRNA pathway protein. This work benefited from input from IGC’s L. Teixeira (Wolbachia) and external TE experts, C. Bergman (UK) and C. Vieira (FR). 4) Following the idea that butterfly eyespots originated from the co-option of ancestral wound-healing machinery, MA Jerónimo studied wound-induced pattern formation in Bicyclus. She implicated immune activation in the development of wound-induced and native wing patterns. 5) L Shirai completed her thesis on the idea that different steps of trait development impact different aspects of trait morphology. She investigated differences within and between species across butterfly wing pattern development. We uncovered inter-specific differences in the timing of pigment deposition, inter-mutant heterochronic and heterotopic changes, and differences in expression dynamics between genes. 6) We published the work of former post-doc RA Keller on body architecture in workers and queens of ant species reporting that i) workers are not just simplified versions of queens; they have a thorax morphology unique among flying insects that confers strength to their heads, and ii) there are two classes of queens’ thorax morphology that co-evolved with two types of behavior during the new colony foundation. This work was done in collaboration with C. Peeters (FR) and published in eLife. It received attention from media and science bloggers nationally and internationally.

► Analysis of expression profiles during the early stages of butterfly pupal wing development when pattern-organizing centers are assigning color fate to epidermal cells. We used microarrays with features representing ca. 17 thousand gene objects to identify genes differentially expressed between time points (heat map) and clusters of genes with distinct temporal dynamics of expression (number in each cluster is shown on the panels in the right). Figure adapted from PhD thesis of Leila Shirai.
Our research focuses on cell cycle progression and the cytoskeleton in normal development and disease. We are particularly interested in the role played by microtubule-organizing structures, such as the centrosome, cilias and flagella. The centrosome is the major microtubule organizer in animal cells, and is very often abnormal in cancers. Cilias and flagella are cellular projections, which are indispensable in a variety of cellular and developmental processes including cell motility, propagation of morphogenic signals and sensory reception. Despite their importance, we know very little about centrosome and cilia biogenesis or how they may go awry in human disease. Our laboratory uses an integrated approach to study those questions, since it combines possibilities of this process. The fruit fly is an excellent organism to study those questions: we combine studies in model organisms with studies in human cells, bioinformatics and extrapolate our findings to humans to test their relevance for human disease. An understanding of the pathways involved in cell cycle and cytoskeleton can generate diagnostic and prognostic markers and hopefully provide novel therapeutic targets in human disease.

Previous Positions:
University College London, UK, 2001

Previous Positions:
Research Associate | University of Cambridge, UK

External website

PUBLICATIONS


COLLABORATIONS

Juliette Amarsheikh (University of California at San Francisco, USA)
Ira Trigo Bandeiras (Instituto de Tecnologia Química e Biológica, Portugal)
Michel Bornens (Institut Curie, France)
Paula Chaves (Instituto de Tecnologia Química e Biológica, Portugal)
David Claviez (University of Cambridge, UK)
Keith Cell (University of Oxford, UK)
Eic Kjems (EMBL, Germany)
David Pellman (Harvard Medical School, USA)
José Pereira-Leal (ICG, Portugal)
Ivo Tellez (ICG, Portugal)

FUNDING

European Research Council, European Commission
Fundações para a Ciência e a Tecnologia, Portugal

PUBLIC ENGAGEMENT IN SCIENCE

Media appearance in newspapers, TV and other channels:
October, November
TED Talks, TagusParque, Oeiras, March
ICG Open Day, 24 - hands on activities, October
Public talk for high school students in the event “A Criançada nas Escolas”, Braga, November.

LAB MEMBERS

Ana Paula (Post-doc)
Mariana Rato (Post-doc/Lab Manager)
Manoela Francisco (Post-doc) (Started in March
Susana Monteagudo (Post-doc)
Debora Teodoro (Post-doc
Sandrinho (Post-doc)
Carla Lopes (Post-doc) (Started in February
Ana Rita Marques (Post-doc)
Cátia Marques (Post-doc)
Zitouni Simeen (Post-doc)
Clia Deshpande (PhD student, IBS 2013)
Catarina Nabais (PhD student, IBS 2014) (Started in August
Suzia Vinoth (PhD student, IBS 2013)
Paula Duarte (Research Assistant)
Susana Mendonça (Research Assistant)
Katharina Danes (Masters student)
Mariana Faria (Post-doc/Lab Manager)
Inês Bento (Post-doc)

PROJECTS RUNNING IN 2014

1. Control of centrosome structure and number
   We have discovered a mechanism by which centrioles duplicate only once per cell cycle, regulated by CDK activity. Additionally, we have evidence that PLK4 autoactivation enforces that centrioles only form close to centrosomes that already exist.

2. Causes and consequences of centrosome and ploidy abnormalities in human cancer
   We have found that centrosome amplification and their clustering in mitosis is a hallmark of cancer. Using Darrëtt’s model, we show that centrosome amplification occurs early during tumorigenesis and is dependent on p53 inactivation.

3. Regulation of cilia biogenesis and maintenance in development and human disease
   We have shown that cilia within an organism, such as Drosophila, are much more diverse than previously thought and that diversity in basal body and transition zone structure is critical to create diversity in function.

4. Regulation of centriole number in development

5. Microtubule regulation in centriole biogenesis mechanism
   We discovered new microtubule regulators that regulate centriole elongation.

6. Centrosomes in evolution
   We have discovered parallels between SPB and centrosome assembly that raise new questions regarding their evolution.

7. A mechanism for maternal gamete centrosome elimination
   We have discovered a mechanism by which centrosomes are inactivated and eliminated in oogenesis. We were able to prevent centrosome loss and show that this leads to problems in embryogenesis after fertilization.
Cells of multicellular organisms cooperate to ensure body development and maintenance throughout life. They do this in a collective distributed manner, without any master or plan. The Quantitative Organism Biology group studies the multilevel mechanisms that give rise to properties of the whole organism, in search for general principles of biological organisation and, eventually, the design of artificial systems. One of our main research interests is the immune system, in which cells collectively ensure body housekeeping and homeostasis, avoid autoimmune diseases, and fight cancer and infections. We also investigate the morphodynamics of cells and tissues during fertilisation and embryonic development of metazoans. Our approach is two fold: on the one hand, we create mathematical models of specific systems aiming to uncover basic principles, and on the other hand, we develop the quantitative methods that assessing the properties and predictions of these models requires.

Cells and whole organisms display a significant phenotypic variation that cannot be ascribed to variation in their genome. In multicellular organisms this variation creates the potential for somatic adaptation by selective expansion of some phenotypic variants in detriment of others. One of the most pervasive forms of somatic variation is the copy number per cell of specific molecular components that control cell physiology, cell cycle and apoptosis. The copy numbers of most molecular components display long-tailed distributions in cell populations of isogenic cells. This is a straightforward consequence of the stochastic nature of biochemical reaction within the cell. In contrast, some cellular components are present in one and only one copy in the cell (not zero and not two copies!). This raises an intriguing question: how can such exquisite regulation of copy numbers be achieved if the biosynthetic reactions are essentially stochastic? We are addressing this question by analysing two specific case studies: the V(D)J recombination reaction in antigen receptor gene loci that produces a unique functional product in lymphocyte precursors and the centriole biosynthesis reaction that produces a single daughter centriole in eukaryotic cells. In both these reactions, the fine regulation of product copy number can be disrupted by specific mutations that...
lead to overproduction. By studying these two distinct systems we aim to find universal principles behind the control of the biosynthesis of a single product and to identify what is peculiar to each system.
Our main goal is to understand how global programmes of gene expression are regulated during vertebrate neurogenesis. Along the neuronal lineage, an intrinsic programme that relies on the activity of transcription factors and the epigenetic landscape coordinates the progression of progenitors throughout distinct cellular stages. Such intrinsic programme integrates information from local extracellular signals (e.g. through cell to cell contact) or from long range cues (e.g. secreted factors), resulting in the progression of a coherent programme of cellular differentiation that requires governing the expression of a large number of genes. In order to understand the regulatory logic of neurogenesis, we focus our studies on proneural transcription factors (e.g. Mash1/Ascl1) as these function as master regulators of neurogenesis by coordinating the various components of the differentiation programme. We investigate how Ascl1 interacts with the chromatin landscape and other transcriptional networks, in particular the Notch pathway. In addition, we are also interested in understanding how key transcriptional networks that underlie neural stem cell function are hijacked during tumorigenesis. In this context we use cancer stem cell models of Glioblastoma Multiforme, the most frequent and aggressive of brain tumours. In our research we use a multidisciplinary approach, combining mouse genetics, genomics and stem cell biology techniques.

REFERENCES


MANUSCRIPTS IN PRESS


2. COLLABORATIONS

Vania Brossard (San Raffaele Scientific Institute, Italy)
François Gullerud (MRC National Institute for Medical Research, UK)
Domingos Henriques (Instituto de Medicina Molecular, Portugal)
Jane E. Johnson (University of Texas Southwestern Medical Center at Dallas, USA)
Desidério Lima (Faculdade de Medicina de Universidade do Porto, Portugal)
Stefan Miron (Justus Liebig University, Germany)
David J. Soldev (St. Jude Children’s Research Hospital, USA)

1. Transcriptional control of vertebrate neurogenesis by the Proneural and Notch pathways.

2. The transcriptional network of the zinc-finger factor ZEB1 and its function in the embryonic nervous system and glioma development.

ASCL1 COORDINATELY REGULATES GENE EXPRESSION AND THE CHROMATIN LANDSCAPE DURING NEUROGENESIS

The generation of new neurons in the embryonic nervous system requires a number of precisely orchestrated steps, whereby proliferating neural progenitors become committed to the neuronal fate, exit cell cycle and undergo a complex programme of migration and differentiation. Proneural transcription factors of the bHLH family, such as Ascl1/ Mash1, are pivotal regulators of the neurogenic process. Ascl1 is expressed in proliferating neural/stem progenitors in the germinal layers of the developing brain and spinal cord regions, where it promotes sequentially the proliferation and differentiation of progenitors towards a neuronal programme. Previous studies have shown that this occurs via the concomitant regulation of distinct transcriptional targets of Ascl1. However, what determines which subsets of genes are regulated by Ascl1 in proliferating versus differentiating progenitors remains poorly understood. Here we used a cellular model of neurogenesis to investigate how Ascl1 activity is restricted by, and impacts the chromatin landscape when promoting the differentiation of adherent cultures of neural stem/progenitor cells. By combining expression profiling with genome-wide mapping of Ascl1 binding sites (ChIP-seq), and DNAse I hypersensitivity sites (DNase-seq), we found that: i) Ascl1 binding occurs most at distal enhancers and is associated with activation of gene transcription; ii) Accessibility of Ascl1 to its binding sites remains largely unchanged in proliferating and differentiating progenitors, as judged by the binding profile of overexpressed Ascl1 in both conditions; iii) In a subset of its target sites, Ascl1 binds to regions of closed chromatin in proliferating cells, promoting chromatin accessibility and the appearance of new regions of open-chromatin; and iv) New regions of open-chromatin are associated with genes expressed de novo during differentiation. Overall, our study suggests that access of Ascl1 to chromatin in proliferating cells is not a major impediment for activation of differentiation target genes. In addition, it reveals a novel function of Ascl1 in promoting chromatin accessibility during neurogenesis, linking the chromatin landscape at Ascl1 target regions with the temporal progression of its transcriptional programme along the neuronal lineage.
network modelling

RESEARCH INTERESTS

With the great advances in molecular biology, genomics, and functional genomics, regulatory and signalling networks are emerging uncovered, opening the way for a better understanding of how cellular processes are controlled. Molecular pathways interplay and operate at diverse levels (transcription and translation of the genetic material, protein modifications, etc.). The complexity of these networks calls for the development of dedicated mathematical and computational models. In this context, our goal is to develop generic tools to model and analyse large signalling and regulatory networks. For this purpose, we mainly rely on a qualitative modelling framework combining the generalised logical formalism, cellular automata and Petri nets.

Our research goes mainly along these lines. First, we devise new methods to efficiently analyse properties of biological relevance in discrete models. Second, methodological advances are made available in the form of novel computational tools or as new functionalities of existing standards and tools with CoLoMoTo.

PROJECTS RUNNING IN 2014

1. Efficient methods to assess the dynamical properties of asynchronous logical models of large signalling networks.
2. Modelling the regulatory control of primary sex determination in mammals.
4. How cells initiate epithelial-to-mesenchymal transition? A computational modelling of cellular and supra-cellular networks to unravel the control of EMT.

MAIN RESEARCH IN 2014

With our work on a discrete model of Drosophila eggshell patterning (Faure et al. 2014), we defined a cellular automata framework that permits the consideration of logical, multi-cellular models. EpiLog, a novel computational tool supports the definition and simulation of these models (http://ginsim.org/epilog).

Logical modelling has proven suitable for the dynamical analysis of large signalling and transcriptional regulatory networks. In this context, model input components are generally meant to convey external stimuli, or environmental cues. In response to such external signals, cells acquire specific gene expression patterns modelled in terms of attractors (e.g. stable states). The capacity for cells to alter or reprogram their differentiated states upon changes in environmental conditions is referred to as cell plasticity. GNSim, our reference tool for the definition and analysis of logical models, has been equipped with novel export functionalities, in particular to enable the use of model-checking techniques. Symbolic model checking allows investigating switches between attractors subsequent to changes of input conditions. As a case study, we consider the cellular network regulating...
One goal of the Network Modelling group is to develop computational means to tackle the complexity of networks controlling crucial cellular processes. (A) GINsim is a software tool supporting the definition and analysis of logical models of regulatory and signalling networks; Public website: http://ginsim.org. (B) EpiLog combines logical models and cellular automata for the qualitative simulation of epithelial patterning; Public website: http://ginsim.org/epilog.
We are interested in how adaptation to stressful environments is affected by interactions between organisms. For this purpose we use a multilevel approach that ranges from genes to ecosystems in the context of experimental evolution with C. elegans and different bacteria. The focus is on intra-population mechanisms, by which negative feedbacks can lead to the maintenance of genetic variability, or on interactions between species, where strong selective pressures occur between predators and prey or host and parasites.

In this context we want to broadly know:
1. If adaptation to a new environment is affected primarily by the type (host/parasite, host/commensal, predator/prey, etc.) or by the strength of interactions;
2. If the strength and type of interactions between organisms can change due to co-evolution during adaptation.

**PUBLICATIONS**


**COLLABORATIONS**

Lilia Perfeito (ICG, Portugal)
Henrique Teotónio (Institute de Biologie de l’École Normale Supérieure, France)

**FUNDING**

Fundação para a Ciência e a Tecnologia, Portugal

**PUBLIC ENGAGEMENT IN SCIENCE**

Workshop Júpiter Ciência 2014 - Theoretical and practical teaching of high school teachers, IGC, July.

IGC Open Day ’14 - hands on activities, October.
Genetic and genomic data are influenced by the demographic events that have shaped the history of populations. Such events include population collapses, expansions, or admixture processes. Our group is interested in developing new and using/testing existing methods to improve our understanding of these events and of the recent evolutionary history of species. We also, and crucially, want to understand the limits of genetic or genomic data as inferential tools. Applications go from human evolution (e.g. the Neolithic transition in Europe) to conservation genetics of wild (e.g. orang-utans, lemurs) and domesticated species (e.g. cattle, sheep).

Work currently done at the Population and Conservation Genetics (PCG) group involves field work in Madagascar, the genetic typing of endangered species (lemurs, endemic rodents), data analysis and simulation. We are also moving towards the use of genomic data. We collaborate with the laboratories Evolution & Diversité Biologique, in Toulouse, where Lounès Chikhi is a Senior researcher (Directeur de Recherche) and with colleagues from various institutions, including several in Portugal, the UK, France (Institut de Mathématiques de Toulouse, Madagascar, (Left) Makaranga, or Malaysia (Danau Girang Field Station).

The PCG has been increasingly involved in Madagascar in the last few years. We have been observing, counting and sampling several groups of vertebrates (lemurs from the Microcebus and Lepilemur genera, rodents from the endemic Endocoicus and invasive Rattus species) and from neutral, selective markers and parasite infection.

Our work is focused in the Northwest and north of Madagascar. This field work led us to become an important actor in the conservation of lemurs in Madagascar. We were therefore invited to an IUCN meeting organised in 2012. During this meeting we evaluated the conservation status of the ca. 100 recognised lemur species present in Madagascar. The IUCN (International Union for the Conservation of Nature) issued a report in 2013, which identified the lemurs as the most threatened group of vertebrates. As a follow-up, we decided with other specialists of Madagascar to write a perspective paper, which appeared in the journal Science in 2014 to call for increased attention to the situation of lemurs in Madagascar. This study attracted attention in the media, and in the conservation and scientific communities. It identified some of the major threats to biodiversity in general and to lemurs in particular and also identified regions of critical importance for the conservation of lemurs.
We are concerned with those properties of the immune system that guarantee tissue integrity as well as tolerance to commensals and food antigens while maintaining the ability to mount efficient responses to infectious agents. We approach the cellular and molecular bases of immune regulation through the analysis of various mouse models, notably addressing the efficiency of lymphocyte homeostasis. Our interests merge within various collaborative works, notably addressing the consequences of deregulated RAG activity on genomic integrity and on the very large diversity of antigen receptors through genomic rearrangement by the RAG recombinases, we also maintain a line of research assessing the consequences of deregulated RAG activity on genomic integrity and on lymphocyte homeostasis. Our interests merge within various collaborative works, notably addressing the efficiency of immunotherapies for Systemic Lupus Erythematosus, Rheumatoid-Arthritis and Type1 diabetes.

**RESEARCH INTERESTS**

PhD in Cellular and Molecular Biology
Université Aix-Marseille, France, 1989

Previous Positions:
- Research Associate | Institut Pasteur, France
- HHMI Research Associate | Harvard Medical School, USA
- Postdoctoral Fellow | Columbia University, USA

**PUBLICATIONS**


**MAIN RESEARCH IN 2014**

1. The contribution of ontogenic and differentiation time windows to the development of immune tolerance to tissues, gut microbiota, tumours and peptide therapeutics.

2. The contribution of immune repertoire, tissue physiology and their regulators to the targeting of autoimmunity.

3. Targets and off targets of the RAG recombinase.


**PROJECTS RUNNING IN 2014**

- Targets and off targets of the RAG recombinase.
- Clinical and pharmaco-economic consequences of anti-TNF drug immunogenicity.
- MAIN RESEARCH IN 2014
- Clinical and pharmaco-economic consequences of anti-TNF drug immunogenicity.
- Projects running in 2014
Different susceptibility of C57Bl/6 and BALB/c mice to heart diseases. Blue panel: Experimental Autoimmune Myocarditis (EAM). Mice were immunized with cardiac α-Myosin emulsified with CFA. After 21 days, hearts were collected and tissue sections colored with H&E to identify nuclei (purple). Sick mice present with enlarged heart and large amount of leucocyte infiltrates. About 65% of BALB/c mice develop EAM while none of the C57Bl/6 do.

Orange panel: Spontaneous Calcinosis. Heart sections of unmanipulated mice colored with Alizarin to identify calcium deposits (dark orange). Around 20% of BALB/c mice present calcinosis, a response to naturally occurring tissue damage. Calcium deposits are not found in C57Bl/6 mice.

In the objective, we first aimed at disentangling the contribution of immune and tissue components in defining mice susceptibility or resistance to autoimmune cardiomyopathy, a project that produced the images shown in the figure.

In keeping with our demonstration that the safety and efficiency of biological therapies would highly benefit from regular immunogenicity assessment (Garcés et al., ARD 2014), we developed and tested the structure required for the systematic monitoring of all patients under biologic treatments at one Hospital in the Lisbon area, a programme to be effectively initiated in 2015 and potentially extended to other institutions.
Obesity

Organisms evolved biological mechanisms that maintain an individual’s body weight within a narrow range of variation. For that purpose, different organs such as brain, fat, liver, bone, pancreas, and even the immune system, integrate nutrient-related and hormonal signals to control weight homeostasis. Our laboratory is interested in the function of the nervous system in weight control, aiming at identifying neurons that play a fundamental role in eating behaviour and metabolism. We rely on newly developed targeted mouse strains that enable the application of state-of-the-art neuro-genetic techniques: we use optogenetics to establish the role of molecularly identified neurons. For this therapeutic strategy take place however, it is fundamental to know what is the molecular machinery neurons regulating feeding behaviour. This can be done with the new translating ribosome affinity purification (TRAP) technology, which enables translational profiling of genetically identified populations of neurons. Thus a rational therapeutic strategy for treating hyperphagia would inactivate appetite neurons. For this therapeutic strategy to take place however, it is fundamental to know what is the molecular machinery neurons regulating feeding behaviour. This can be done with the new translating ribosome affinity purification (TRAP) technology, which enables translational profiling of genetically identified populations of neurons. The TRAP method involves transgenic tissue-specific expression of the fusion protein GFP-L10a. In this method, GFP serves an epitope tag that can be used to specifically precipitate polysomes. TRAP shortcuts dissociation steps and targets with neuromodulatory activity enriched in those key neurons. We believe that our experimental approach will pave the way for the identification of novel molecular targets with potential in the treatment of obesity.

PhD in Neurobiology
The Rockefeller University, USA, 2005

Previous Positions:
- Adjunct Research Associate | The Rockefeller University, USA
- Research Associate | The Rockefeller University, USA
- Postdoctoral Associate | The Rockefeller University, USA

- Collaborations
Roger Adam (University of Utrecht, The Netherlands)
Ivan Anaco (Tate University, USA)
Dennis Baturky (Department of Physiology, Istanbul Medipol University, Turkey)
Dennis Budayray (Medical Research Council, MBI, UK)
Marcelo Dietrich (Yale University, USA)
Henning Voss (Wellcome Trust, USA)
Weimin Zeng (Tsinghua University, China)
Manuel Zimmer (Institute of Molecular Pathology, Austria)

- Publications

- Funding
Fundação para a Ciência e a Tecnologia, Portugal

- Lab Members
Andrea Barreiro (Post-doc) | Started in April
Elisa Santos (Post-doc) | Started in February
Maria Inês Mahú (PhD student, IBB 2014) | Started in August
Roksana Maria Progalakis (External PhD student) | Started in February
Matilde Pereira (Master’s student) | Started in July
Nadia Kubasova (Research Technician)

- Research Interests

- Projects Running in 2014
1. Translational profiling of hypothalamic neurons controlling eating behaviour.
2. Neurons controlling lipolysis.
As sessile organisms, plants have evolved unique strategies to cope with environmental challenges that affect their growth and development. These range from morphological and physiological changes to alterations at the cellular level, but the basis for adaptation or acclimation lies ultimately at the level of the genome. The Plant Molecular Biology group uses Arabidopsis thaliana as a model system to investigate how plants perceive and respond to environmental stress at the molecular level. In particular, we are focusing on the role of RNA alternative splicing in the regulation of gene expression. The versatility of this posttranscriptional regulatory mechanism suggests an important contribution in ensuring the developmental plasticity and stress tolerance essential for plant survival. Another major ongoing project in the lab is uncovering a role for membrane transporters of the Major Facilitator Superfamily (MFS) in plant development and responses to abiotic stress. Interestingly, the functional analysis of these membrane proteins is revealing striking exceptions of the biological impact of alternative splicing in plants.

To pursue our general working hypothesis that alternative splicing plays a key role in plant responses to environmental stress, we have been following up on our functional characterization of SR proteins, which constitute a highly conserved family of major regulators of this important posttranscriptional regulatory mechanism. We found that the Arabidopsis SR-like protein SR45 regulates sugar signalling during early seedling development via modulation of the levels of the energy-sensing SNRK1 protein kinase and broadly controls alternative splicing in vivo including that of the SR45 gene itself. The endogenous splicing targets of the plant-specific SCL30a SR protein, which we have shown confers drought and salt stress tolerance during seed germination in Arabidopsis via modulation of the vacuolar acid (ABA) stress signalling pathway, are currently being identified by whole transcriptome analysis using next generation sequencing.

In 2014, we also reported the functional characterization of two novel Arabidopsis membrane transporters of the Major Facilitator Superfamily (MFS). Zinc-induced Facilitator 2 (ZIF2) is a tonoplast-localized root transporter that positively regulates plant zinc tolerance. Elevated zinc levels enhance translation of the ZIF2 gene by promoting an intron retention event in the 5’ untranslated region (5’UTR). Finally, we showed that this zinc-responsive activation of ZIF2 protein production is dependent on a secondary structure element present in the retained intron. On the other hand, ZIF-like 2 (ZFL2) is a root plasma-membrane transporter that modulates plant potassium and cesium homeostasis.

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Our results indicated that ZIFL2 promotes cellular potassium efflux in the root, thereby restricting potassium/cesium xylem loading and subsequent root to shoot translocation under high potassium conditions or in the presence of external cesium.

ZIF2 promoter is also active in floral buds.
Differential interference contrast microscopy image of GUS-stained transgenic plant carrying the ProZIF2:GFP-GUS construct.

ZIFL2 transporter does not co-localize with a tonoplast marker.
Confocal microscopy images of tobacco leaf epidermal cells transiently co-expressing a ZIFL2-GFP fusion (A) with tonoplast marker γ-TIP–mCherry (B). Merged image is shown in C. The GFP and mCherry signals are visualized by green and red coloration, respectively.
In 2014, we have accomplished a milestone in our cancer and ageing programme. We finalized one of the most comprehensive characterizations of ageing performed in a vertebrate - the zebrafish. This was done in WT individuals ranging from 3 to 36 months and was compared to telomerase mutants. The study included detailed histological characterization of selected tissues (gut, kidney, muscle, testes and brain) and quantification of molecular markers for cell proliferation, DNA damage, apoptosis and cell senescence. We also measured telomere length in these organs and analysed their transcription profile. We found that, much like human ageing, tissue and organ dysfunction occurs with distinctive rhythms in different organs. We discovered that, as individuals age, some organs accumulated short telomeres with DNA damage and this phenomenon preceded cell proliferation decline and tissue dysfunction. Conclusively, we showed that telomerase mutants suffer from premature ageing while still juveniles and die of similar causes as old individuals (mostly from wasting and infections).

Unexpectedly, but consistent with the previous observation, telomerase mutants accelerate the onset of cancer, an old age disease, to very young ages. This result has opened a clear path in understanding one of the key questions in the lab: why does the incidence of cancer increase with age?

1. The role of telomeres in ageing and cancer.
2. Establishing anti-telomerase therapeutics for invasive melanoma in zebrafish.
3. Telomerase-dependent rejuvenation in zebrafish.
4. Consequences of genome instability to adaptation and speciation.
We continued analysing data from our previous project “Lupus and its compensation in unaffected relatives by T-cell regulation” (PIC/IC/82746/2007). Results can be summarized as follows: FOXP3+ regulatory T-cells (Tregs) in Systemic Lupus Erythematosus (SLE) are functionally deficient and characterized by the reduction or absence of surface CD25 (the IL-2 receptor alpha chain). In the context of previous results indicating that unaffected relatives of SLE patients, other than the patients themselves, are able to compensate pathogenic autoimmune reactions by functional Tregs, we are studying them systematically for their Treg properties. This allowed us to distinguish two components contributing to Treg CD25 expression and its reported SLE-characteristic reduction:

1. In both SLE patients and unaffected first-degree relatives, we found surface CD25 strongly reduced in relation to control subjects already in the earliest identifiable subset, circulating CD4+FOXP3+CD45RO-CD31+ non-activated recent thymic emigrant (RTE) Tregs.

2. Unaffected relatives clearly differed from patients in properties of activated CD4+FOXP3highCD45RO+ Tregs, which upregulated CD25 versus non-activated CD45RO- Tregs to similar extents in relatives and unrelated control subjects, while not in SLE patients.

These two components were also found affected by polymorphisms in two different regions of the IL2RA locus that encodes CD25. Only the first component, RTE Treg CD25, along with the genetic variants influencing it, was significantly related to numbers and frequencies of circulating activated Tregs in unaffected relatives, while the second component, CD25 upregulation upon Treg activation, was related to the generation of FOXP3lowCD45RO+ cells reported dysfunctional in other contexts.

Our results point to an intrathymic effect present in an extended risk population, responsible for reduced CD25 in early Tregs and a subsequently decreased activation capacity. This effect seems compensated by functionally independent CD25 upregulation upon Treg activation, which is selectively deficient in SLE patients.

We further completed the project “IgE as a biomarker of Regulatory T Cell activity in autoimmune diseases” (EXP/ DTP-PIC/0644/2012). Results are currently on the way to be published.
Activity-dependent plasticity of synaptic connections is a key mechanism for learning. Long-Term Potentiation (LTP) and Long-Term depression (LTD), the cellular models of activity-dependent learning require de novo protein synthesis of plasticity-related proteins (PRPs) for its maintenance. To maintain the input-specificity of LTP and LTD a cellular mechanism has to target PRPs specifically to activated synapses. Previous studies have proposed that potentiated synapses set up “synaptic tags”, which target or capture PRPs (plasticity-related proteins) in activated synapses allowing the maintenance of synaptic plasticity an input-specific way. We propose that the synaptic tag is a structural change of the synapse that turns it permissive to synaptic plasticity. Our hypothesis is that activity modulation of the synaptic actin cytoskeleton leads to the capture of PRPs in activated synapses regulating the protein composition of the postsynaptic density and therefore the expression and maintenance of LTP. To test this we follow an electrophysiological and pharmacological approach, and test whether altering the dynamics of actin has an impact on the induction and maintenance of synaptic plasticity.

Recently, we have shown that pharmacological modulation of actin dynamics bi-directionally interferes with the ability of activated synapses to capture proteins. Synaptic capture is blocked if actin de-polymerization is inhibited whereas synaptic capture is restored by inhibition of actin polymerization. Interestingly, we also found that inhibition of actin polymerization can rescue the impairment in synaptic capture observed when CaMKII is inhibited. Taken together, these reports suggest that modulation of the actin cytoskeleton dynamics, presumably through CaMKII activation, constitutes an activity-dependent cellular mechanism allowing capture of PRPs in an input-specific manner.

To further test the role of actin in synaptic plasticity maintenance we are addressing:

1. Activity dynamics of synaptic actin cytoskeleton as the synaptic-tag.
2. The compartmentalization of synaptic plasticity: assessing the spatial rules of synaptic cooperation and competition.

**Main Research in 2014**

Activity-dependent plasticity of synaptic connections is a key mechanism for learning. Long-Term Potentiation (LTP) and Long-Term depression (LTD), the cellular models of activity-dependent learning require de novo protein synthesis of plasticity-related proteins (PRPs) for its maintenance. To maintain the input-specificity of LTP and LTD a cellular mechanism has to target PRPs specifically to activated synapses. Previous studies have proposed that potentiated synapses set up “synaptic tags”, which target or capture PRPs (plasticity-related proteins) in activated synapses allowing the maintenance of synaptic plasticity an input-specific way. We propose that the synaptic tag is a structural change of the synapse that turns it permissive to synaptic plasticity. Our hypothesis is that activity modulation of the synaptic actin cytoskeleton leads to the capture of PRPs in activated synapses regulating the protein composition of the postsynaptic density and therefore the expression and maintenance of LTP. To test this we follow an electrophysiological and pharmacological approach, and test whether altering the dynamics of actin has an impact on the induction and maintenance of synaptic plasticity.

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To further test the role of actin in synaptic plasticity maintenance we are addressing:

1. Activity dynamics of synaptic actin cytoskeleton as the synaptic-tag.
2. The compartmentalization of synaptic plasticity: assessing the spatial rules of synaptic cooperation and competition.
We study collective phenomena, such as self-organization, criticality, and pattern formation, arising from spatial and temporal constraints in physical and biological systems, with a current focus on infectious disease ecology and evolution. The central theme of our research derives from a conceptual model of pattern immunity whose collective outcome—the reinfection threshold—underlies a phenomenological transition in epidemic dynamics, with practical implications ranging from extreme geographical variability in the effect of vaccination programs to destabilized transmission favouring polymorphism in antigenically diverse pathogens. We are interested in reducing concepts and methodologies by performing specific experiments in the laboratory and in natural populations.

**REFERENCES**


**MAIN RESEARCH IN 2014**

We have been developing theory and methods to overcome current limitations in the assessment of interventions for biomedical and biological control. The novelty of our approach lies on a formal integration between laboratory and field study arms, through mathematical and statistical models.

**MANUSCRIPTS IN PRESS AND ACCEPTED**


**COLLABORATIONS**

Stephen Cordon (Liverpool School of Tropical Medicine, UK)
Marc Lapichard (Harvard School of Public Health, USA)
Catarina Rebêlo (Faculdade de Ciências da Universidade de Lisboa, Portugal)
Rafael Sá-Leão (Instituto de Tecnologia Química e de Engenharia, Portugal)
Andrew Wilage (Virginia Institute of Marine Science, USA)

**FUNDING**

Pires, Portugal

**LAB MEMBERS**

Ana Isabel Franco (Post-doc)
Eudália Gomes (Post-doc)
Caetano SM Mendes (PhD student, IGC 2015)

**PUBLICATIONS (cont.)**


The Science and Policy group works under the premise that it is possible to use the scientific method to improve the decision-making process. By gathering large amounts of data and using a broad range of approaches, we ask how political decisions can be more informed and how can scientists and the scientific method help in this process.

Current research includes:
- using internet search engines and social networks to try identify disease outbreaks and group behaviours,
- pooling available (but dispersed) information to study public understanding of science and risk communication,
- generating data (from large scale surveys to text mining techniques) to understand public policies and how to help scientists become effective advisors.

Our ultimate goals are to engage scientists and researchers in the policy-making process and to contribute to a more knowledgeable and critical society.

We have been developing several tools to manage and analyse large datasets, with the goal of extracting useful information to be used for political decisions. We will briefly describe four ongoing projects.

   From worldwide Google Trends data and Twitter we have helped answer the long-standing question of whether human reproduction cycles are biological or cultural. We have managed to infer private behaviour, from internet searchers and tweets, and predict patterns of regional sexual trends. We are preparing a paper with collaborators from Indiana University to be submitted during 2015.

2. Scientific and technological risk regulation in the social network age.
   We have also analysed Google, weather and WHO Influenza data to try to predict flu peaks. These are compared by modelling several seasons and doing real time monitoring of different platforms. We have very promising results, which are being complemented with a machine learning approach to several other Portuguese databases, including an emergency phone line and the citizen participatory platform Influenzanet. Taken together, our large datasets and complementary approaches were very successful in predicting the flu onset, in December 2014. We are now working with the Portuguese School of Public Health, responsible for tracking influenza, to implement a real-time monitoring system using our tools. This will be of great use to the local political decision makers and can be expanded to include data from other countries.

   We are also participating in a large scale project to analyse parliamentary data. For this we are developing several machine learning and sentiment analysis tools, in Portuguese, and specific to political discourse.

4. Different technologies create different risks: an assessment of the risk literacy in natural and social scientists
   Finally, the group has been working on several public understanding of science projects. From these, we highlight another large-scale approach, in which we analysed European-wide data on interest, knowledge and perception of science (Eurobarometer, PISA scores, etc) and compared these with several trends and indicators (World Bank, OECD, among others). Our results have shown a non-intuitive relation between investment and perception and we are in the process of expanding the analysis to include surveys and possibly focus groups.
Gordo, Isabel
Group Leader at IGC since 2004

PhD in Evolutionary Biology
University of Edinburgh, UK, 2002

Previous Positions:
Research Associate | University of Oxford, UK
Post-doc | IGC, Portugal

External website

RESEARCH INTERESTS

The area of our research interests is Evolutionary Biology. We combine both theoretical and empirical work with the aim at understanding the major forces that shape variation in populations.

We use E. coli as a model organism to test theoretical predictions about the genetics of adaptation in the context of environmental changes due to abiotic and biotic factors. Main topics of current work are evolution of antibiotic resistance caused by chromosomal mutations, adaptation to cells of the innate immune system, transition of commensalism to pathogenesis and evolution in the gut microbiota.

PUBLICATIONS


COLLABORATIONS

Thomas Batallón (University of Karlsruhe, Germany)
Paulo Carneiro (Universidade Federal Rural de Pernambuco, Brazil)
José de Araújo (ICG, Portugal)
Miguel Gradinho Ferreira (ICG, Portugal)
Michael Haber (Universität zu Köln, Germany)
Gabriel Mancos (Université Lyon 1, France)
Wile Martinon (Wellcome Trust Sanger Institute, UK)
Eduardo Rocha (Institut Pasteur, France)
Miguel Soares (ICG, Portugal)
Linda Wolfl (Estonian University, Estonia)
Karmen Xavier (ICG, Portugal)

FUNDING

European Research Council, European Commission
Fundação para a Ciência e a Tecnologia, Portugal

PROJECTS RUNNING IN 2014

1. Adaptation within ecosystems.
2. Epistasis and antibiotic resistance.
3. Adaptation of commensal bacteria to the mammalian gut.

Adaptation to novel environments involves the accumulation of beneficial mutations. If these are rare the process will proceed slowly with each one sweeping to fixation on its own. On the contrary if they are common in clonal populations, individuals carrying different beneficial alleles will experience intense competition and only those clones carrying the stronger effect mutations will leave a future line of descent. This phenomenon is known as clonal interference and the extent to which it occurs in natural environments is unknown. One of the most complex natural environments for E. coli is the mammalian intestine, where it evolves in the presence of many species comprising the gut microbiota. We have studied the dynamics of adaptation of E. coli populations evolving in this relevant ecosystem. We show that clonal interference is pervasive in the mouse gut and that the targets of natural selection are similar in independently E. coli evolving populations. These results illustrate how experimental evolution in natural environments allows us to dissect the mechanisms underlying adaptation and its complex dynamics and further reveal the importance of mobile genetic elements in contributing to the adaptive diversification of bacterial populations in the gut.

PUBLIC ENGAGEMENT IN SCIENCE

Media appearance in newspapers and other channels, January and March.
IGC stand at NOS Alive'14 – scientific speed dating activity, July.
IGC Open Day’14 – public talk and hands-on activities, October.

MAIN RESEARCH IN 2014

Adaptation of commensal bacteria to the mammalian gut

Epistasis and antibiotic resistance

Adaptation within ecosystems

LAB MEMBERS

Isabel Gordo (Post-doc)
Roberto Batallón (Post-doc) | Started in November
Paulo Carneiro (Post-doc) | Started in December
Nelson Fonseca (Post-doc) | Started in April
Ilda Pereira (Post-doc)
Ricardo Pia (Post-doc)
Ana Magalhães Sousa (Post-doc)
Richard Pia (PhD student, IGC, 2013) | Left in August
Sara Soares (PhD student, IBS, 2015)
Ilda Filipe (PhD student)
Teresa Costa (PhD student)
Plinio Lourenço (External Masters student) | Left in December
Franko Al (Research Assistant) | Left in August
Plinio Lourenço (Research Assistant) | Left in September
Ricardo Pia (Research Assistant) | Started in April
Plinio Lourenço (Research Assistant) | Started in October
Catarina Fonseca (Research Assistant)
Catarina Bourgard (Laboratory Manager) | Left in March
Daniela Amorim (Laboratory Manager, Research assistant) | Started in March

Catafago, Isabel (Research Assistant)
Catarina Pinto (Research Assistant)
Antónia Pinto (Research Assistant) | Started in October
Hugo Barreto (Research Assistant) | Started in April
Maria Azevedo (Research Assistant) | Left in September
Hajrabibi Ali (Research Assistant) | Left in August
Marta Lourenço (External Masters student) | Left in December
Henrique Costa (External Masters student)
João Batista (External PhD student)
Ricardo Ramiro (Post-doc)
João Proença (Post-doc)
Nélson Frazão (Post-doc) | Started in April
Paulo Durão (Post-doc)
Roberto Balbontin (Post-doc) | Started in November
Ana Magalhães Sousa (Post-doc)
Miguel Godinho Ferreira (Post-doc)
Jocelyne Perotte (Post-doc, IGC, Portugal)
Lindi Wahl (Western University, Canada)
Miguel Soares (IGC, Portugal)
Eduardo Rocha (Institut Pasteur, France)
Ville Mustonen (Wellcome Trust Sanger Institute, UK)
Gabriel Marais (Université Lyon 1, France)
Michael Lässig (Universität zu Köln, Germany)
Miguel Ferreira (Alternative)
Our work focuses on mechanisms of resistance to the ubiquitous intracellular protozoan parasite, Toxoplasma gondii, a malaria relative, which infects about 40% of the human race. We study immunity of mice against T. gondii because the primary hosts of the parasite, in which it makes gametes and does meiosis, is cats, so the T. gondii life cycle, and its abundance in our environment, is thus driven by an infectious cycle between cat and mouse. Mouse immunity against T. gondii is based on a mechanism absent in humans, inducible GTPases (IRG proteins) that cooperatively destroy the vacuole in which the parasite lives. This mechanism has in turn been targeted by the parasite, via a family of kinases that inactivate IRG proteins. Both the IRG proteins and the kinases are massively polymorphic, consistent with a complex co-evolutionary dynamic. Our work stretches from ecological studies on wild mice to cell biological, biochemical and structural studies.

RESEARCH INTERESTS

Our work focuses on mechanisms of resistance to the ubiquitous intracellular protozoan parasite, Toxoplasma gondii, a malaria relative, which infects about 40% of the human race. We study immunity of mice against T. gondii because the primary hosts of the parasite, in which it makes gametes and does meiosis, is cats, so the T. gondii life cycle, and its abundance in our environment, is thus driven by an infectious cycle between cat and mouse. Mouse immunity against T. gondii is based on a mechanism absent in humans, inducible GTPases (IRG proteins) that cooperatively destroy the vacuole in which the parasite lives. This mechanism has in turn been targeted by the parasite, via a family of kinases that inactivate IRG proteins. Both the IRG proteins and the kinases are massively polymorphic, consistent with a complex co-evolutionary dynamic. Our work stretches from ecological studies on wild mice to cell biological, biochemical and structural studies.

PUBLICATIONS


COLLABORATIONS

John Boothroyd (Stanford University, USA)
Veli Hornung (University of Bonn, Germany)
Eicke Latz (University of Bonn, Germany and University of Massachusetts, USA)
David Sibley (Washington University St Louis, USA)

FUNDING

Deutsche Forschungsgemeinschaft, Germany
Janody, Florence
Group Leader of IGC since 2006

The actin cytoskeleton controls numerous cellular processes. Actin filaments (F-actin) are not found in the cells as disorganized meshworks, but rather as networks with precise organizations, assembled at specific locations. Numerous lines of evidence indicate that the geometrical, mechanical and dynamic properties of each F-actin network are specifically adapted to perform a particular cellular function. We have reported reciprocal feedbacks between F-actin and the activity of various oncoproteins, including Src kinase, c-Jun N-terminal kinase and Yorkie in Drosophila epithelia.

We aim to determine how distinct F-actin networks are built by signal transduction pathways. What are the composition and properties of these networks? What is the molecular function of these networks in transducing signalling activities?

Our work will have major repercussions in the cell biology field, as it will permit to explore the extensive diversity of F-actin networks built within a cell and reveal the mechanisms by which cells, that contain a complex mixture of F-actin networks built within a cell, reveal the mechanisms by which cells, that contain a complex mixture of F-actin-regulatory proteins in a common cytoplasm, assemble distinct F-actin-based structures at specific subcellular locations. In addition, our work will have a major impact in the cancer field as it will allow understanding how F-actin alterations impact on growth control mechanisms and cancer development.

PhD in Cell Biology, Structural Biology and Microbiology
Université de la Méditerranée, France, 1999

Previous Positions:
Research Associate | Developmental Biology Institute of Marseille Luminy, France
Research Associate | Skirball Institute, USA

PUBLICATIONS


MANUSCRIPTS ACCEPTED


COLLABORATIONS

- Fernando Casares (Universidad Pablo de Olavide, Spain)
  (Biotechnology Centre, Germany)
  (ICG, Portugal)
- Raquel Severino (Universidade de Trás-os-Montes e Alto Douro, Portugal)
- Gaspar P., Holder M., Russell M., Collonson L., Janody F. and Tapon N.

FUNDING

- Fundação para a Ciência e a Tecnologia, Portugal
excess to sustain tissue growth (Amandio et al., 2014).

To characterize the molecular mechanism by which CP limits Yki-mediated tissue growth, we screen for additional actin regulators involved. We have identified the actin-associated LIM domain protein Zyxin (Zyx) as a key player. Using a zyx mutant allele generated by TALEN endonucleases, we show that Zyx antagonises the FERM-domain protein Expanded (Ex), an upstream Yki regulator, to control tissue growth, eye differentiation and F-actin accumulation. Zyx membrane targeting promotes the interaction between the transcriptional co-activator Yki and the transcription factor Scalloped (Sd), leading to activation of Yki target gene expression and promoting tissue growth. Finally, we show that Zyx’s growth-promoting function is dependent on its interaction with the actin-associated protein Enabled (Ena) via a conserved LPPPP-motif, and is antagonised by CP. Because vertebrate Zyx relocates to strained or severed actin filaments our observations argue that the antagonism between Zyx/Ena and CP on F-actin links mechanical forces to Yki oncogenic activity (Casper et al., accepted).

▶ (A) Zyxin/Enabled antagonises Expanded and Capping Protein to couple F-actin and Yoriki-dependent organ growth (B-G) Removing zyxin function suppresses the eye defects induced by the loss of expanded. (B, D, F) Scanning electron micrographs or (C, E, G) retinas at 40 h of pupal development for the genotypes indicated. Retinas are stained with anti-Disc-large (Dlg) to outline cell shapes.
In addition to genomic information embedded in the primary DNA sequence, additional epigenetic information is propagated along cell divisions that “memorizes” gene activity states and specific chromatin structures. Epigenetic modes of inheritance impact many aspects of biology that includes development, gene regulation and disease. Several molecular components such as histone proteins and modifications thereof have been implicated in this process but in most cases we don’t understand the logic of how something other than DNA can be faithfully duplicated when a cell divides. We have a broad interest in how this works. We use the mammalian centromere as a model for chromatin-based epigenetic inheritance. We employ molecular genetic and cell biological tools with a focus on novel fluorescent labelling techniques, high-end microscopy and the latest tricks in genetic engineering of human cells to tackle a wide range of problems in this emerging and fascinating area of biology.

PhD in Molecular Genetics
Leiden University, The Netherlands, 2002

Previous Positions:
Post-doc | Ludwig Institute for Cancer Research, La Jolla, USA

External website

**PUBLICATIONS**


**COLLABORATIONS**

Ben E. Black (University of Pennsylvania, USA)
Don K. Cleveland (Ludwig Institute for Cancer Research, San Diego, USA)
Ivan Correa (New England BioLabs, USA)
Daniel R. Foltz (University of Virginia, USA)
Robert Kingston (Harvard University, USA)
Jagesh Shah (Harvard University, USA)

**FUNDING**

EMBO Installation Grant
European Research Council

**PUBLIC ENGAGEMENT IN SCIENCE**

Media appearance on TV, newspapers and other channels, January and July.

ICG Open Day ’14 - hands on activities, October.

Centromeres form the site of chromosome attachment to microtubules during mitosis and are responsible for driving chromosome segregation. Identity of these loci is maintained epigenetically by nucleosomes containing the histone H3 variant CENP-A. The amount of centromeric CENP-A has direct implications for both the architecture and epigenetic inheritance of centromeres. In 2014 our main achievement has been to determine this number, how copy number is regulated and how it impacts on centromere function. Using complementary fluorescence-based strategies, we determined that typical human centromeres contain ~400 molecules of CENP-A, which is controlled by a mass-action mechanism. This number, despite representing only ~4% of all centromeric nucleosomes, forms approximately 50-fold enrichment to the overall genome. In addition, although pre-assembled CENP-A is randomly segregated during cell division, this amount of CENP-A is sufficient to prevent stochastic loss of centromere function and identity. Finally, we produced a statistical map of CENP-A occupancy at a human neocentromere and identified nucleosome positions that feature CENP-A in a majority of cells. Combined we arrive at a quantitative view of the centromere that provides a mechanistic framework for both robust epigenetic inheritance of centromeres and the paucity of neocentromere formation.
Mallo, Moisés
Group Leader of IGC since 2001

Our group is interested in several aspects of vertebrate embryonic development. The ultimate goal of our research is to understand the molecular mechanisms that translate patterning information into morphogenetic processes during formation of the vertebrate embryo. More recently, we have also become interested in the role that those processes played in the evolution of the vertebrate body plan. In general, most of our work uses the mouse as the model system, and our approaches have a main focus on in vivo functional analyses, but we are incorporating other model systems to our approaches, mostly as a consequence of the recent Evo-Devo twist in our research. Some of the active projects in the laboratory are outlined below.

RESEARCH INTERESTS

Previous Positions:
- Junior Group Leader | Max Planck Institute of Immunobiology, Freiburg, Germany
- Postdoctoral Fellow | Roche Institute of Molecular Biology, New Jersey, USA

Institutional Role at IGC:
- Head of the Transgenics Unit

PUBLICATIONS


COLLABORATIONS

Denis Duboule (University of Geneva, Switzerland)

PROJECTS RUNNING IN 2014

1. The molecular mechanism of Hox group 6 rib-promoting activity.
2. The mechanisms controlling the activity of axial progenitors.
3. The role of specific peptide motifs and posttranslational modifications in activity of Hox group 10 genes.

MAIN RESEARCH IN 2014

Extension of the vertebrate body results from the concerted activity of many signals in the posterior embryonic end. Among them, Wnt3a has been shown to play relevant roles in the regulation of axial progenitor activity, mesoderm formation and somitogenesis. However, its impact on axial growth remains to be fully understood. Using a transgenic approach in the mouse, we found that the effect of Wnt3a signaling varies depending on the target tissue. High levels of Wnt3a in the epiblast prevents formation of neural tissues, but did not impair axial progenitors from producing different mesodermal lineages. These mesodermal tissues maintained a remarkable degree of organization, even within a severely malformed embryo. However, from the cells that failed to take a neural fate, only those that left the epithelial layer of the epiblast activated a mesodermal program. The remaining tissue accumulated as a folded epithelium that kept some epiblast-like characteristics. Together with previously published observations, our results suggest a dose-dependent role for Wnt3a in regulating the balance between renewal and selection of differentiation fates of axial progenitors in the epiblast. In the paraxial mesoderm, appropriate regulation of Wnt/β-catenin signaling was required not only for somitogenesis, but also for providing proper anterior-posterior polarity to the somites. Both processes seem to rely on mechanisms with different requirements for feedback modulation of Wnt/β-catenin signaling, once segmentation occurred in the presence of high levels of Wnt3a in the presomitic mesoderm, but not after permanent expression of a constitutively active form of β-catenin. Together, our findings suggest that Wnt3a/β-catenin signaling plays sequential roles during posterior extension, which are strongly dependent on the target tissue. This provides an additional example of how much the functional output of signaling systems depends on the competence of the responding cells.

LAB MEMBERS

Ana Casacca (Post-doc)
Ana Rita Aires (PhD student, PIBS 2011)
Csilla Iva (PhD student, PIBS 2010)
Irina Vanita Laheres (PhD student, PIBS 2011)
André Dias (Masters student) Started in September
Ana Novo (Research Technician)

FUNDING

Fundação para a Ciência e a Tecnologia, Portugal

PUBLIC ENGAGEMENT IN SCIENCE

IGC Open Day’14 – public talk and hands on activities, October.
Media appearance on TV and newspapers, coverage of the Mallo e Castro Award, November.

Sustained Wnt3a expression affects the function of axial progenitors. Lateral (A,C) and ventral (B,D) views of wild type (A,B) and Cdx2P-Wnt3a (C,D) transgenic embryos stained by carmine. Transgenic embryos develop normal heads and necks but their trunks and tails are strongly affected. The red arrow indicates the border between these two areas. The trunks are strongly reduced as seen by the short distance between the limb primordia (white arrow).
Changes in the environment profoundly shape developmental and behavioural responses in all organisms, a process known as phenotypic plasticity. We are, however, only beginning to understand the mechanisms that integrate information from the environment to coordinate this plasticity. In my laboratory, we seek to understand how environmental cues influence development and behaviour and how these interactions evolve to generate species-specific phenotypes. We approach this problem at multiple biological levels with the goal of understanding:

1) the mechanisms that allow the environment to modify the synthesis of hormones necessary for development;
2) how organs interpret hormonal cues to coordinate their development with that of the whole body, and;
3) how the choices animals make while foraging impact their development and life history.

**PROJECTS RUNNING IN 2014**

1. The ontogeny of foraging behaviour.
2. Mechanisms underlying nutritional plasticity in body and organ size.
4. Evolution of niche specialization and foraging strategies.

**NUTRITION-DEPENDENT REGULATION OF BODY SIZE IN DROSOPHILA MELANOGASTER**

Organisms of all phyla regulate their body size in response to a number of environmental factors, including nutrition. Both the rate of growth and the length of the growth period determine final body size. Nutrition regulates growth rates via the insulin and target of rapamycin (TOR) pathways. In insects, a size-dependent checkpoint known as critical weight determines when growth ceases. Insulin and TOR signaling in the prothoracic gland (PG) regulates critical weight by controlling the production of the steroid hormone ecdysone. Thus, nutrition directly affects both the rate and duration of the growth period.

Over the past year, we have described how organs coordinate their development with that of the whole body and how the developmental hormone juvenile hormone regulates body size and perturbs insulin signaling in Drosophila. We have also investigated how organs coordinate their development with the whole body in varied environments.

**PUBLIC ENGAGEMENT IN SCIENCE**

- LabEscolas project - Tutorship of high-school students, IGC, January - June.
- Media appearance in newspapers and other channels, June and November.
- Workshop Inspirar Ciência 2014 - Theoretical and practical teaching of high school teachers, IGC, July.
- Children’s European Schools - Webinar for basic and high school students from Europe, July.
- IGC Open Day 2014 - Hands on activities and participation in the organizing committee, October.
We are interested in how environmental conditions, especially temperature and nutrition, affect body and organ size, Life history traits, and foraging strategies in species of the fruit fly, *Drosophila*.
Sepsis is a life-threatening condition most often initiated by a bacterial infection. It arises as a systemic inflammatory response syndrome, but if not promptly recognized and treated can progress to severe sepsis and septic shock and ultimately multi-organ failure and death. Recently, our laboratory used a drug screen to identify the clinically approved group of anthracyclines as potent in vivo inhibitors of two pro-inflammatory key initiators of sepsis, tumour necrosis factor and interleukin-1β. In vivo, anthracyclines confer strong protection of both sepsis and septic shock, and ultimately multi-organ failure and death. Based on our recent discovery of anthracyclines as potent effective drugs in the CLP mouse model of sepsis, without modifying the bacterial burden and their dependence on the activation of DDR for protection, we propose that the identification of the molecular events downstream of the DDR has the potential to provide a molecular framework to explain the mechanisms of tissue tolerance to infection and other deleterious or lethal stressors.

We aim to explore our remarkable findings and to determine how anthracyclines protect from sepsis in model organisms, downstream of their dependence on the activation of DDR for protection, we propose that the identification of the molecular events downstream of the DDR has the potential to provide a molecular framework to explain the mechanisms of tissue tolerance to infection and other deleterious or lethal stressors.

1. Molecular mechanisms of induced protection against sepsis by DNA damage responses.
2. shRNA-based dissection of phagosome-to-cytosol antigen export in dendritic cells.
3. Effect of sleep disorders on circadian rhythms.
We study how chromosome architecture contributes to faithful genome segregation. Genome stability relies on two major changes in chromosome organization: 1) The two-sister DNA molecules remain tightly associated with each other from the moment of DNA replication until the later stages of the subsequent mitosis; 2) At the onset of nuclear division, chromatin is converted into compact structures with the right mechanical properties (size, flexibility, and rigidity) to facilitate their segregation.

Our laboratory adopts a multidisciplinary approach, combining Drosophila genetics, acute protein inactivation, 4D-live cell imaging and biophysical/mathematical modelling to evaluate how dynamic mitotic chromosomes are assembled and how their morphology influences the mechanical aspects of chromosome movement and cell cycle checkpoint signalling. In parallel we aim to dissect how different cells respond to compromised chromosome cycle checkpoint signalling. In parallel we aim to model how different cells respond to compromised chromosome cycle checkpoint signalling.

We show that full sister chromatid separation is not sufficient to elicit a robust response in Drosophila cells.

We have also developed a mathematical modelling for SAC response to premature loss of chromatid cohesion. We show that full sister chromatid separation is not sufficient to elicit a robust response in Drosophila cells. We explain how sister chromatid cohesion defects may give rise to aneuploid cells.

All together these results provide a theoretical model describing several feedback loops involved in the poor SAC response to premature loss of cohesion. We show that full sister chromatid separation is not sufficient to elicit a robust response in Drosophila cells. We explain how sister chromatid cohesion defects may give rise to aneuploid cells. A manuscript describing these results is currently under preparation and will be submitted soon.

Sister chromatid cohesion, mediated by the cohesin complex, is essential for the fidelity of mitosis as precocious sister chromatid separation leads to random chromosome segregation. Mitotic errors are prevented by the Spindle Assembly Checkpoint (SAC), a surveillance mechanism that inhibits anaphase onset until all chromosomes are properly aligned and bioriented. Biorientation, in turn, depends on sister chromatid cohesion. It should therefore be expected that the SAC arrests mitosis when loss of sister chromatid cohesion occurs. However, cumulative evidence suggests that the SAC is not robust enough to detect and halt cell division in the present of cohesion loss. The mechanism behind this poor response is not properly understood. To address this issue we made used of a system to acutely induce sister chromatid separation (TEV protease mediated cleavage) in Drosophila developing brains to probe for the efficiency of the SAC in response to premature loss of chromatid cohesion. We show that full sister chromatid separation is not sufficient to elicit a robust checkpoint response and cells abnormally exit mitosis with high segregation errors after a short mitotic delay. Using quantitative imaging analysis we show that the weak checkpoint response is caused a gradual declining efficiency in the error correction machinery, leading to abnormal stabilization of tensionless kinetochore-microtubules interactions and consequent weak SAC signalling.

We have also developed a mathematical modelling for SAC response to cohesion loss, in collaboration with Prof. Bela Novak (University of Oxford) to provide a theoretical model describing several feedback loops involved in the poor SAC response to premature cohesion loss. All together these results explain how sister chromatid cohesion defects may give rise to aneuploid cells. A manuscript describing these results is currently under preparation and will be submitted soon.

Previous Positions:
Postdoctoral Research Associate | Department of Biochemistry, University of Oxford, UK

PhD in Biochemistry
Universidade de Coimbra, Portugal, 2007

Research Interests
We study how chromosome architecture contributes to faithful genome segregation. Genome stability relies on two major changes in chromosome organization:

1. The two-sister DNA molecules remain tightly associated with each other from the moment of DNA replication until the later stages of the subsequent mitosis;
2. At the onset of nuclear division, chromatin is converted into compact structures with the right mechanical properties (size, flexibility, and rigidity) to facilitate their segregation.

Our laboratory adopts a multidisciplinary approach, combining Drosophila genetics, acute protein inactivation, 4D-live cell imaging and biophysical/mathematical modelling to evaluate how dynamic mitotic chromosomes are assembled and how their morphology influences the mechanical aspects of chromosome movement and cell cycle checkpoint signalling. In parallel we aim to dissect how different cells respond to compromised chromosome cycle checkpoint signalling.

We show that full sister chromatid separation is not sufficient to elicit a robust response in Drosophila cells.

We have also developed a mathematical modelling for SAC response to premature loss of chromatid cohesion. We explain how sister chromatid cohesion defects may give rise to aneuploid cells.

All together these results provide a theoretical model describing several feedback loops involved in the poor SAC response to premature loss of cohesion. We show that full sister chromatid separation is not sufficient to elicit a robust response in Drosophila cells. We explain how sister chromatid cohesion defects may give rise to aneuploid cells. A manuscript describing these results is currently under preparation and will be submitted soon.

Sister chromatid cohesion, mediated by the cohesin complex, is essential for the fidelity of mitosis as precocious sister chromatid separation leads to random chromosome segregation. Mitotic errors are prevented by the Spindle Assembly Checkpoint (SAC), a surveillance mechanism that inhibits anaphase onset until all chromosomes are properly aligned and bioriented. Biorientation, in turn, depends on sister chromatid cohesion. It should therefore be expected that the SAC arrests mitosis when loss of sister chromatid cohesion occurs. However, cumulative evidence suggests that the SAC is not robust enough to detect and halt cell division in the present of cohesion loss. The mechanism behind this poor response is not properly understood. To address this issue we made used of a system to acutely induce sister chromatid separation (TEV protease mediated cleavage) in Drosophila developing brains to probe for the efficiency of the SAC in response to premature loss of chromatid cohesion. We show that full sister chromatid separation is not sufficient to elicit a robust checkpoint response and cells abnormally exit mitosis with high segregation errors after a short mitotic delay. Using quantitative imaging analysis we show that the weak checkpoint response is caused a gradual declining efficiency in the error correction machinery, leading to abnormal stabilization of tensionless kinetochore-microtubules interactions and consequent weak SAC signalling.

We have also developed a mathematical modelling for SAC response to cohesion loss, in collaboration with Prof. Bela Novak (University of Oxford) to provide a theoretical model describing several feedback loops involved in the poor SAC response to premature cohesion loss. All together these results explain how sister chromatid cohesion defects may give rise to aneuploid cells. A manuscript describing these results is currently under preparation and will be submitted soon.

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The main research interest of my lab is the integrative study of social behaviour that combines the study of proximate causes and ultimate consequences (gene modules, hormones, neural circuits, cognitive processes) and ultimate effects (evolutionary consequences). In particular, we aim to understand how brain and behaviour can be shaped by social environment, and how social cognitive, neural and genetic mechanisms underlying plasticity in the expression of social behaviour have evolved. Current research questions centre on four topics:

1. Evolution of social cognition and of its neuromolecular mechanisms – we aim to understand if social plasticity is as an organism’s performance trait that impacts Darwinian fitness and may itself be subject to selection.
2. Genomic and epigenomic mechanisms of social plasticity – we seek to understand how the same genome can produce different social phenotypes in response to key social cues in the environment.
3. Neuroendocrinology of social interactions and of social plasticity – this research aims to understand how brain and behaviour can be shaped by social context (social eavesdropping); and (iii) learn associatively and collect and use social information in order to adjust their behaviour in relevant settings. In 2014, our research has focused on three broad questions, for which a brief description of main achievements is provided below:

1. Evolution of social cognition and of its neuromolecular mechanisms. We have progressed in the establishment of zebrafish as a relevant model for the comparative study of the neuromolecular mechanisms of social cognition. Specifically, we have shown that zebrafish are a suitable model for the study of social cognition and of its neuromolecular mechanisms.

2. Genomic and epigenomic mechanisms of social plasticity. We have shown in zebrafish that: (i) acute social interactions elicit major changes in zebrafish that (ii) acute social interactions elicit major changes in the expression of social behaviour.

3. COPEWELL: A new integrative framework for the study of fish welfare based on the concepts of allostatics, appraisal and coping styles.

4. Neural mechanisms of cognitive bias. The main research interest of my lab is the integrative study of social behaviour that combines the study of proximate causes and ultimate consequences. We address these questions using a combination of methods, evolutionary and neuroethology studies both in zebras and in non-model fish species that can be studied in ecologically relevant settings. In 2014, our research has focused on three broad questions, for which a brief description of main achievements is provided below:

1. Evolution of social cognition and of its neuromolecular mechanisms. We have progressed in the establishment of zebrafish as a relevant model for the comparative study of the neuromolecular mechanisms of social cognition. Specifically, we have shown that zebrafish are able to (i) recognize particular conspecifics (social memory), (ii) collect and use social information in order to adjust their behaviour to social context (social eavesdropping); and (iii) learn associatively and from conspecifics (e.g. observational conditioning of fear response).

2. Genomic and epigenomic mechanisms of social plasticity. We have shown in zebrafish that (i) acute social interactions elicit major changes in the expression of social behaviour.

3. COPEWELL: A new integrative framework for the study of fish welfare based on the concepts of allostatics, appraisal and coping styles.

4. Neural mechanisms of cognitive bias.
changes in the brain transcriptome; (ii) specific social experiences are paralleled by specific brain gene expression profiles; and (iii) cognitive appraisal of the interaction outcome is needed to trigger a genomic response. In a non-model blenniid species that has alternative reproductive tactics, we established that the tactics are sequential and that there are alternative life-history pathways, and we have also characterized the brain transcriptome of each tactic and of the switch between tactics using RNAseq.

3. Neuroendocrinology of social interactions and of social plasticity. Using cichlid fish as a model we have shown how cognitive variables modulate the response to social challenges. We have also progressed in the study of the role of the nonapeptides of the vasopressin-oxytocin (VP-OXT) family on social behaviour, namely in social cooperation in a cleaner fish mutualism (collaboration with Bhasary lab in Neuchâtel) and in social competition in cichlid fish dominance hierarchies. Finally, we started developing relevant transgenic zebrafish lines to study the role of this nonapeptide system on social behaviour and we have already been successful (collaboration with Levkowitz lab, Weizmann Inst.) in having one stable OXT-GAL4:UAS-NTR line that allows visualization and silencing of OXT neurons, and CRISPR KO lines for the 2 oxytocin receptors.

**MAIN RESEARCH IN 2014** (cont.)

**FUNDING**

BIAL
European Commission, Framework Programme 7
Fundação para a Ciência e a Tecnologia, Portugal

**PUBLIC ENGAGEMENT IN SCIENCE**

IGC Open Day ’14 – hands on activities, October.

**COLLABORATIONS**

Jörg Becker (IGC, Portugal)
Miguel Godinho Ferreira (IGC, Portugal)
Hans Hofmann (University of Texas at Austin, USA)
Koichi Kawakami (National Institute of Genetics, Mishima, Japan)
Gil Levkowitz (Weizmann Institute, Israel)
Daniel Petersen (The Chicago Medical School at Rosalind Franklin University of Medicine and Science, USA)
Svante Winberg (Uppsala University, Sweden)

**MAIN RESEARCH IN 2014**

1. Behavior and brain development. In the non-model blenniid species, we have characterized the brain transcriptome of the different reproductive tactics and the switch between them and we have identified a number of key genes involved in the switch process.

2. Social behaviour and brain development. Using zebrafish as a model, we have shown how the social environment can modulate the development of the brain and behavior. We have also progressed in the study of the role of the nonapeptides of the vasopressin-oxytocin (VP-OXT) family on social behaviour, namely in social cooperation in cleaner fish mutualism (collaboration with Bhasary lab in Neuchâtel).

**NEW RESEARCH IN 2015**

3. Neuroendocrinology of social interactions and of social plasticity. Using cichlid fish as a model we have shown how cognitive variables modulate the response to social challenges. We have also progressed in the study of the role of the nonapeptides of the vasopressin-oxytocin (VP-OXT) family on social behaviour, namely in social cooperation in a cleaner fish mutualism (collaboration with Bhasary lab in Neuchâtel) and in social competition in cichlid fish dominance hierarchies. Finally, we started developing relevant transgenic zebrafish lines to study the role of this nonapeptide system on social behaviour and we have already been successful (collaboration with Levkowitz lab, Weizmann Inst.) in having one stable OXT-GAL4:UAS-NTR line that allows visualization and silencing of OXT neurons, and CRISPR KO lines for the 2 oxytocin receptors.
1. Inhibition of Interferon responses by African Swine Fever Virus.

The objective of the project is to determine the mechanism and consequences of three non-homologous non-evasion genes of ASFV. The ASFV A276R gene from MGF360 inhibited the induction of IFN-beta via both the TLR3 and the cytosolic pathways, targeting IRF3, but not IRF7 nor NF-κB. Interestingly, the protein co-localizes with PML bodies which are critical for the host anti-virus response. The ASFV A528R inhibited the induction of both NF-κb and IRF3 branches of the type I IFN induction signalling pathway and the impact of IFN response via both IFN type I and type II stimulation. The ASFV I329L gene is a functional viral TLR3 homologue inhibiting the induction of IFN at the level of TRIF. Deletion of one or more of these genes is a rational strategy for construction of a deletion mutant vaccine. Finally, our work clearly demonstrates that non-homologous, unassigned viral genes may be viewed as a repository of host evasion strategies, only identifiable through functional assays.


The importance of herpesviruses is evident from their ubiquitous prevalence in the human population and the diverse range of diseases that they provoke. Their ability to establish latency provides a compelling example of how herpesviruses successfully evade the immune system and manipulate cellular biology. One promising approach for the development of novel anti-viral strategies is to study viral proteins involved in these host-pathogen interactions. We have focused on the induction of IL-8 by HCMV as this enhances viral replication and dissemination of the virus by neutrophils. We have identified the HCMV UL76 gene, conserved in all herpesviruses, as an inducer of IL-8, and thus with an important impact on HCMV pathogenesis. The induction of IL-8 by UL76 results from activation of the DNA Damage response, which may also explain why UL76 also induces cell cycle arrest. These findings are a clear example of how one virus host evasion molecule manipulates intracellular signalling pathways with different outcomes that will be beneficial for viral infection.

Finally, the fact that UL76 is a non-homologous gene substantiates the premise that many such pathogen genes without homology may indeed have evolved for host manipulation, and are a repository of potential useful tools for experimental manipulation in health and disease.
Our previous research in genetics of inflammatory responses to malaria infection drove us to ask how infection/inflammation impacts on cellular metabolism and organ physiology. One line of research will be focused on evaluating the role of foetal-derived trophoblasts, an intriguing cell type that coapt functional roles of maternal-fetal exchanges, blood microcirculatory regulation and inflammatory responses. This research will impact our understanding of the involvement of foetal factors in vaso-inflammatory placental disorders and may unveil pharmacological targets to promote foetal viability and protection mechanisms valuable in abortion prevention. The liver is another target organ of maternal-fetal exchanges, blood microcirculatory impairments in the diabetes pathogenesis. Project running in 2014: Insulin clearance (dys)regulation – clarifying the mist. Diabetes is frequently associated with fatty liver disease. We have set-up mouse models of non-alcoholic fatty liver disease (NAFLD) induced by hypercaloric diets. Using different diets we found that effects of fructose supplementation in potentiating NAFLD and other dysmetabolism parameters. We have found a 2-fold reduction at G17 and G18 and negatively correlated to maternal parasitemia. These results indicate that infection impacts NO production that could compromise the progression of normal gestation. This work raises the possibility that treatment with NO donors could be an adjuvant to improve pregnancy outcomes.

Penha Gonçalves, Carlos
Group Leader at IGC since 2005

PhD in Immunology
University of Umeå, Sweden, 1999

Previous Positions:
Post-doc | Cambridge Inst. of Medical Research, UK

Institutional Role at IGC:
Head of Genomics Unit
Member of the Ethics Committee

REFERENCES

1. Malaria in pregnancy: impact of Plasmodium infection in placental vasoactive regulation. Malaria infection during pregnancy leads to placental cells (trophoblasts) dysfunction and impacts maternal-fetal gas and nutrient exchanges. We have recently shown in the mouse placenta that infected erythrocytes (IEs) preferentially accumulate in areas of low maternal blood flow suggesting that apart from molecular interactions placental microcirculatory dynamics also play a role in parasite sequestration. We found that receptors for bradykinin (B2R), vascular endothelial growth factor (KDR) and endothelial nitric oxide synthase (eNOS) are down-regulated at gestational day (G)18 (final-stage pregnancy) in infected placentas. Nitrite production in maternal sera and in placenta also showed approximately 2-fold reduction at G17 and G18 and negatively correlated to maternal parasitemia. These results indicate that infection impacts NO production that could compromise the progression of normal gestation. This work raises the possibility that treatment with NO donors could be an adjuvant to improve pregnancy outcomes.

2. Liver dysmetabolism: insulin clearance (dys)regulation – clarifying the mist. Diabetes is frequently associated with fatty liver disease. We have set-up mouse models of non-alcoholic fatty liver disease (NAFLD) induced by hypercaloric diets. Using different diets we found that effects of fructose supplementation in potentiating liver esteross and fibrosis is rooted in an inflammatory response involving activation of liver macrophages and expression of pro-inflammatory genes in non-parenchymal cells. Using a cohort of prediabetic Portuguese adults we are investigating the association of diabetes susceptibility genes with insulin metabolism providing causal links of specific metabolic impairments in the diabetes pathogenesis.
In 2014, we pursued the development of novel methods for the study of evolutionary cell biology. We focused both at the level of sequence analyses as well as the level of phenotypic analyses. On the first we studied evolutionary patterns in coiled coil forming sequences to develop a new substitution model that substantially improves the quality of phylogenetic inference of coiled coil proteins. This analysis revealed that coiled coil sequences carry substantial phylogenetic information, in contrast to the common lore that their divergence makes them unsuitable for evolutionary studies. This work has been submitted for publication. On the level of phenotypic evolution, we developed two novel approaches. The first is termed Maximum Parsimony Landscapes and are used to reconstruct ancestral states of phenotypes for which the cost of gain or loss cannot be estimated. The second is termed the Morphological Diversity Index and permits the quantification of the occupancy of a phenotypic space, and hence the identification of constraints that can reveal signs of selection.

Other work in the lab involved the generation of genome-scale data on novel bacteria and protozoan species that are important in the study of specific evolutionary transitions, as well as the characterisation bacterial and protozoan communities in marine and freshwater samples. Furthermore, we continued to pursue research in biomarkers of cancer progression in collaboration with clinical centres.
Can we predict evolution? This is one of the most fundamental questions in biology today. If we can predict evolution, we can control it. Doing so will change the way we understand biology, the way we use living organisms in biotechnology, the way we treat disease and indeed the way we see ourselves.

The Evolution and Genome Structure research group aims to create a predictive framework of evolutionary biology by addressing how variations in genetic background, in general, and chromosome structure in particular affect the evolutionary path of populations. We use experimental evolution in microorganisms as a method as it allows the precise control of genetic background and of the relative weights of selection and drift. When combined with whole genome sequencing and high-throughput methods to track populations, this approach is very powerful in explaining fitness from biological processes.

Explaining how the genetic background (particularly chromosome structure) affects the rate of fitness change under these conditions. Among other applications, this will be important to understand why some populations are more resilient to bottlenecks than others. The third project running in the lab addresses how the presence of genomic instability affects the adaptation rate. These two projects are still in their infancy so there are no results yet.

The main project in the lab aims at characterizing the adaptive potential (evolvability) of strains with different genetic backgrounds. Specifically, we want to address the problem of how changes in chromosome structure affect the adaptation rate in fission yeast (Schizosaccharomyces pombe). During these months, we successfully demonstrated that different chromosomal rearrangements adapt at different speeds, proportional to their initial fitness differences. This pattern has been seen in other species and contexts and points to a general phenomenon. For the first time, we are demonstrating that it holds for fission yeast and in the presence of chromosomal rearrangements. We are now looking into the genetics behind these adaptive differences: do different strains adapt at different speeds because they are accumulating different mutations? Or, is it that they are accumulating the same mutations, but these have different effects? For this, we are sequencing ancestral and evolved strains using the Illumina Miseq instrument acquired by the IGC. These results will not only elucidate the mechanisms behind the differences in evolvability, but also shed light into why the different chromosomal rearrangements have different fitnesses in the first place. For example, if different rearrangements accumulate different mutations, these will likely be directly compensating for the initial defect caused by the rearrangement. We are also currently looking into how different fitness-related traits responded to selection in order to build a phenotype-based model that can explain and predict differences in evolvability. Meanwhile, we started a second related project, which addresses how different strains respond to decreased levels of selection. Under these conditions, mutations accumulate close to the rate at which they appear. Since most mutations are deleterious, populations tend to lose fitness under relaxed selection. We are measuring how the genetic background (particularly chromosome structure) affects the rate of fitness change under these conditions. Among other applications, this will be important to understand why some populations are more resilient to bottlenecks than others. The third project running in the lab addresses how the presence of genomic instability affects the adaptation rate. These two projects are still in their infancy so there are no results yet.

1. How does chromosome structure affect the tempo and mode of adaptation?
2. Explaining fitness from biological processes.
3. Differences in mutation accumulation in S. pombe due to the presence of chromosomal rearrangements.
4. How does genomic instability affect the tempo and mode of adaptation?
We are interested in the informational properties of natural and artificial systems, which enable them to adapt and evolve. This means both producing computational models of biological systems to understand the evolutionary role of information, as well as abstracting principles from biology to produce adaptive information technology. Our current research projects are on complex dynamics in biological networks (gene regulation, cell signaling, and metabolic networks), text and literature mining (in proteomics, protein-protein interaction and pharmacokinetics), computational social science, complex networks, machine learning, computational models of RNA editing, artificial immune systems, evolutionary systems, artificial life, cognitive science, and biosemiotics.

Recent highlights for our group were the development of a method to characterize brain regions and networks in terms of information-theoretic measures. The method allows us to study how much the DSI-inferred structural connectivity (the connectome) of the human brain predicts fMRI recordings of resting-state activity. We are very confident that this method represents only a first step in understanding brain function.

In collaboration with Olaf Sporns and other neuroscientists, our group developed a method to characterize brain regions and networks in terms of information-theoretic measures. The method allows us to study how much the DSI-inferred structural connectivity (the connectome) of the human brain predicts fMRI recordings of resting-state activity. We are very confident that this method represents only a first step in understanding brain function. Another highlight for our group was the development of a method to evaluate the controllability of complex systems: a Preliminary Study. Our current research projects are on complex principles from biology to produce adaptive information systems, which enable them to adapt and evolve. This means both producing computational models of biological systems to understand the evolutionary role of information, as well as abstracting principles from biology to produce adaptive information technology. Our current research projects are on complex dynamics in biological networks (gene regulation, cell signaling, and metabolic networks), text and literature mining (in proteomics, protein-protein interaction and pharmacokinetics), computational social science, complex networks, machine learning, computational models of RNA editing, artificial immune systems, evolutionary systems, artificial life, cognitive science, and biosemiotics.

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perform automatic fact-checking online, in collaboration with several
network scientists. Traditional fact checking by journalists cannot keep
up with the enormous volume of information that is generated online.
Computational fact checking enhances our ability to evaluate the
veracity of dubious information. We demonstrated that human fact
checking can be approximated quite well by finding the shortest path
between concept nodes of a very large concept graph derived from
Wikipedia. We obtained very good results examining tens of thousands
of claims related to history, entertainment, geography, and biographical
information. Our work represents a significant step toward scalable
computational fact-checking methods that may one day mitigate the
spread of harmful misinformation (Ciampaglia et al., In Press).

On the biomedical front, we continued to work on automatic extraction
of drug-drug interactions (DDI) from the published scientific literature.
DDI is a major cause of morbidity and mortality and a subject of intense
scientific interest. While evidence for DDI ranges in scale from intracellular
biochemistry to human populations, previous literature mining methods
had not been used to extract specific types of experimental evidence
which are reported differently for distinct experimental goals. In our work
this year, we demonstrated that biomedical literature mining can aid
DDI research by extracting evidence for large numbers of potential
interactions from published literature and clinical databases quite
effectively (Kolchinsky et al., In Press).

Finally, we made an important contribution to network science, by
demonstrating an isomorphism between distance and Fuzzy graphs. This
allows the transfer of an enormous body of mathematical methods to
be ported from the field of Fuzzy Set theory into network science which
greatly enriches the toolbox available to analyse weighted graphs
(Simas & Rocha, In Press).
Inflammation is an immediate response to foreign challenge and/or tissue injury characterised by local and transient extravasation of soluble molecules and leukocytes from blood to non-lymphoid tissues. While the physiologic purpose of inflammation is to restore homeostasis there are many instances where inflammation becomes pathological. Moreover, there is a general consensus that some of the major causes of human morbidity and mortality are in fact due to pathological conditions in which inflammation and/or immunity are the underlying cause of disease. The research effort developed in our laboratory is aimed at understanding the cellular and molecular mechanisms assuring that in the overwhelming majority of cases inflammation exerts its physiologic purpose without becoming pathological. Our body of work supports the notion that one of such mechanisms relies on the expression of cytoprotective genes that allow inflammation to progress without causing irreversible tissue damage.

**MAIN RESEARCH IN 2014**

1. Macrophage control of homeostasis.
2. Interplay between heme catabolism and gasotransmitters in disease tolerance.
3. The DNA damage response controlled by atm in disease tolerance.
4. The heat shock response controlled by Hsf1 in disease tolerance.
5. The oxidative stress response controlled by Nrf2 in disease tolerance.
6. Natural antibodies in malaria transmission.
7. Targeting heme with single domain antibodies.

**PROJECTS RUNNING IN 2014**

1. Macrophage control of homeostasis.
2. Interplay between heme catabolism and gasotransmitters in disease tolerance.
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4. The heat shock response controlled by Hsf1 in disease tolerance.
5. The oxidative stress response controlled by Nrf2 in disease tolerance.
6. Natural antibodies in malaria transmission.
7. Targeting heme with single domain antibodies.

**LAB MEMBERS**

- Patricia Bastos Pereira (Post-doc) | Started in April
- Bini Blamireh (Post-doc)
- Ana Maria Carvalho (Post-doc)
- Luísa Dell'oro (PhD) (Post-doc) | Started in September
- Roballo Cosmelei (Post-doc)
- Susana Ramos (Post-doc)
- Socorro Vieira (Post-doc)
- Ana Silva (PHD student, 2021)
- Sumanta Singh (PhD student, 2022)
- Bohlman Yvone (PhD student, 2020)
- Sofia Gozzelino Ribeiro (Research Assistant)
- Inês Cabral (Research Assistant) | Started in March
- Carolina Maia (Research Assistant) | Started in November
- Babasunonen Sainu (Research Assistant) | Started in February
- Sofia Cabral (Research Technician)
- Sofia Rebeato (Laboratory Manager)

**PUBLICATIONS**


**RESEARCH INTERESTS**

Inflammation is an immediate response to foreign challenge and/or tissue injury characterised by local and transient extravasation of soluble molecules and leukocytes from blood to non-lymphoid tissues. While the physiologic purpose of inflammation is to restore homeostasis there are many instances where inflammation becomes pathological. Moreover, there is a general consensus that some of the major causes of human morbidity and mortality are in fact due to pathological conditions in which inflammation and/or immunity are the underlying cause of disease. The research effort developed in our laboratory is aimed at understanding the cellular and molecular mechanisms assuring that in the overwhelming majority of cases inflammation exerts its physiologic purpose without becoming pathological. Our body of work supports the notion that one of such mechanisms relies on the expression of cytoprotective genes that allow inflammation to progress without causing irreversible tissue damage.

**DESCRIPTION**

- PhD in Science
  - University of Louvain, Belgium, 1995
- Previous Positions:
  - Invited Professor I Univ de Lisboa, Portugal
  - Lecturer | Harvard Medical School, Boston, USA
  - Instructor in Surgery | Harvard Medical School, Boston, USA
  - Research Fellow | Harvard Medical School, Boston, USA
- **Institutional Role at IGC:**
  - Head of Histopathology Unit

**PUBLICATIONS**

involvement of additional stress responsive programs in a process we refer to as tissue damage control, which confers disease tolerance to infection, that is, an evolutionary conserved host defense strategy that does not interfere with the host’s pathogen load. We are also interested in understanding how symbiotic relationships with microbes modulate disease tolerance as well as resistance to infection.
The Evolution and Development lab aims at exploring the interface between the fields of evolution and developmental biology with the ultimate purpose of contributing to the understanding of the rules by which this interplay shapes organisms across evolutionary time. In particular, research carried out in the lab focuses on evolutionary novelties, that is, new traits (either morphological, physiological or behavioural) that may participate in the emergence of adaptive radiations into novel niches. We approach this concept experimentally at different levels of biological organisation and through both the comparative method and experimental evolution. Specifically, we look into novelty at: a) the genetic level, studying gene expression evolution upon gene duplication; b) the cellular level, approaching immune function diversity in Drosophila and other arthropods; c) the morphological level, studying the evolutionary origin of dorsal appendage formation in the Drosophila clade; and d) the organismal level, by following and characterizing the adaptation of D. melanogaster populations to pathogen exposure.

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PhD in Evolution and Development, Genetics
University of Cambridge, UK, 2001

Previous Positions:
Post-doc | Princeton University, USA
Post-doc | University of Western Ontario, Canada

Institutional Role at IGC:
Director of the IGC PhD Programme - IBB

Main Research in 2014

2. Drosophila hematopoiesis.
3. Immunity in the spider mite Tetranychus urticae.

Publications


Collaborations

Sara Magathans (Faculdade de Ciências, Universidade de Lisboa, Portugal)
Fernanda Reich (Centre de Biologie du Développement, France)
Luís Teixeira (IGC, Portugal)

Funding

Fundação para a Ciência e a Tecnologia, Portugal

Public Engagement in Science

Public talk for undergraduate biology students, FCUL, Lisbon, February.
Enhanced lashing of two recently duplicated paralogs reveals the regulatory elements driving shared and specific paralog expression domains.

 Enhancer bashing of two recently duplicated paralogs reveals the regulatory elements driving shared and specific paralog expression domains.

MAIN RESEARCH IN 2014 (cont.)

relying on structure-dependent signalling events to promote blood homeostasis, creates a new paradigm for addressing outstanding questions in Drosophila hematopoiesis and establishing further parallels with vertebrate systems.

We had previously shown that the genome of the spider mite Tetranychus urticae is missing important elements of the canonical Drosophila immune pathways necessary to fight bacterial infections.

We compared the consequences of bacterial infection in T. urticae, which feeds on virtually aseptic plant cell contents, to infection in Sancassania berlesei, a litter-dwelling mite. Whereas in S. berlesei infections are kept under control, T. urticae does not mount a response and dies from uncontrolled bacterial proliferation. Furthermore, in accordance with its ecology, the spider mite harbours 1,000 less commensal bacteria than S. berlesei. We show an association between life-style and the loss of induced immunity in T. urticae suggesting an evolutionary link between the shaping of the microbiota by ecological conditions and the architecture of the immune response.
Multicellular organisms and microorganisms are continuously interacting. Many of these interactions are mutually beneficial. However, multicellular organisms have to actively thwart invasion by opportunistic or overtly pathogenic microbes. We are studying the interaction of the model organism Drosophila melanogaster with different microorganisms, in particular intracellular ones. D. melanogaster has been successfully used as a model system to study innate immunity against many pathogens. Recently it has been shown that there are innate immune pathways against viruses conserved between insects and mammals. We are investigating mechanisms of resistance to viruses in the fruit fly. Interestingly, we have found that the intracellular bacteria Wolbachia confer resistance to RNA viruses in D. melanogaster. We want to understand the molecular basis of this induced resistance. We are also interested in the interplay between Drosophila and Wolbachia itself. These endosymbionts are one of the most widespread intracellular bacteria in the world but little is known, at the molecular level, on how the hosts control Wolbachia or Wolbachia manipulate the hosts. Finally, we are studying also what constitutes the gut microbiota of the hosts. Finally, we are studying also what constitutes the hosts control the world but little is known, at the molecular level, on how these endosymbionts interact with the host.

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During 2014, we have investigated how different Wolbachia strains give protection to Drosophila. We have found that the higher the Wolbachia density the higher the protection but also the higher the cost. Moreover, no immune activation is associated with this protection. This has been done in Drosophila melanogaster and Drosophila simulans and resulted in two publications (Chrostek et al. 2014 PLOS One and Martinez et al. 2014 PLOS Pathogens; the latter in collaboration with F. Jiggins). We have also investigated the basis of a pathogenic Wolbachia-polymerase and identified the genetic cause of this phenotype. This allowed us to conclude that Wolbachia can evolve rapidly through gene amplification and that mutation can be broken down by a single genomic change (Chrostek and Teixeira, accepted in PLOS Biology).

We have also focused in other mechanisms of Drosophila protection against viruses. In collaboration with E. Sucena and S. Magalhães we have studied how Drosophila adapts to viral challenges. We have identified genes that are under selection by viral infection in an experimental evolution setup (Martins et al. 2014 PNAS). Finally, we analysed how Drosophila responds to virus upon oral infection. We found that the Toll pathway is essential for the host resistance to this mode of infection but not systemic infection. We have therefore identified an inducible anti-viral pathway that is also route specific (Ferreira et al. 2014 PLOS Pathogens).

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physical principles of nuclear division

Telley, Ivo
Group Leader at IGC since 2013

► RESEARCH INTERESTS

We are broadly interested in the physical aspects of nuclear division (mitosis) and nuclear positioning inside large egg cells. We approach this topic by means of micro-mechanical engineering, biochemistry and live imaging rather than phenotypic profiling of genes. An integrative understanding of the chemo-mechanical processes behind mitosis is sought. Our research focus is two-fold: Firstly, we aim to decipher the molecular basis, the kinetics of the molecular machines, and the mechanical scaffold that facilitates movement. Addressing the mechanics of mitosis in embryo cells will help understand early defects in embryo development that have been found by genetic screens. Secondly, we are working towards a systems level understanding of how the mitotic spindle achieves the eccentric movement of segregating chromosomes. Directed force generation lies at the heart of chromosome segregation. Thus, our lab strives to be able to measure tension generation and the mechanical response of the cytoskeleton.

► COLLABORATIONS

Mónica Bettencourt Dias (IGC, Portugal)
Thomas Surrey (CRUK London Research Institute, UK)

► FUNDING

FP7, Marie Curie Actions - Career Integration Grant European Commission
Fundação para a Ciência e a Tecnologia, Portugal

► PROJECTS RUNNING IN 2014

1. Physical principles of nuclear migration and position in Drosophila syncytial embryos.
2. Cytoskeletal dynamics during inter-nuclear spacing in the Drosophila syncytial embryo.
4. The mechanics of nuclear division.
5. Spatial regulation of centriole biogenesis.

► MAIN RESEARCH IN 2014

The intracellular positioning of the nucleus has gained substantial interest among biologists due its relevance in cell cycle, differentiation, migration, and polarity. Abnormal positioning has been related to cell and tissue function deficiency, and severe defects in embryogenesis. Membrane linkers and cytoskeletal and molecular motor dynamics are essential factors for nuclear movement. However, understanding the coordination and the quantification of force generating elements for nuclear positioning are current challenges. In Drosophila embryos, nuclei undergo rapid successive divisions without cytokinesis and, therefore, a vast number of nuclei share the same intracellular space in a syncytium. They need to be evenly distributed throughout a large cytoplasmic volume and brought to the cell cortex to form the blastoderm. The regular arrangement of the nuclei is vital to later embryo development, and defects that perturb this distribution are lethal. How the regular nuclear distribution during early divisions is achieved and maintained is an interesting yet unresolved question. In each division cycle a single nucleus gives rise to two sister nuclei that are separated by the mitotic spindle.

One of our main research tracks is to understand the principles underlying the regular arrangement and precise positioning of nuclei, and the mechanism that maintain the regularity of the nuclear distribution during perturbations. For this, we are measuring time-resolved nuclear positions starting at the earliest stage of Drosophila embryo development to understand causality and regulation of nuclear positioning. We infer on how predefined external factors (e.g. neighbor nuclei, cytoplasmic volume, geometry) influence the dynamics of the cytoskeletal machinery surrounding a nucleus, with focus on microtubules, actin, and associated molecular motors and linking proteins. Furthermore, we investigate how the non-sister nuclei remain separated and do not collide with each other. We particularly focus on the microtubule-based molecular interactions that regulate the distance between neighboring non-sister nuclei. We know that the microtubule cytoskeleton plays a key role in nuclear transport, and its dynamics is greatly determined by the microtubule-organizing center, the centrosome. Therefore, our research also aims at understanding the role of the centrosome and its spatial regulation during every nuclear division cycle.
Bacteria use small chemical molecules called autoinducers to communicate with one another by a process called quorum sensing. This process enables a population of bacteria to regulate behaviours, which are often crucial for successful bacterial-host relationships whether symbiotic and pathogenic. In this laboratory biochemical and genetic approaches are used to study the molecular mechanisms underlying quorum sensing, with an emphasis on systems promoting bacterial inter-species communication. This research includes an integrated study involving elucidation of the chemical molecules that are used as signals, the network components involved in detecting the signals and processing information inside individual cells, and finally characterisation of the behaviour of the bacterial community in multi-species bacterial consortia. Our ultimate goal is to understand how bacteria use inter-species cell-cell communication to coordinate population-wide behaviours in consortia and in microbial-host interactions.

**RESEARCH INTERESTS**

Bacteria use small chemical molecules called autoinducers to communicate with one another by a process called quorum sensing. This process enables a population of bacteria to regulate behaviours, which are often crucial for successful bacterial-host relationships whether symbiotic and pathogenic. In this laboratory biochemical and genetic approaches are used to study the molecular mechanisms underlying quorum sensing, with an emphasis on systems promoting bacterial inter-species communication. This research includes an integrated study involving elucidation of the chemical molecules that are used as signals, the network components involved in detecting the signals and processing information inside individual cells, and finally characterisation of the behaviour of the bacterial community in multi-species bacterial consortia. Our ultimate goal is to understand how bacteria use inter-species cell-cell communication to coordinate population-wide behaviours in consortia and in microbial-host interactions.

**PUBLICATIONS**


**COLLABORATIONS**

1. Joaquim Demengeot (IGC, Portugal)
2. Isabel Cordon (IGC, Portugal)
3. Stephanie Miller (Swarthmore College, USA)
4. Luis Teixeira (IGC, Portugal)
5. Caires Lisboa (University of Valencia, Spain)
6. Rita Ventura (Instituto de Tecnologia Química e Biológica, Portugal)
7. Isabel Gordo (IGC, Portugal)
8. Jocelyne Demengeot (IGC, Portugal)
9. Cristina Barroso-Batista (IGC, Portugal)
10. Ana Rita Oliveira (Trainee)
11. Joana Dias (Technician) | Started in March
12. Filipe Vieira (External Masters student)
13. Rita Valente (PhD student, PIBS 2008)
14. Jessica Thompson (Post-doc)
15. Pol Nadal (Post-doc)
16. Ana Rita Oliveira (Trainee)
17. Luís Teixeira (IGC, Portugal)
18. Jocelyne Demengeot (IGC, Portugal)
19. Isabel Gordo (IGC, Portugal)
20. Rita Ventura (Instituto de Tecnologia Química e Biológica, Portugal)
21. Howard Hughes Medical Institute, USA

**FUNDING**

1. Fundação para a Ciência e a Tecnologia, Portugal
2. Howard Hughes Medical Institute, USA
3. João XXI funds, University of Coimbra, Portugal

**PUBLIC ENGAGEMENT IN SCIENCE**

1. Media appearance in newspapers and other channels, March.
2. LabEScola project – workshop of high-school students and hosting students’ internships, IGC, from January to July.
3. IGC stand at NOS Alive’14 – scientific speed dating activity, Algés, July.
4. IGC Open Day 14 – hands on activities, October.

**LAB MEMBERS**

- Joaquim Demengeot (Post-doc)
- Jessica Thompson (Post-doc)
- Cécilia Cordon (PhD student, PIBS, 2011)
- Rita Valente (PhD student, PIBS, 2008)
- Filipa Vieira (External Masters student)
- Joana Almeida (Technician)
- Joana Dias (Technician) | Started in March
- Ana Rita Oliveira (Trainee)

**MAIN RESEARCH IN 2014**

AI-2 is a universal signal for bacterial communication that can mediate inter-species bacteria communication and regulate important bacterial behaviours, including virulence and biofilm formation.

We had previously shown that Escherichia coli is capable of interfering with AI-2-mediated bacterial behaviours and of terminating quorum sensing signalling interfering with the communication of other species. In a recent work published in *PNAS* we completed the elucidation of the pathway that *E. coli* uses to sequester and destroy AI-2. We showed that *E. coli* uses a very unique enzyme for the degradation of AI-2. This enzyme has all the sequence and structural features of a Class I aldolases but it acts as a thiolase, an activity not previously described for this large family of enzymes. With this work we identified the products that link AI-2 degradation to the Gut Are Dominated by Soft

**PROJECTS RUNNING IN 2014**

1. Inter-species cell-cell signalling: its role in bacteria consortia.
2. Identification of microbiota-derived functions favoring expansion of enteric bacteria in antibiotic-treated mice.
3. Inhibition of bacterial plant virulence by interference with interspecies cell-cell communication.
Research at the Plant Development group is concerned with developing integrated models of cellular growth and morphogenesis using the pollen tube as a biological model, ion dynamics as an experimental paradigm and theoretical modelling as an integrative tool. We have characterized novel ion channels involved in pollen tube growth and morphogenesis, by means of imaging, electrophysiology, genetics and molecular biology, and, furthermore, unravelled some of the genetic and cellular mechanisms behind pollen tube guidance and fertilization in plants. Our group has provided novel insight into the transcriptional status of plant male gametes and its consequences for plant reproduction and improvement. The members of the group have been pivotal in the strengthening of the imaging, transcriptomics and vibrating probe electrophysiology services of the IGC. We have several collaborations with theoretical, animal developmental, evo-devo and other groups at the IGC, apart from external collaborations with research groups in Portugal and abroad.

### Publications


### Collaborations

- Liam Dolan (Oxford University, UK)
- Alice Cheung (University of Massachusetts, USA)
- Gerhard Obermeyer (University of Salzburg, Austria)
- Matthew Gilliham (University of Adelaide, Australia)
- Zach Lipman (Cold Spring Harbor Laboratory, USA)
- Rainer Hedrich (University of Würzburg, Germany)

### Funding

**Fundação para a Ciência e Tecnologia, Portugal**

### Projects Running in 2014

1. **A systems approach to apical cell growth.**

The aims of this project are the definition of electrical equivalent models based on the individual fluxes described, modelling of internal ion concentrations based on membrane activity, and the description of glutamate receptors as possible calcium channels in pollen. We established numerical methods to model how membrane activity results in specific patterns of cytosolic free concentration of a given ion.
PROJECTS RUNNING IN 2014

1. Elucidating the molecular patterning underpinning T cell activation in HIV infected cells.
2. Elucidating how HIV-1 alters the spatial organization of signalling pathways to enhance signalling outcomes that are favourable for HIV pathogenicity.

MAIN RESEARCH IN 2014

MEMBRANE SIGNALLING PATTERNING IN HIV INFECTION

From viral entry to immune escape, HIV pathogenesis occurs at a spatial dimension beyond the reaches of conventional microscopy. Super-Resolution microscopy allows the visualization of biological processes at single-molecule resolution. Using Super-Resolution microscopy we have recently found that HIV alters the organization of the signalling pathways that drive T cell activation. In this project, we will exploit the connection between the molecular patterning of the signalling pathways that control T cell activation and increased HIV pathogenesis. With this goal, we will develop new methods to push forward the current limits in super-resolution microscopy.

ROLE OF SIGNALLING COMPARTMENTALIZATION IN HIV DRIVEN IMMUNE ACTIVATION

Immune activation is the strongest predictor of progression to AIDS. Although the mechanisms underlying HIV-driven inflammatory activation remain unknown, it does persist in antiretroviral treated patients, making it an attractive potential therapeutic target. While for other cells of the immune system it is clear that signalling compartmentalization is pivotal in duration and type of the inflammatory response ensued, whether signalling compartmentalization plays a similar role in T cell inflammatory responses is not known. In this project, we want to confront the increased immune activation observed upon HIV infection with HIV-altered signalling compartmentalization.

RESEARCH INTERESTS

An open question in biology is how spatial organization conditions molecular mechanisms and ultimately cellular function. T cell function is primarily to fight infection. We study how the organization of signalling pathways within specialized domains control signalling outcomes that determine T cell function and the pathogenicity of HIV-1 infection.

We have found that T cell activation does not solely rely on the lateral organization of molecules embedded in the plane of the T cell plasma membrane, but also relies on preformed vesicular ‘packets’ that are released on demand to the T cell plasma membrane. Specifically, signalling cascades are assembled at discrete membrane domains, ‘signalling nanoterritories’, upon vesicle release. These findings add an extra dimension, vesicle delivery, to the plasma membrane compartmentalization of T cells. We have recently found that HIV-1 exploits the interconnectivity between vesicular traffic, signalling compartmentalization and T cell activation to create an appropriate signalling equilibrium favourable for viral replication. In particular, HIV-1 reorganizes the nanoscale organization of T cell signalling to control the infected cell life-span.

Our research focuses on elucidating the molecular patterning underpinning T cell function and HIV-1 pathogenicity using a combination of cellular biology and super-resolution microscopy approaches.

PUBLICATIONS


COLLABORATIONS

Ricardo Henriques (University College London, UK)
Ana Espada Sousa (Instituto de Medicina Molecular, Portugal)

FUNDING

Fundação para a Ciência e a Tecnologia, Portugal
The following groups develop their research at external associated institutes and research centres, maintaining strong scientific collaborations with IGC groups, and access to IGC facilities.

**GASTRULATION** • José António Belo, Group Leader
Centro de Biomedicina Molecular e Estrutural, Universidade do Algarve, Portugal, & CEDOC – Chronic Diseases Research Center, Faculdade de Ciências Médicas, Universidade Nova de Lisboa, Portugal

**NEURAL CIRCUITS AND BEHAVIOUR** • Megan Carey, Group Leader
Champalimaud Neuroscience Program, Portugal

**NEUROBIOLOGY OF ACTION** • Rui M. Costa, Group Leader
Champalimaud Neuroscience Programme, Portugal

**NEO-VASCULARIZATION** • Sérgio Dias, Group Leader
Instituto de Medicina Molecular, Lisbon, Portugal

**EVOLUTIONARY ECOLOGY OF MICROORGANISMS** • Francisco Dionsio, Group Leader
Faculdade de Ciências da Universidade de Lisboa, Portugal

**NEUROETHOLOGY** • Susana Lima, Group Leader
Champalimaud Neuroscience Programme, Portugal

**SYSTEMS NEUROSCIENCE** • Zachary Mainen, Group Leader
Champalimaud Neuroscience Programme, Portugal

**EARLY FLY DEVELOPMENT** • Rui Martinho, Group Leader
Universidade do Algarve, CEME, Portugal

**BEHAVIOUR AND METABOLISM** • Carlos Ribeiro, Group Leader
Champalimaud Neuroscience Programme, Portugal

**SYSTEMS IMMUNOLOGY** • José Faro, Group Leader
Universidad de Vigo, Spain

**DOPAMINE IN ACTION LEARNING** • Joseph Paton, Group Leader
Champalimaud Neuroscience Programme, Portugal

**MOLECULAR IMMUNOLOGY** • Bruno Silva Santos, Group Leader
Instituto de Medicina Molecular, Portugal

**DEVELOPMENT AND EVOLUTIONARY MORPHOGENESIS** • Solveig Thorsteinsdóttir, Group Leader
Faculdade de Ciências da Universidade de Lisboa, Portugal

**INNATE BEHAVIOUR** • Maria Luísa Vasconcelos, Group Leader
Champalimaud Neuroscience Programme, Portugal

**HUMAN MOLECULAR GENETICS AND FUNCTIONAL ANALYSIS UNIT** • Astrid Vicente, Group Leader
Instituto Nacional de Saúde Dr. Ricardo Jorge, Lisbon, Portugal, & Center for Biodiversity, Functional and Integrative Genomics (BioFIG), Universidade de Lisboa, Portugal
animal house facility

Rebelo, Manuel
Head of Facility since 2014

PhD in Immunology
Universidade de Lisboa, Portugal, 2005

Other position at IGC:
Member of the Ethics Committee

The Animal House Facility is organized in several areas, specifically prepared for each model organism hosted at the IGC.

Rodent Facility:
The facility is composed by 1 Production Unit, 4 Experimental Areas, 1 Quarantine, 1 Germ-Free and 1 Gnotobiology Services. It is part of the Infrafrontier-I3-European Mouse Mutant Archive (EMMA) consortium (www.infrafrontier.eu) and the European Consortium for Gnotobiology (www.ecgnoto.eu). In 2014, it hosted over 170 mouse strains, 1 rat strain and was used by 22 research groups and 2 Services.

Fish Facility:
The facility has 1 Production/Experimental area, another Experimental area with 3 slots for behavior setups, 1 Quarantine and 1 microinjection room. In 2014, it hosted 150 zebrafish lines and was used by 4 research groups.

Fly Facility:
The facility hosts thousands of mutant lines. It is composed of 2 controlled-temperature walk-in chambers, 2 controlled-temperature small rooms, 1 food preparation room, 2 procedure labs and 1 Quarantine. In 2014, 10 research groups used the facility.

Frog Facility:
The facility has 2 aquatic habitat systems and benches for experimental work. In 2014, 1 research group used the facility.

FACILITY STAFF

Jocelyne Demengeot (Scientific Coordinator) | Started in January
Ana Coelho Rogers (Manager of Fish Facility) | Started in January
Joana Bom (Manager of Germ-Free/Gnotobiology Facility)
Liliana Vieira (Manager of Fly Facility)
Moisés Franco (Technician)
Ana Sofia Leocádio (Technician) | Left in August
Ana Dinis Pereira (Technician)
Marília Pereira (Technician) | Started in November
Ana Ribeiro (Technician)
Karen Ruiz (Technician) | Left in August
Liliana Vale (Technician)
Adérito Vieira (Technician)
Carla Almada (Caretaker)
Sara Carvalho (Caretaker) | Left in February
Sandra Cristovao (Caretaker) | Started in March
Cláudia Gafaniz (Caretaker)
Joélly Gomes (Caretaker)
João Lopes (Caretaker)
Carina Monteiro (Caretaker)
Pedro Pinto (Caretaker)
Levi Pires (Caretaker)
Olinda Queirós (Caretaker) | Left in March
Graça Ramalho (Caretaker)
Marco Rocha (Caretaker)
Cátia Silva (Caretaker)

PUBLICATIONS


PUBLIC ENGAGEMENT IN SCIENCE

Hosting internships of students from LabEscolas project, July.
IGC Open Day ’14 – Top Models room, October.

EU-FP7 INFRAFRONTIER-I3 AND EUROPEAN MOUSE MUTANT ARCHIVE (EMMA)

The Infrafrontier-I3 consortium aims at building a world-class research infrastructure for mutant mouse analysis and archiving that provides the biomedical research community with the tools needed to unravel the role of gene function in human disease. Integrated in the Infrafrontier-I3 is EMMA, a not-for-profit repository for the collection, archiving (via cryopreservation) and distribution of mutant mouse strains used in basic biomedical research. This grant maintains a state-of-the-art Mouse Germ-Free Facility, used by European and IGC researchers.

HOST MICROBE INTERACTION

This FCT funded project (REG/PMI/MIU/0038/2012) aims at enhancing the capacity of the Instituto Gulbenkian de Ciência to study evolutionary conserved mechanisms regulating host-microbial interactions under homeostasis as well as in the context of infection in mice. In this frame, the Animal House Facility implemented, tested and adapted to experimentation the Gnotobiology and the BSL2 facilities.

EUROPEAN CONSORTIUM FOR GNOTOBILOGY

This consortium aims at developing new tools and technologies in the field of gnotobiotic and Germ-free mice. It also aims at harmonizing procedures across facilities in Europe.

CONGENTO

CONGENTO was selected to be part of the National Roadmap of Research Infrastructures (RI) that FCT launched in 2013. The goal of CONGENTO is to provide services, making available state of the art technologies in the 3 most commonly used genetically tractable organisms worldwide (mouse, zebrafish and Drosophila). It is a completely innovative infrastructure at the National and International level. The IGC is part of this RI, together with Champalimaud Foundation, I3M and CEDOC.

COLLABORATIVE PROJECT WITH UNIVERSITY OF SÃO PAULO – USP (BRAZIL)

Since 2008, the IGC has a collaborative project with USP (Brazil) in the field of cryopreservation of mouse germline, sharing knowledge and human resources to implement the latest developments in our common routines. In 2014, the project was extended to the zebrafish model, in which the IGC is helping on the implementation of the new Fish Facility in USP.
RODENT FACILITY

- 6 autoclaves
- 6 IVCs (Individually Ventilated Cages) rack systems
- 3 AHU Smart Flow model, with touch screen for all IVC racks
- 4 cage washers
- 1 bedding disposal station
- 7 conventional biosafety cabinets
- 1 movable biosafety cabinet CS5
- 8 isolators for Germ-free
- 2 ISOcage isolator rack system (72 cages each)
- 1 biosafety Cabinet for ISOcage rack system
- 1 ISOTEC transfer chamber with socket connector for 270 DPTE isolators door
- 5 stainless steel cylinders for 350 DPTE isolators door
- 3 stainless steel cylinders for 270 DPTE isolators door
- 3 transport cars for cylinders
- 1 plastic emergency cylinder for 350 DPTE isolators door
- 1 paracetamol acid sterilizer and compressed air pump
- 1 osmosis reverse system
- 1 vapour-phase hydrogen peroxide decontamination system
- 1 transfer and decontamination chamber
- 1 animal transfer chamber

FISH FACILITY

- 1 ZebTEC system with 6 racks, total capacity of 300 aquariums (3.5L)
- 1 ZebTEC system with 2 racks, total capacity of 100 aquariums (3.5L) + 60 aquariums (1L)
- 7 stand-alones, total capacity of 250 aquariums (3.5L) + 100 aquariums (1L)
- 1 zebrafish system for Quarantine, capacity for 126 aquariums (3.5L)
- 20 glass aquariums (6L)
- 100 breeding aquariums
- 3 osmosis reverse systems
- 2 microinjectors
- 4 stereoscopes
- 3 fluorescent stereoscopes
- 1 microscope
- 1 heat shock bath
- 3 incubators

FLY FACILITY

- 2 controlled-temperature walk-in chambers
- 2 controlled-temperature rooms
- 9 incubators
- 16 working stations with CO₂ output pedal system
- 4 working stations with CO₂ output flow buddy system
- 1 microinjector
- 1 boiling pan for food preparation, 80L capacity
- 3 food dispensers
- 2 heat shock baths

FROG FACILITY

- 1 Xenopus stand-alone with chillers, total capacity of 9 aquariums (27L each)
- 1 aquatic habitat system with 9 tanks
- 1 cooler/heater system for the aquatic habitat system
- 1 incubator
An important component of the Unit’s activity during 2014 was the implementation of the CRISPR/Cas9 system for the production of mutant mice, to make it available for the different research groups at the Institute. We have successfully used this technique to inactivate genes, to introduce a small tag into the coding region, and to modify target sites for transcription factors and microRNAs. We produced both mouse lines and embryos in the FVB and C57BL/6 backgrounds with approximately 15% efficiency.

This year we have injected one ES cell line, which gave three chimeras (nearly 100% chimerism) and resulted in germ line transmission.

As usual, production of transgenics was the main task of the unit. We injected a total of 31 different constructs that produced 377 transgenic embryos that were analyzed at the embryonic and fetal stages. Our efficiency remained high (around 30%). This year, we also had a strong effort in the production of transgenics with BACs. We produced a total of 27 different lines with a transgenic efficiency ranging the 26%.

Generating Mutant Mice Using the CRISPR/Cas9 Technology

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Production of Chimeric Mice by Blastocyst Microinjection of Mouse Embryonic Stem Cells

This year we have injected one ES cell line, which gave three chimeras (nearly 100% chimerism) and resulted in germ line transmission.

Major Projects & Accomplishments

PRODUCTION OF TRANSGENIC MICE AND EMBRYOS

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Equipment & Infrastructure

- 1 Microinjection setup with Nikon inverted microscope equipped with DIC optics, and three-dimensional Narishige micromanipulators
- 1 Microinjection setup with Leica inverted microscope equipped with DIC optics, and three-dimensional, power assisted, Narishige micromanipulators
- 2 FemtoJet pumps
- 1 Sutter P-87 Flaming/Brown micropipette puller
- 1 Zeiss SV6 Stereomicroscope with training head
- 2 Standard Zeiss SV6 Stereomicroscopes
- 1 CO2 incubator
- 1 Ultrasonic Cleaning Device

Funding

Calouste Gulbenkian Foundation
Fundação para a Ciência e a Tecnologia
The Plant Facility at the IGC ensures the growth and maintenance of Arabidopsis thaliana and Physcomitrella patens plants, the model organisms used by the plant research groups hosted by the Institute.

The facility consists of a custom-built greenhouse with lighting control and temperature regulation and three custom-made fully controlled growth chambers with short-day, long-day and continuous light settings, as well as a walk-in plant growth room and five small reach-in chambers that allow the performance of cell-based assays and more precise phenotypical analyses.

Four research groups (Plant Molecular Biology, Plant Stress Signaling, Cell Biophysics and Development, and Plant Genomics) make use of the IGC Plant Facility.

**Users:**
- Baena-González, Elena
- Becker, Jörg
- Duque, Paula
- Feijó, José A.

**DESCRIPTION**

- **FACILITY STAFF**
  - Vera Nunes (Technician)

- **PUBLICATIONS**

**EQUIPMENT & INFRASTRUCTURE**

- 1 Walk-in Chamber (Aralab 10,000 EH 2009)
- 3 Regular Reach-in Chambers (Aralab S600PLH)
- 2 Double Reach-in Chambers (Aralab D1200PL)
- 3 Custom-made fully controlled plant growth rooms
- 1 Custom-built greenhouse with lighting control and temperature regulation
- 1 Temperature-controlled room for plant drying and seed production
- “Soil house” for planting, seed harvesting, plant crossing, etc.

**FUNDING**

- European Molecular Biology Organization (EMBO)
- Instituto Gulbenkian de Ciência
**DESCRIPTION**

The Histopathology Unit provides a wide range of services related to tissue preparation. These include collection, fixation, processing, embedding, sectioning and staining of animal tissue samples. The unit also provides microscopy assistance as well as training to new users in sample preparation and sectioning.

**FACILITY STAFF**

- Alistair Martin Robson (Pathologist)
- Marta Pinto (Technician)
- Joana Rodrigues (Technician)

**EQUIPMENT & INFRASTRUCTURE**

- **Equipment & infrastructure (cont.)**

  - Vibratome: similar to a microtome but uses a vibrating razor blade to cut through tissue. The vibration amplitude, the speed, and the angle of the blade can all be controlled. Fixed or fresh tissue pieces are embedded in low gelling temperature agarose. The resulting agarose block containing the tissue piece is then glued to a metal block and sectioned while submerged in a water or buffer bath. Individual sections are then collected with a fine brush and transferred to slides or multiwell plates for staining.

- **Funding**

  - Calouste Gulbenkian Foundation
IMPLEMENTATION OF A HARDWARE VIRTUALIZATION INFRASTRUCTURE
In cooperation with the IT team, we have implemented a virtualization infrastructure that allows us to more easily and flexibly provide the IGC with web services and other computational services such as a local Chipster server.

IMPLEMENTATION OF A LOCAL GALAXY COMPUTATIONAL SERVER
We have implemented a local installation of a galaxy server to help IGC users run and share their bioinformatic analysis. Whenever necessary we have also developed our own Galaxy tools for local IGC needs. This service is running on top of our virtualization infrastructure, and in cooperation with the IT team we have also begun linking it to the IGC farm infrastructure.

DEVELOPMENT OF A MISEQ SEQUENCING QUALITY ASSESSMENT PIPELINE FOR THE GENOMICS UNIT
We have developed a pipeline to report on the MiSeq sequencing quality, including raw read quality, contamination analysis, and coverage. This pipeline has been implemented as a Galaxy tool and is run by the Genomics Unit.

PhD FORMS
We have implemented a web application for the registration of applicants for the IGC PhD programme. This application has also been used for the PGCD programme, as well as the registration of new PI applying to the IGC.

GENETIC VERSUS EPIGENETIC CONTRIBUTIONS TO AUTHENTIC AND CRYPTIC RSS TARGETING BY THE RECOMBINASE
In collaboration with the group of Jocelyne Demengeot, we are modeling the influence of genetic and epigenetic cues in the process of VDJ recombination in the tcr-beta locus. To build and evaluate our models we are making use of targeted sequencing of V and J loci, as well as publicly accessible epigenetic data.

CONTRIBUTIONS TO RESEARCH CARRIED OUT IN 2014 BY IGC AND EXTERNAL GROUPS
We have provided support for 27 groups (of which 6 external). Support examples include: NGS data analysis and consulting (RNA-Seq, miRNA-Seq, Rad-Seq, Exome-Seq, Genome Resequencing); sequence multi-alignment and phylogenetic analysis; general biological information (gene annotation, SNPs, linkage analysis, primer design); genomic data integration; consulting and development of custom analysis solutions.
support to research • core facilities
bioinformatics & computational biology unit

EQUIPMENT & INFRASTRUCTURE

- One heavy calculation server used for support and hosted projects
- Two virtualization servers dedicated to hosting web services and other computational resources
- Six workstations of which two have analysis software for user access
- Four smaller servers to support virtualization services
- Transfac Software License (single user)

FUNDING
Calouste Gulbenkian Foundation
Fundação para a Ciência e a Tecnologia

UBI's work supports IGC's scientific outcome.

Person-month spent in each item of the UBI’s mission (from a total of 42 person/month). User support is the task where the UBI spends most of its resources. In 2014, a significant effort was put into developing our computing infrastructure.
The Gene Expression Unit provides DNA microarray services, ranging from experimental design over complete sample processing to expert advice on data analysis. We have been an Affymetrix Core Lab with reference status for GeneChip technology in Portugal since 2002. Running a total of 226 microarrays we have contributed to 18 in-house and national projects in 2014 alone. In addition we have added 1950 DNA/RNA samples on our Bioanalyser. Services include:

- Gene Expression Profiling (3’ IVT and Gene ST arrays)
- Genotyping & Cytogenetics (SNP 6.0, Cytoscan HD and Cytoscan 750K arrays)
- MicroRNA Profiling (miRNA 4.1 arrays)
- Custom assay projects
- RNA and DNA quality analyses (Bioanalyser)
- Data analysis training (dChip and Chipster)

In June 2013 the IGC has acquired an Illumina MiSeq unit for NGS services. Standard NGS services offered are: Illumina amplicon sequencing (16S metagenomics) and re-sequencing of genomes.

**Publications**


In June 2013, the IGC has acquired an Illumina MiSeq unit for NGS services. Standard NGS services offered are:

- Illumina amplicon sequencing (16S metagenomics) and re-sequencing of genomes.
- AluPCR and re-sequencing of genomes.
support to research • core facilities

gene expression unit

► MAJOR PROJECTS & ACCOMPLISHMENTS (cont.)

● NGS SERVICE (IN COLLABORATION WITH GENOMICS UNIT)
  Re-sequencing (E. coli) & 16S metagenomics (Evolutionary Biology Lab, IGC)
  Re-sequencing (E. coli) & 16S metagenomics & de novo (Pectobacterium carotovorum) (Bacterial Signaling Lab, IGC)
  Amplicon re-sequencing & 16S metagenomics (Lymphocyte Physiology Lab, IGC)
  Re-sequencing (S. cerevisiae) (Evolution and Genome Structure Lab, IGC)
  Re-sequencing (S. cerevisiae) & custom project (Integration profiling) (Telomeres and Genome Stability Lab, IGC)
  RADSeq custom project (Eco-Evolutionary Genetics Lab, IGC)
  Amplicon re-sequencing (Plant Genomics Lab, IGC)
  16S metagenomics (Plant Genomics Lab, IGC)
  Amplicon re-sequencing (Lupus and Autoimmune Immune Repertoires Lab, IGC)
  Re-sequencing & de novo (Computational Genomics Lab, IGC)
  Amplicon re-sequencing (Population and Conservation Genetics Lab, IGC)
  Re-sequencing (Burkholderia) (Biological Sciences Research Group, Instituto Superior Técnico, Lisbon)
  Re-sequencing (S. cerevisiae) (CREM, Faculdade de Ciências e Tecnologia, Universidade Nova de Lisboa)
  Re-sequencing (S. aureus) (Laboratory of Bacterial Cell Biology, Instituto de Tecnologia Química e Biológica, Oeiras)
  Re-sequencing (S. epidermidis) (Laboratory of Molecular Genetics, Instituto de Tecnologia Química e Biológica, Oeiras)
  16S metagenomics (Department of Biology, Universidade de Minho, Braga)
  Re-sequencing (Streptococcus pneumoniae R6) (Laboratory of Bacterial Cell Surfaces and Pathogenesis, Instituto de Tecnologia Química e Biológica, Oeiras)
  Re-sequencing (Codium vermilara) (Department of Biology, Universidade de Aveiro)
  Re-sequencing (S. cerevisiae) (Biological Research Center of the Hungarian Academy of Sciences)

► EQUIPMENT & INFRASTRUCTURE

• GeneAtlas System
• Scanner 3000 7G with Autoloader
• Fluidics Station 450
• Hybridization Oven 645
• Bioanalyzer 2100
• MiSeq System

► FUNDING
Fundação para a Ciência e a Tecnologia
The Unit provides technological support and expertise for research at the genome scale and is composed by Genotyping and Sequencing Services.

The Genotyping Service offers the Sequenom iPLEX technology, allowing rapid SNP genotyping assays with up to forty SNPs assayed simultaneously. The facility collaborates with investigators on SNP choice and SNP Assay Design, Sequenom Procedure and Data Management for Genetic Studies, providing access to the BC/GENE interface software. Genotyping Service also offers a backcrossing service for users of genetically modified mice and mouse breeders.

The Sequencing Service offers DNA sequencing and fragment analysis using multiplex with automatic technology, allowing rapid SNP genotyping assays with up to forty SNPs assayed simultaneously. The facility collaborates with investigators on SNP choice and SNP Assay Design, Sequenom Procedure and Data Management for Genetic Studies, providing access to the BC/GENE interface software. Genotyping Service also offers a backcrossing service for users of genetically modified mice and mouse breeders.

The Genomics Unit supports to research (NGS).

Gene Expression Unit
Since June 2013 the CFX384 (BioRad) Real-Time PCR systems. Expression are also available with 7900 HT (ABI) and sequencer ABI 3130XL. SNP genotyping and gene fragment analysis using multicapillary with automatic.

The Sequencing Service offers DNA sequencing and fragment analysis using multiplex with automatic sequencer ABI 3130XL. SNP genotyping and gene expression are also available with 7900 HT (ABI) and CFX384 (BioRad) Real-Time PCR systems.

Since June 2013 the Genomics Unit collaborates with the Gene Expression Unit for Next Generation Sequencing (NGS).

PhD in Immunology
University of Linköping, Sweden 1999

Other position at IGC:
Group Leader of the Disease Genetics group
Member of the Ethics Committee

External website

Facility tour for PhD students from the Netherlands, October.
Facility tour for high-school teachers, July.
Facility tour for high-school students, February and April.
Facility tour for IGC Sponsor (Everything is New). May
Facility tour for high-school teachers, July.
Facility tour for PhD students from the Netherlands, October.

PUBLICATIONS (cont.)


PUBLIC ENGAGEMENT IN SCIENCE

Facility tour for high-school students, February and April.
Facility tour for IGC Sponsor (Everything is New). May.
Facility tour for high-school teachers, July.
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MAJOR PROJECTS & ACCOMPLISHMENTS

• GENOTYPING SERVICE

In a total number of 144 chips, 1, 905, 024 SNP genotypes have been produced since January 2014 until January 2015. Four In-House, three Associated and seven non IGC groups have used the Genotyping Service.

• DNA SEQUENCING

Twenty-seven internal and six IGC associated and one external groups have used the ABI 3130XL Sequencing Service, with a total of 21,494 samples sequenced during the period of January 2014 until December 2014.

• FAST REAL-TIME PCR SYSTEM

Twenty-seven In-House and four IGC Associated groups have used the RT-PCR equipment on a regular basis (a total of 2625 hours), to detect gene expression of several genes in different projects.
**EQUIPMENT & INFRASTRUCTURE**

- Two robotic pipetting devices, robot PlateMate 2x2 (Matrix)
- Five thermocycling machines - ABI 9700 equipped with 2x384 blocks
- Chip spotting robot (MassARRAY, Nanodispenser)
- SNP detection, MALDI-TOF technology - MassARRAY Compact (Sequenom)
- ABI 3130XL
- 7900 HT (ABI) Fast Real-Time PCR
- CFX384 (BioRad) Real-Time System

**FUNDING**

Fundo para a Ciência e a Tecnologia
Since then, the UIC has grown in personnel and technological spectrum to anticipate the demands of a growing base of users. Because cellular imaging and cytometry have been in high demand, and new systems and techniques are continuously developed, the facility expanded significantly to facilitate accessibility while introducing the latest innovations to the whole research community.

To provide more dedicated and focused services on specific technical areas, the UIC was restructured in 2013 as three autonomous sub-units, that retain the "UIC" brand of excellence:

- **Advanced Imaging**
- **Flow Cytometry**
- **Electron Microscopy**

The **Unit of Imaging and Cytometry (UIC)** has been at the forefront of major technological developments at IGC, since its formal creation in 2003.

The UIC offers a wide range of services to the research community, including:

- Access to Sequencing Services – RT-PCR
- Fluorescence Imaging
- Confocal Microscopy
- Electron Microscopy
- Flow Cytometry
- Imaging Data Analysis

The UIC is equipped with state-of-the-art imaging and cytometry technologies, including:

- **Confocal Microscopy**
- **Fluorescence Microscopy**
- **Flow Cytometry**
- **Electron Microscopy**

The UIC also provides training and support to researchers for the effective use of these technologies.
The UIC Advanced Imaging Unit provides access and support to high-end light microscopy imaging needs of the whole IGC community. The Unit currently stands as an international reference laboratory, with cutting-edge techniques ranging from super-resolution, high-end widefield and confocal systems, (with high-throughput/screening capabilities), multiphoton, light-sheet microscopy, optical tomography and bioluminescence/fluorescence animal imaging. Some of these techniques are unique in Portugal and were developed in-house.

The Unit is also responsible for general maintenance of optical instruments, including satellite microscopes throughout the IGC. Users are trained through regular workshops on basic and advanced light microscopy techniques, equipment setup, experimental design, collection of high quality data, and image processing and analysis.

In the last five years, work conducted at the UIC resulted in more than 140 publications, 15 with UIC personnel co-authorship. The unit is also a member of the Portuguese Platform for Bioimaging, a consortium of the Portuguese ESFRI roadmap.

The UIC: Advanced Imaging Unit

Martins, Gabriel
Head of Facility since 2013

PhD in Cell Biology and Anatomy
School of Medicine and Biomedical Sciences, USA, 2004

External website

/> DESCRIPTION

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/> FACILITY STAFF

Emilio Gualda (Developer Engineer)
Ana S. Gonçalves (Microscopy Technician)
Nuno Pimpão Martins (Microscopy Technician) | Started in February
Hugo P. Peres (Microscopy Technician) | Started in June
Maria Nascimento (Post-Doc.) | Started in April, left in September

/> PUBLICATIONS


/> PUBLIC ENGAGEMENT IN SCIENCE

Facility tour for university students, March
Facility tour for high-school students, May
Media appearance in newspapers and TV, May-Jun
IGC Open Day: “The fluorescence world” activity, October
Talk for high-school students, Escuela Ibn Mucina, Maccabeche, December

/> MAJOR PROJECTS & ACCOMPLISHMENTS

NON-INVASIVE WHOLE BRAIN IMAGING IN BEHAVING ANIMALS USING LIGHT-SHEET MICROSCOPY

This project involved developments to our light-sheet microscope to allow automated high-throughput collection and imaging of 3D samples. This also involved development of the control and analysis software using the popular software ImageJ. Emilio Gualda was the PI of this exploratory FCT project.

MICROFLUIDICS LIGHT-SHEET MICROSCOPY FOR CELL DIFFERENTIATION AND DRUGS SCREENING IN NEUROSPHERES AND ZEBRAFISH

The UIC collaborates with Neuroscience Programme at Champalimaud Center for the Unknown (CCU) in the development of a light-sheet microscope for functional imaging in zebrafish able to record neuronal activity in transgenic zebrafish with calcium indicators (GCaMP) at 100 frames per second.

STUDY OF THE DIVERSITY AND EVOLUTION OF PERMIAN VERTEBRATES FROM NIASSA, MOZAMBIQUE

This project involves analysis of 3D images of fossils by synchrotron radiation tomography, using advanced morphometrical analysis. Gabriel Martins from the UIC participates in this project, which involves the PALNIASSA project, the Museu da Lourinhã and the Museu Nacional de Geologia from Mozambique.

/> EQUIPMENT & INFRASTRUCTURE

INSPECTION WIDE-FIELD LIGHT MICROSCOPES
• Olympus BH2
• Olympus IMT-2
• Leica DMLB2

RESEARCH WIDEFIELD LIGHT MICROSCOPES
• Leica inverted DMI8E2
• Leica upright DMRA2
• Custom-built Nikon high-throughput microscope setup
• Zeiss high-throughput Biosafety B2 level microscope
CONFOCAL MICROSCOPES

- Confocal Leica SP5 (with HyD detectors)
- Confocal Leica SP5 Inverted with environmental control
- Confocal Zeiss LSM 510
- Confocal Andor Spinning disk (with EM-CCD intensified camera)
- Nikon TIRF/spinning disk with environmental control
- Light-sheet (SPIM and DSLM) microscope
- Confocal Andor W-1 wide FOV Spinning disk (with sCMOS camera) with micromanipulation apparatus.
- DeltaVision - Deconvolution microscope system from Applied Precision, Inc. (full featured system with EM-CCD intensified camera)
- Whole-animal imager, Hamamatsu Aequoria with EMCCD camera
- OPenT- optical tomography scanner

FUNDING

Calouste Gulbenkian Foundation
European Molecular Biology Organization (EMBO)
Fundação para a Ciência e a Tecnologia
2014 was a year of technical advancement in the IGC EMF. The first High Pressure Freezer in Portugal was installed in May. This technique uses ultra rapid cryo-immobilization to improve sample preservation. In addition, an adapted Olympus light microscope (donated by the European Molecular Biology Laboratory in Heidelberg, Germany) allows scientists to combine the dynamic imaging of light microscopy with the high-resolution contextual imaging of electron microscopy. These two advancements enable scientists to investigate their biological questions at a new level of detail.

Overall, in 2014 we contributed to 25 research projects, 15 for the IGC scientists, 10 for external groups. Our samples ranged in size from proteins, to full organs and across many different model organisms.

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8. Tranfield, Erin M.
Head of Facility since 2013

At the Electron Microscopy Facility at the Instituto Gulbenkian de Ciência we believe that electron microscopy is a powerful tool that can be used to address research questions in the life sciences. With this in mind we aim to:

- provide centralized, high quality electron microscopy infrastructure to support scientific investigation;
- offer electron microscopy services, mentorship and skill training;
- collaborate with researchers within our institute, our country and the scientific community to foster knowledge of technical developments in electron microscopy.

The Electron Microscopy Facility has been expanding its technical expertise and in 2014 we added a high pressure freezer, an automated freeze substitution system and a light microscope for correlative Light and Electron Microscopy studies to our available resources.

FACILITY STAFF

- André Barros (Technician)
- Sara Bonucci (Technician)
- Ana Catarina Carneiro (Technician)
- Ana Laura Sousa (Technician)

PUBLIC ENGAGEMENT IN SCIENCE

- IGC Open Day 2014 - “The secret world of cells” hands-on activity, October.
- Facility tour for high-school students, December.

EQUIPMENT & INFRASTRUCTURE

- 1 Reichert Cryo-ultramicrotome
- 1 Wohlenberg High Pressure Freezer
- 1 Leica Automatic Freeze Substitution Unit
- 1 Hitachi Transmission Electron Microscope
- 1 Pelco Microwave Processing System
- 1 Carbon Coater
- 1 Fluorescence Light Microscope

FUNDING

- Calouste Gulbenkian Foundation
- European Molecular Biology Laboratory (EML) Heidelberg, Germany (Donation)
The aim of the Flow Cytometry Facility is to provide high-quality technical and scientific support in multiparameter cell sorting and flow cytometry analysis to all researchers at the IGC as well as to outside groups and companies. The facility provides a unique service to allow ready access to a wide range of technologies and expertise in an integrated manner that helps drive research forward efficiently. The IGC Flow Cytometry Facility currently stands as a national and international reference for Flow Cytometry and high-throughput cell sorting. The unit is well equipped with two multicolor high-speed cell sorters, live flow analyzers and a multiple analyte reader. All users receive basic training in the systems in use, in troubleshooting, and advice on experimental design and data analysis.

Due to the high-demand for new flow instruments and techniques, the facility is continuously expanding and introducing the latest innovations in Flow Cytometry to the research community.

**FACILITY STAFF**
- Cláudia Andrade (Technician)
- Cláudia Bispo (Technician)

**PUBLICATIONS**

**PUBLIC ENGAGEMENT IN SCIENCE**
- IGC Open Day 24 – visit to the laboratories, October.
- Facility tour for high-school students, throughout the year.

**EQUIPMENT & INFRASTRUCTURE**

**CELL SORTERS**
- 1 MoFlo (4 lasers, 9 fluorescence detectors) Beckman Coulter
- 1 FACSAria (3 laser, 9 fluorescence detectors) BD Biosciences

**ANALYzers**
- 1 FACSCan (1 laser, 3 fluo-detectors) BD Biosciences
- 1 FACSCalibur (2 lasers, 4 fluo-detectors) BD Biosciences
- 1 CyAn ADP (3 lasers, 9 fluo-detectors, HTS plate loader) Beckman Coulter
- 1 SORP LSR Fortessa (3 lasers, 12 fluo-detectors, Small Particle Detection Option, HTS plate loader) BD Biosciences
- 1 Muse Cell Analyzer (1 laser, 2 fluo-detectors) Merck-Millipore
- 1 Magpix Multiplex Analyte Reader, Merck-Millipore

**QUALITY CONTROL SOFTWARE TOOL FOR INSTRUMENT PERFORMANCE EVALUATION**

Cláudia Bispo has been developing an open source Python-based software tool - FlowQC - that allows Quality Control data collection, processing, and display of different QC metrics - PMT voltages, laser time delays, MFIs, SDs, CVs, and others, for any instrument in a Core Facility using any preferred set of QC particles.
In 2014, the Administrative Unit was composed of 5 project managers, 2 of which also provided support to the IGC Directors and to the purchasing sector respectively, 2 secretaries to the Directors, 1 general secretary and the coordinator. The Administrative Unit is responsible for: 1) post-award project management of externally financed projects; 2) administrative assistance to the IGC Directors, researchers and visitors; 3) support to purchasing; 4) accounting (insertion of payment entries on SAP for fellowships and voluntary social security refunds and associated filing processes).

**PROJECT MANAGEMENT**

The unit offered post-award project management to around 65 PIs and/or Unit Heads and managed approximately 143 projects. The key activities included support for execution and control of projects, financial reporting according to funding agency regulations and all procedures regarding recruitments within these projects.

**SUPPORT TO PURCHASING**

Core activities were the monitoring and assistance of the purchasing process through LabOrders and common email, attendance of supplier doubts and claims and analysis and follow up of non-compliant invoices to be freed for payment.

**ADMINISTRATIVE SUPPORT**

In addition to admin support to in-house researchers, the Unit also organised logistics for 42 Seminar Visitors, 25 incoming researchers and 52 visa-related issues. We managed 2 IEFP applications and 48 importation processes for incoming scientific products from abroad.

**SERVICE STAFF**

- Liliana Rodrigues (Secretary to the Director)
- Olena Shydenko (Secretary to the Deputy Directors/Admin Project Manager)
- Tatiana Rocha (Admin Project Manager)
- Cláudia Vieira (Admin Project Manager) Left in July
- Rita Gusmão (Admin Project Manager/Purchasing Support Officer)
- Joana Gusmão (Purchasing Support Officer)
- André Sousa (Purchasing Support Officer) Started in September
- Ana Maria Santos (Secretary)
- Andréia Mariano (Administrative assistant) Started in October

**SERVICE STAFF**

- Fátima Mateus (Accounts Officer)
- Vítor Santos (Accounts and Information Officer)
- Abílio Simões (Stores Manager)
- Ana Sofia Oliveira (team responsible PWC)
- João Braga (Accounts officer PWC)
- João Correia (Accounts officer PWC)
- Tânia Lobão (Accounts officer PWC)
- António Bretanha (Procurement FlyBridge)
- Filipe Silva (Auditor Deloitte)

**THE ADMINISTRATIVE UNIT**

The Administrative Unit organised 7 major scientific events for the IGC in 2014:

- IGC Scientific Advisory Board
- Annual PhD student meeting (MeeCeS)
- EMBO Microscopy course
- EMBO Conference on Centrosomes
- EU Life Strategy Meeting
- Post-doc Retreat
- Auto-Immune Diseases Conference (with Hospital Curry Cabral)

**ACCOUNTING & INTERNAL AUDIT**

This service provides support in all administrative and accounting matters, including ordering and stores, financial and fiscal support.

The accounts office provides support in preparing financial reports of research projects, and in general accounting and management of projects.

The Accounting and financial reporting of research projects is executed by an external society: PWC.

The Procurement is executed by an external society: FlyBridge.

The internal auditing is executed by an external society: Deloitte.
The IGC Informatics Unit (ITI) manages most of the ICT needs of the IGC including the development and maintenance of the IT and communications infrastructure, direct support to IGC users (helpdesk), training and consulting as a service, development and maintenance of the scientific computation farm, and application development. These services are multilayered and can be engaged fully or partially as needed.

Most of the IGC infrastructure relies on the use of Open Source technologies and the competence of our dedicated staff to maintain a competitive level of service. Notable exceptions are the dedicated administrative applications that also rely on commercial applications and external consultants to maintain them.

The IGC has a modern IT infrastructure with a local data center, redundant internet lines, Gigabit Ethernet to the desktop, campus-wide Wi-Fi, centralized file storage, internal helpdesk, knowledge base servers and fully integrated and automated intranet and user management.

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Equipment Maintenance is a technical platform for ensuring effective equipment acquisition, distribution and usage. We work closely with scientific facilities in order to provide cutting edge service and a smooth workflow, ensuring high equipment up-time.

Our services include: equipment repair and maintenance, building of small hardware apparatus, etc.

During 2014 we reached 180 sensors spread at the institute, which monitor from -80’s freezers to general HVAC chillers. We run a seminar series “Tech Minutiae” with the aim of raising awareness, amongst scientists, of the most cutting edge techniques.

Moreno, Nuno
Head of Unit since 2008

PhD in Biology and Biophysics
Universidade Nova de Lisboa, Portugal, 2009

► SERVICE STAFF
Ana Homem (Sterilization room management)
Tiago Vale (Hardware engineer)

► PUBLICATIONS

This service provides support in all general maintenance (excluding scientific equipment and units), in electricity, AVAC, buildings, gardening, cleaning and gives support to other activities that needs it (garbage - general and biohazard - reconstruction and adaptation, etc.).

Leite, José Mário
Head of Unit since 2014

Other position at IGC
Deputy Director

► SERVICE STAFF
Pedro Alves (Engineer for infrastructure)
Filipa Pardelha (Project Manager / Application Specialist)

► EXTERNAL SUBCONTRACTING
Cofeley VERKO
The Occupational Health & Biosafety Unit is focused on promoting protection of all workers and visitors of Instituto Gulbenkian de Ciência. Our biosecurity programme also aims to protect the environment and the community in which we live. The IGC firmly believes in the promotion of safety standards for academic research and is fully committed to improving the safety conditions of researchers. The Biosafety unit works to implement rules that meet the best biosafety practices recommended by the European Union and the World Health Organization. It is our mission to provide a better and safer working environment for all of our workers.

Among the services we provide are:

- Training of personnel to work with radioactive isotopes. Our radiation room is licensed by Direção Geral da Saúde (DGS) and we have permission to work with P-32, P-33, S-35, C-14 and H-3.
- The IGC has a Biosafety Level 2 containment facility that is under the supervision of the biosafety officer with an implemented training programme.
- Assisting scientists with the biosafety procedures to adopt in their labs.
- Guidance on biological and chemical waste disposal and decontamination procedures.
- Setting up and implementing emergency procedures and protocols.

Carneiro, Tiago
Head of Unit since 2012

Margarida Meira
Librarian

PhD in Biomedical Sciences

The Instituto Gulbenkian de Ciência’s library is an open access, specialized library in biomedicine. Its bibliographic collection covers Biology, Biochemistry, Genetics, Pharmacology, Microbiology, Physiology, Immunology, Virology, Cell Biology, Neuroscience and Developmental Biology.

The library is intended for researchers, faculty and visiting scientists, students and staff of the IGC, but is also opened to external users, either from the national scientific community or from higher education institutions. It aims to provide access to useful, diversified and up-to-date information, to improve services provided, to acquire, register, maintain and distribute scientific information of interest to or produced by researchers and students who work at the IGC.

The IGC library has a collection of printed journals in the field of health sciences, which spans almost 30 years. Currently it subscribes approximately 336 international scientific journals in electronic version.

In addition, since 2004, the library belongs to the national consortium Biblioteca do Conhecimento Online (b-on), which provides online access to the contents of about 22,000 international scientific journals and 18,000 e-books from 19 publishers, as well as to an important scientific bibliographic database - the Web of Science, which provides access to titles, abstracts and citation and impact factor reposts of approximately 8,500 journals, with records since 1945.
In 2014, this service supported researchers in attracting several external competitive research funds. IGC researchers secured or signed contracts for a total of 22 new external competitive research grants (14 FCT; 3 EU-FP7; 1 ERC; 1 AICR-UK; 1 EMBO Installation Grant; 1 ECCO Grant; 1 University Cologne: UoC Cooperation), 2 prizes (Best Oral Communication in an International Meeting; 1 Nikon Small World in Motion Photomicrography Competition) as well as 7 other type of funds (1 EMBO Conference Series; 1 EMBO Practical Course; 2 FCT FACC Conferences in Portugal; 2 Tebu Bio Travel Grants; 1 EMBO Short-term Fellowship) in a total amount of 3,247,635 EUR.

In addition, support was provided to attract several competitive national and international Individual PhD and Post-doctoral Fellowships (1 EMBO long-term fellowship, 1 FCT BCC fellowship, 1 FCT PhD fellowships and 5 FCT Post-doctoral fellowships) and 9 FCT Investigator Research positions.

The Research Funding Affairs’ responsibilities cease with contract signature and after passing all grant information to the Administrative and Project manager Unit and finance staff.

The services offered to researchers entail:
1) Identifying, in a timely manner, calls for proposals that might interest the IGC, evaluating the conditions and preferences for grant applications (eligibility, deadlines, how to apply and prepare full proposals, filling-in forms and web-pages, knowing how it works, what are the specific targets, what is behind each call, etc) and disseminating these opportunities through several means: the Grant Information website, monthly newsletter, online calendar, emails, meetings, etc;
2) Supporting proposal development and submission, namely: arranging administrative forms, host documents and signatures, assisting with scientific proposal writing and budget;
3) Post-award negotiation with funding agencies of contracts and agreements;
4) Grant application training for research staff and graduate students.

In addition, this team also monitors the impact of the services offered through the quantification of the following criteria: number of applications submitted, secured grants and prizes, diversity of grant agencies and amounts raised.
support to research

research structures & networks

**RESEARCH STRUCTURES**

*LABORATÓRIO ASSOCIADO ITQB (LA-ITQB)*

**Coordinator:** Cláudio M. Soares (ITQB Director)

Since January 2011, following a re-structure, the LA-ITQB brings together the Instituto de Tecnologia Química e Biológica (ITQB-UNL), the Instituto Gulbenkian de Ciência (IGC), the Instituto de Biologia Experimental e Tecnológica (IBET) and the Centro de Estudos de Doenças Crónicas (CEDOC-UNL). The current LA-ITQB is a successor of a previous, smaller consortium, set up in 2001, between ITQB, IBET, and a few groups of IGC, as one of the first Associated Laboratories in Portugal. In its present form, it is a much wider partnership whose main aim is to carry out a collaborative research programme, underpinned by a strong communications network and sharing of infrastructures, namely libraries, scientific facilities, academic services, and administrative support.

It is currently one of the broadest Associated Laboratories in terms of scientific expertise, spanning research areas from Chemistry to Medicine, along the following research themes:

- Theme 1 - Synthesis, structure, and function of biologically important molecules.
- Theme 2 - From genetics, cell and developmental biology to pathogenesis and novel therapies.
- Theme 3 - Computational and theoretical biology: from biochemistry to medicine.
- Theme 4 - Host-microbe and host-cancer interactions.
- Theme 5 - Plant genomics and stress responses.
- Theme 6 - Evolution of ecosystems, biological risk, and food safety.

*THE EUROPEAN MOUSE MUTANT ARCHIVE (EMMA)*

**Head of the Portuguese node:** Jocelyne Demengeot

The laboratory mouse is the most important mammalian model for studying genetic and multi-factorial diseases in Man. The European Mouse Mutant Archive (EMMA) is a not-for-profit repository for the collection, archiving (via cryopreservation) and distribution of relevant mutant strains that are essential for biomedical research.

EMMA draws on the expertise of 16 leading research institutes across Europe, including the IGC, in Portugal. The IGC offers the crucial Germ-Free Service that generates, breeds and houses mice that are free of all microorganisms. These germ-free animals are crucial in studies aimed at understanding the effects of microorganisms on a host, or dissecting the molecular mechanisms underlying the function of the immune system.

The germ-free facility of the IGC has generated more than 20 different strains of germ-free mice, requested by researchers from Portugal, Germany, USA, France and the UK. The facility has the capacity to temporarily host scientists wishing to carry out their own research with the mice at the IGC itself.

EMMA is part of the Infrafrontier Project, that links two complementary infrastructure networks with the aim of establishing a sustainable research infrastructure for systematic phenotyping, archiving and distribution of mouse models. IGC is one of the Infrafrontier partners, together with research facilities, government departments and funding agencies from 13 European countries, Canada and Israel.

*NATIONAL ROADMAP OF RESEARCH INFRASTRUCTURES OF STRATEGIC RELEVANCE*

In 2013, FCT opened a call for research infrastructures to be included in the National Roadmap of Research Infrastructures of Strategic Relevance. This call aimed at assessing the existing research infrastructures, identifying national priority areas and introducing Portugal into the group of European countries who have produced their own national roadmaps in alignment with the European Strategic Forum on Research Infrastructures (ESFRI). In total, 40 infrastructures in all scientific domains were integrated in the Portuguese Roadmap, of which 23 are aligned with ESFRI.

Four research structures of the IGC were selected to be included in the National Roadmap of Research Infrastructures:

1. **BioData.pt**: Portuguese Biological Data Network (coordinated by José Pereira-Leal, IGC)
2. **PPBI**: Portuguese Platform of BioImaging (coordinated by Paula Sampaio, Instituto de Biologia Molecular e Celular)
3. **GenomePT**: National Facility for Genome Sequencing and Analysis (coordinated by Manuel Santos, University of Aveiro)
4. **CONCENETO**: Consortium of Genetically Tractable Organisms (coordinated by Rui Costa, Champalimaud Foundation)

**EU-LIFE**

EU-LIFE is a new alliance that gathers thirteen renowned European research centres in life sciences: CRG-Centre for Genomic Regulation, (Barcelona, Spain); VIB (Flanders, Belgium); Institut Curie (Paris, France); MDC-Max Delbrück Center for Molecular Medicine, (Berlin, Germany); Gulbenkian Institute of Science (Oeiras, Portugal); CeMM-Research Center for Molecular Medicine of the Austrian Academy of Sciences (Vienna, Austria); EIO-European Institute of Oncology, (Milan, Italy); CEITEC-Central European Institute of Technology (Brno, Czech Republic); Netherlands Cancer Institute – Antoni van Leeuwenhoek (Amsterdam, Netherlands); FIMM-Institute for Molecular Medicine Finland (Helsinki, Finland); BRIC-Biotech Research and Innovation Centre (Copenhagen, Denmark); Babraham Institute (Cambridge, UK).
RMI- Friedrich Miescher Institute for Biomedical Research (Basel, Switzerland).

Partners in EU-LIFE operate with similar principles of excellence, external review, integrity and independence, competitiveness, internationality, and social responsibility. EU-LIFE partners believe that they can join forces to better address complex questions in research, training and research management, thereby contributing to pushing European science forward. Specific working groups join efforts, share best practice, brainstorm, and design common activities in areas of common interest such as technology transfer, international collaboration, translational research, science communication, competitive funding strategies, recruitment and training.

● **EMBnet - THE EUROPEAN MOLECULAR BIOLOGY NETWORK**

**Head of the Portuguese node: Pedro Fernandes**

The European Molecular Biology Network (EMBnet) Node is an international foundation that aggregates National Nodes and Specialist Nodes (industrial and research), that provide Bioinformatics infrastructural facilities in a geographically distributed way. Since its creation in 1988, EMBnet has evolved from an informal network of individuals in charge of maintaining biological databases into the only organization worldwide bringing bioinformatics professionals to work together to serve the expanding fields of genetics and molecular biology. Although composed predominantly of academic nodes, EMBnet gains an important added dimension from its industrial members. The success of EMBnet is attracting increasing numbers of organizations outside Europe to join. With members in more than 30 countries, it promotes useful exchanges between them and facilitates the location of resources and people. EMBnet runs EMBnet Journal and produces training and reference materials such as the EMBnet Quick-Guides. The IGC is a member of EMBnet since 1992. The role of the node has evolved according to the needs of the Portuguese community. One of its main activities, training and tuition in Bioinformatics, is strongly supported in EMBnet’s pool of professional teaching staff.

● **GOBLET - GLOBAL ORGANISATION FOR BIOINFORMATICS LEARNING, EDUCATION AND TRAINING**

GOBLET provides a global, sustainable support and networking structure for bioinformatics educators/trainers and students/trainees. This includes a training portal for sharing materials, tools, tips and techniques, guidelines and best practice documents, facilities to help train the trainers, and offering different learning pathways for different types of learners. It facilitates capacity development in bioinformatics in all countries and develops standards and guidelines for bioinformatics education and training. IGC is a member of GOBLET.
publications

peer-reviewed publications

IN-HOUSE PUBLICATIONS


40. Galhardo, L, Oliveira, RF. (2014). The effects of social isolation on steroid hormone levels are modulated by previous social status and context in a cichlid fish. Horm. Behav. 65: 1–5.


96. Oliveira, CA, Uceda, S., Oliveira, TF, Fernandes, AC, Garcia-Marques, T., Oliveira, RF (2014). Testosterone response to competition in males is unrelated to opponent familiarity or threat appraisal. Front. Psychol. 5: 1240.


► EPUB AHEAD OF PRINT


publications ● peer reviewed


► IGC CURRENT ADDRESS


► ASSOCIATED GROUPS


prizes & honours
prizes & honours

- Amorim, Maria João
  FCT Investigator
  Fundação para a Ciência e a Tecnologia, Portugal

- Athanasiadis, Alekos
  FCT Investigator
  Fundação para a Ciência e a Tecnologia, Portugal

- Beldade, Patrícia
  FCT Investigator
  Fundação para a Ciência e a Tecnologia, Portugal

Editorial Board
- Frontiers in Ecology and Evolution
- Frontiers in Cell and Developmental Biology
- EvoDevo
- Journal of Experimental Zoology - Molecular and Developmental Evolution

Hewitt Prize Committee for the Council for the European Society for Evolutionary Biology (ESEB)
European Society for Evolutionary Biology (ESEB)

Scientific Council
European Society for Evolutionary Biology

Vice-president
Portuguese Society for Evolutionary Biology

- Baena-González, Elena
  FCT Investigator
  Fundação para a Ciência e a Tecnologia, Portugal

- Castro, Diogo
  Member of the Board
  Portuguese Society for Developmental Biology

- Chelo, Ivo
  FCT Investigator
  Fundação para a Ciência e a Tecnologia, Portugal

- Chrostek, Ewa
  Best PhD student talk
  8th International Wolbachia meeting

- Domingos, Ana
  EMBO Installation Grant
  European Molecular Biology Organization (EMBO) and Fundação para a Ciência e a Tecnologia, Portugal

- Duque, Paula
  FCT Investigator
  Fundação para a Ciência e a Tecnologia, Portugal

  Member of the Scientific Advisory Board
  Plant-KBBE funding initiative

  Member of Editorial Board
  Scientific Reports, Nature Publishing Group (NPG)

- Godinho Ferreira, Miguel
  Member of the FCT Scientific Council for Life and Health Sciences
  Fundação para a Ciência e a Tecnologia, Portugal

- Goisés, Gabriela
  Special Visiting Researcher, Science without Borders
  Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES), Brazil

- Gordo, Isabel
  Panel Member for the ERC-Consolidator Grant panel in Life Sciences (LS8)
  European Research Council

- Jansen, Lars
  ERC Consolidator Grant
  European Research Council

- Lafuente, Elvira
  Best PhD Student Poster
  Portuguese Society for Evolutionary Biology

- Mallo, Moisés
  Academic Editor
  PLoS ONE

Editorial Board member
ISRN Developmental Biology

Prémio Melo e Castro 2014
Santa Casa da Misericórdia de Lisboa, Portugal

- Martins, Gabriel
  1st Place - Nikon Small World in Motion Competition 2013
  Nikon Instruments Inc.

- Oliveira, Raquel
  ERC Starting Grant
  European Research Council
Prizes & Honours

- **Perfeito, Lília**
  FCT Investigator
  Fundação para a Ciência e a Tecnologia, Portugal

- **Rocha, Luís**
  Editorial Board
  - PLoS ONE
  - Frontiers in Robotics and AI: Computational Intelligence
  - Immune Computation
  - International Journal of Signs and Semiotic Systems
  - Member
  - National Academy of Sciences Keck Futures Initiative, Complex Systems Review Panel
  - Conference Programme Committee
    - SSCI 2014: IEEE Symposium Series on Computational Intelligence 2014
    - BICT 2014: 8th International Conference on Bio-inspired Information and Communications Technologies
    - IBERAMIA 2014: 14th Ibero-American Conference on Artificial Intelligence
    - PSB 2014: Pacific Symposium on Biocomputing 2014
    - BioLINK 2014: Supporting BioScience through Text Mining
    - PACBB'14: International Conference on Practical Applications of Computational Biology & Bioinformatics 2014
    - Conference Programme Committee, Best paper award committee chair and Boolean and Neural Network session chair
    - ALIFE 14: the 14th International Conference on the Synthesis & Simulation of Living Systems

- **Soares, Helena**
  FCT Investigator
  Fundação para a Ciência e a Tecnologia, Portugal

- **Telley, Ivo**
  FCT Investigator
  Fundação para a Ciência e a Tecnologia, Portugal

- **Xavier, Karina**
  NIH Travel Grant
  National Institutes of Health
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<td>Teaching at other PhD programmes</td>
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PhD programme in 
integrative biology &
biomedicine (IBB)

Sucena, Élio
Director of the programme since 2013

► DESCRIPTION

The IGC PhD programme offers students from all over the globe and diverse academic backgrounds the opportunity to learn biology from a combination of resident institute researchers and invited faculty from many prestigious biological research institutions. In addition, our students attend classes at the Champalimaud Foundation, the Instituto de Tecnologia Química e Biológica and the University of Cologne/ MPI for Plant Breeding Research in the context of a bilateral student exchange agreement. This intensive academic semester culminates with students choosing research groups to join and writing their thesis projects. The IBB programme puts strong emphasis on the student’s involvement in determining his/her project from its conception. Students also benefit from many educational courses and workshops throughout their PhD, including a bioinformatics training program, weekly seminars and an annual retreat. The IBB programme is supported by the Fundação para a Ciência e a Tecnologia and the Calouste Gulbenkian Foundation.

► STUDENTS ADMITTED IN 2014

<table>
<thead>
<tr>
<th>Name</th>
<th>Nationality</th>
<th>First Degree</th>
<th>Institution</th>
</tr>
</thead>
<tbody>
<tr>
<td>Catarina Nabais</td>
<td>Portugal</td>
<td>MSc (Evolutionary Biology &amp; Development)</td>
<td>Universidade de Lisboa, Portugal</td>
</tr>
<tr>
<td>Delphine Pessoa</td>
<td>Belgium/Portugal</td>
<td>MSc (Biometrics &amp; Computational Biology)</td>
<td>Universidade de Lisboa, Portugal</td>
</tr>
<tr>
<td>Diego André dos Santos</td>
<td>Portugal</td>
<td>MSc (Biometrics &amp; Computational Biology)</td>
<td>Universidade de Lisboa, Portugal</td>
</tr>
<tr>
<td>Inês Calêndia de Souza</td>
<td>Portugal</td>
<td>MD (Medicine)</td>
<td>Universidade Nova de Lisboa, Portugal</td>
</tr>
<tr>
<td>José de Arlindo Santos</td>
<td>Portugal</td>
<td>MSc (Molecular Biology &amp; Genetics)</td>
<td>Universidade Nova de Lisboa, Portugal</td>
</tr>
<tr>
<td>Lok Ran Pahari</td>
<td>Nepal</td>
<td>MD (Medicine)</td>
<td>Nepal Medical College Teaching Hospital, Nepal</td>
</tr>
<tr>
<td>Maria Inês Mamo</td>
<td>Portugal</td>
<td>MSc (Biomedical Research)</td>
<td>Universidade de Lisboa, Portugal</td>
</tr>
<tr>
<td>Mihailo Mihajlovic</td>
<td>Montenegro</td>
<td>MSc (Molecular Biology &amp; Physiology)</td>
<td>University of Belgrade, Serbia</td>
</tr>
<tr>
<td>Praveen Jain</td>
<td>India</td>
<td>MSc (Microbiology)</td>
<td>The Manipal Academy of Tropical Medicine, India</td>
</tr>
<tr>
<td>Ioanna Olimpeodriti</td>
<td>Greece</td>
<td>BSc (Biology)</td>
<td>University of Athens, Greece</td>
</tr>
</tbody>
</table>

► COURSES IN 2014

● History of Biological Concepts
  January 13-17
  Organisers: Lars Jansen and Élio Sucena (IGC, Portugal)
  Faculty: William Bynum, Helen Bynum (University College London, UK), William Martin (Heinrich-Heine-Universität Düsseldorf, Germany), Jonathan Howard, António Coutinho, Christen Mirth, Rui Oliveira (IGC, Portugal), Joe Paton (Champalimaud Neuroscience Programme, Portugal)

● Statistics and Quantitative Biology
  January 20-24
  Organiser: Jorge Carreira (IGC, Portugal)
  Faculty: Nuno Sepúlveda (London School of Hygiene & Tropical Medicine, London, UK), Jorge Carreira (IGC, Portugal)

● Molecular and Structural Biology
  January 27-31
  Organisers: Alekos Athanasiadis and Lars Jansen (IGC, Portugal)
  Faculty: Ben E. Black (Perelman School of Medicine, University of Pennsylvania, USA), Anna Akhmanova (Utrecht University, The Netherlands), Sandra Ribeiro (Instituto de Biologia Molecular e Celular, Portugal), Manuel Santos (Universidade de Aveiro, Portugal), Claudio Soares (Instituto de Tecnologia Química e Biológica, Portugal)

● Inside the Cell
  February 3-7
  Organisers: Raquel Oliveira and Colin Adrain (ICC, Portugal)
  Faculty: Seamus Martin (Trinity College Dublin, Ireland), Camilla Sjögren (Karolinska Institute, Sweden), Helder Maiato (Instituto de Biologia Molecular e Celular, Portugal), Sérgio Almeida (Instituto de Medicina Molecular, Portugal), Dani Bodo; José Planells (ICC, Portugal)

● Cell Biology
  February 10-14
  Organisers: Mónica Dias and Florence Jonasdy (ICC, Portugal)
  Faculty: Manuel Théry (Institut de Recherches en Technologies et Sciences pour le Vivant, Creteil, France), Ewa Paluch (Laboratory for Molecular Cell Biology, University College London, UK), Thomas Leclerc (Institut de Biologie du Développement de Marseille, CNRS, France), Maria João Amorim, José Pereira-Leal (ICC, Portugal)
COURSES IN 2014 (cont.)

● Developmental Biology
February 17-21
Organisers: Diogo Castro, Maísa Mallo and Joaquim Léon (IGC, Portugal)
Faculty: Anne Grapin-Botton (University of Copenhagen, Denmark), Valerie Wilson (University of Edinburgh, UK), Benedikt Berringeirg (University of Mainz, Germany), Fernando Roch (Centre de Génétique Moléculaire, CNRS, Toulouse, France), Élio Sucena (IGC, Portugal), Susana Lopes (Chronic Diseases Research Center, Portugal), Rui Martinho (Universidade do Algarve, Portugal), Leonor Saúde (Instituto de Medicina Molecular, Portugal), Ana Tavares (IGC, Portugal)

● Biophysics
February 24-28
Organisers: Filipa Alves and Ivo Telley (IGC, Portugal)
Faculty: Jaap Kaandorp (University of Amsterdam, The Netherlands), Silvia Ponce Dawson (Universidad de Buenos Aires, Argentina), Jochen Guck (Dresden University, Germany), António Jacinto and Susana Lopes (Chronic Diseases Research Center, Portugal)

● Systems Biology
March 3-7
Organizer: Claudine Chaouiya (IGC, Portugal)
Faculty: Didier Corse (Université libre de Bruxelles, Belgium), Attila Csikasz-Nagy (King’s College London, UK), Nils Blüthgen (Charité-Universitätsmedizin Berlin, Germany), Edda Schulz (Génétique et biologie du développement at Institut Curie, France)

● Evolution
March 17-21
Organisers: Isabel Gordo and Lounès Chikhi (IGC, Portugal)
Faculty: Gilles Guillot (Technical University of Denmark, Denmark), Sylvain Cardon (University of Montpellier, France), Cristina Vieira (University of Lyon, France), Pedro Vale (University of Edinburgh, UK), José Álvarez, Ivo Chela, Lilia Perfeito, João Alpedinha, Jorge Sousa, Rasmus Heller (IGC, Portugal)

● Evolution, Development and Ecology
March 24-28
Organisers: Patricia Beldade and Christen Mirth (IGC, Portugal)
Faculty: Christian Borendre (Université Nice Sophia Antipolis, France), Johannes Jaeger (Centre de Regulació Genòmica, Barcelona, Spain), Abderrahman Khila (Institut de Génomique Fonctionnelle de Lyon, France), Élio Sucena (IGC, Portugal)

● Ecology
March 30 - April 4
Organiser: Sara Magalhães (Faculdade de Ciências da Universidade de Lisboa, Portugal)
Faculty: Marc-André Selouse (Centre d’Écologie Fonctionnelle et Evolutive, CNRS, Montpellier, France), Michael Wade (Indiana University, USA), Sara Magalhães (Faculdade de Ciências da Universidade de Lisboa, Portugal)

● Immunochemistry
April 1-16
Organisers: Luis Teixeira and Miguel Soares (IGC, Portugal)
Faculty: Dieter Ebert (Basel University, Switzerland), Paul Schmid-Hempel (Eidgenössische Technische Hochschule Zürich, Switzerland), Ruslan Medzhitov (Yale University, USA), Csaba Reis e Sousa (London Research Institute, UK), Max Cooper (Emory Vaccine Center, USA), David Schneider (Stanford University, USA), Wolf-Dietrich Hardt (Eidgenössische Technische Hochschule Zürich, Switzerland), Jonathan Howard, António Coutinho, Jocelyne Demengeot (IGC, Portugal)

● Introduction to Neuroscience
April 28 - May 2
Organisers: Rui Oliveira (IGC and Instituto Superior de Psicologia Aplicada, Portugal) and Champalimaud Neuroscience Programme, Portugal
Faculty: Zach Mainen, Joe Paton, Megan Carey, Luisa Vasconcelos, Michael Orger, Carlos Ribeiro, Nicolas Morgenstern, Rui Costa, Alfonso Renart, Marta Moita, Susana Lima (Champalimaud Neuroscience Programme, Portugal), Rui Oliveira (IGC and Instituto Superior de Psicologia Aplicada, Portugal), Ana Domingos (IGC, Portugal)

● Plant Science
May 5-9
Organiser: Isabell Witt (Max Planck Institute for Plant Breeding Research, Germany)
Faculty: Jochen Guck (Dresden University, Germany), António Jacinto and Susana Lopes (Chronic Diseases Research Center, Portugal), José Feijó (University Maryland, USA, and IGC, Portugal), Jörg Becker (IGC, Portugal)

● From Cells to Organisms
May 12-16
Organisers: Karina Xavier and Miguel Godinho-Ferreira (IGC, Portugal)
Faculty: Stijn Speevers, Henning Freiigmann (Max Planck Institute for Plant Breeding Research, Germany), Ute Höcker, Maria Alberi (Institute for Genetics, Germany), Andreas Weber (Heinrich-Heine-Universität Düsseldorf, Germany), Martin Hüsken (Biocentre, University of Trieste, Italy), José Feijó (University Maryland, USA, and IGC, Portugal), Jörg Becker (IGC, Portugal)

● Hypothesis Driven Research
May 19-23
Organiser: Élio Sucena (IGC, Portugal)
Faculty: Élio Sucena, Jocelyne Demengeot (IGC, Portugal)
The Graduate Programme Science for Development (PGCD) is an advanced training programme designed to prepare students from the various Portuguese Speaking African Countries (PALOP) to pursue research careers in Science and Technology, particularly in the Life Sciences. It is currently being developed as a partnership between the IGC and the Ministry of Higher Education, Science and Innovation (MESCI) of Cape Verde, with three main goals: 1) To train the next generation of excellent Portuguese-speaking African students, giving them the opportunity to learn advanced science and become scientists; 2) To improve the quality of science education and scientific research in the Portuguese-Speaking African Countries; 3) To use science and technology as effective tools for development.

The programme will offer basic training in the life sciences, paying particular attention to Plant Biology, Marine Biology and Tropical Diseases. In addition to the science curriculum, the PGCD will offer a course in English, the language of science. The programme's structure will consist of one year of graduate courses, taking place in Praia, Cape Verde, followed by a 3 to 4 year research period leading to PhD thesis. The research period will be divided between the home countries and select institutes and universities abroad.

More information, including the final list of students, can be found at the Programme’s website.

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**STUDENTS ADMITTED IN 2014**

<table>
<thead>
<tr>
<th>Name</th>
<th>Nationality</th>
<th>First Degree</th>
<th>Institution</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ana Paula de Sousa Montero</td>
<td>Cape Verde</td>
<td>MSc (Chemical Engineering)</td>
<td>Universidade de Cabo Verde, Portugal</td>
</tr>
<tr>
<td>Semedo d’Aguiar</td>
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</tr>
<tr>
<td>Anelmo Angelo Adolfo Langa</td>
<td>Mozambique</td>
<td>MSc (Marine Sciences)</td>
<td>University of Dares-Salam, Tanzania</td>
</tr>
<tr>
<td>Cintia Patrícia Horta Reves</td>
<td>Cape Verde</td>
<td>MSc (Biomedical Engineering)</td>
<td>Universidade de Cabo Verde, Portugal</td>
</tr>
<tr>
<td>Daniel Augusta Zacarias</td>
<td>Mozambique</td>
<td>MSc (Water &amp; Coastal Management)</td>
<td>Universidade do Algarve, Portugal</td>
</tr>
<tr>
<td>Denise de Oliveira Coutinho</td>
<td>Cape Verde</td>
<td>BSc (Microbiology &amp; Immunology)</td>
<td>Universidade Federal do Rio de Janeiro, Brazil</td>
</tr>
<tr>
<td>Edison Sá Fernandes Corvalho</td>
<td>Cape Verde</td>
<td>MSc (Marine Biology)</td>
<td>Universidade de Cabo Verde, Portugal</td>
</tr>
<tr>
<td>Elaine Ochóia Ade de Carvalho</td>
<td>Angola</td>
<td>MSc (Medical Parasitology)</td>
<td>IMET, Universidade Nova de Lisboa, Portugal</td>
</tr>
<tr>
<td>Elves Helena Coates Duarte</td>
<td>Cape Verde</td>
<td>MSc (Medical &amp; Veterinary Entomology)</td>
<td>Bicer e Montpellier</td>
</tr>
<tr>
<td>Hugo Aluquerarure Mário</td>
<td>São Tomé e Príncipe</td>
<td>BSc (Biology)</td>
<td>Inst. Sup. Politécnico, São Tomé e Príncipe</td>
</tr>
<tr>
<td>Júlio Monteiro Rodrigues</td>
<td>Cape Verde</td>
<td>MSc (Epidemiology &amp; Endemic Disease Control)</td>
<td>FioCruz, Brasil</td>
</tr>
<tr>
<td>Lisaro Gonçalves Cunha</td>
<td>Mozambique</td>
<td>MSc (Toxicology &amp; Environmental Contamination)</td>
<td>ICBAS, Universidade do Porto, Portugal</td>
</tr>
<tr>
<td>Neide Vazela Rodrigues</td>
<td>Cape Verde</td>
<td>MSc (Molecular &amp; Cell Biology)</td>
<td>Universidade de Aveiro, Portugal</td>
</tr>
<tr>
<td>Osvaldo Frederico Inlamea</td>
<td>Mozambique</td>
<td>BSc (Veterinary Medicine)</td>
<td>UEM-Moçambique</td>
</tr>
<tr>
<td>Santos Lopes Tavares Martins</td>
<td>Cape Verde</td>
<td>MSc (Marine Biology)</td>
<td>Universidade de Cabo Verde, Portugal</td>
</tr>
<tr>
<td>Vinícius M'Bana</td>
<td>Guinea-Bissau</td>
<td>BSc (Biotechnology)</td>
<td>FCT, Universidade Nova de Lisboa, Portugal</td>
</tr>
</tbody>
</table>

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**COURSES IN 2014**

- **English**
  - January 6-10
  - Organiser: Jacob Cullen (Language Link, Cabo Verde)

- **Biostatistics**
  - January 13-17
  - Organiser: Jorge Carneiro (IGC, Portugal)
  - Faculty: Filipa Alves (IGC, Portugal)
COURSES IN 2014 (cont.)

- **Evolution and Ecology**  
  January 20-24  
  *Organiser:* Filipa Vala (Faculdade de Ciências da Universidade de Lisboa, Portugal)  
  *Faculty:* Tiago Paixão (Institute of Science and Technology, Austria) Rui Castanheira (IGC, Portugal), Sara Magalhães (Faculdade de Ciências da Universidade de Lisboa, Portugal)

- **Molecular Biology**  
  January 27-31  
  *Organiser:* Christen Mirth (IGC, Portugal)  
  *Faculty:* Maria João Amorim (IGC, Portugal)

- **Genomes and DNA**  
  February 3-7  
  *Organiser:* Miguel Godinho Ferreira (IGC, Portugal)  
  *Faculty:* Luis Jansen (IGC, Portugal), Rui Martinho (Universidade do Algarve, Portugal)

- **Inside the Cell**  
  February 10-14  
  *Organiser:* Pedro Carvalho (Centre de Regulació Genòmica, Spain)  
  *Faculty:* Joana Loureiro (Rochester University, EUA), Nuno Santos (Faculdade de Medicina da Universidade de Lisboa, Portugal)

- **The Working Cell**  
  February 17-21  
  *Organiser:* Mónica Dias (IGC, Portugal)  
  *Faculty:* Raquel Oliveira (IGC, Portugal), Susana Godinho (Queen Mary University of London, UK), Dina Calado (London Research Institute, UK), Joana Paredes (PATIMUP, Portugal)

- **Bioinformatics**  
  February 24-28  
  *Organiser:* José Leal (IGC, Portugal)  
  *Faculty:* Ana Teresa Vasconcelos (Laboratório Nacional de Computação Científica, Brazil), Claudia de Moraes Russo (Universidade Federal do Rio de Janeiro, Brazil), Ricardo Leite (IGC, Portugal)

- **Genetics and Development**  
  March 3-7  
  *Organiser:* António Jacinto (Chronic Diseases Research Center, Portugal)  
  *Faculty:* Leona Saade (Instituto de Medicina Molecular, Portugal), Rita Flor (IGC, Portugal)

- **Introduction to Marine Biology**  
  March 10-14  
  *Organiser:* Mike Weber (Centro de Investigação em Biodiversidade e Recursos Genéticos, Portugal)  
  *Faculty:* Jaime Paiva (Estação Lisboa da Avenida and Faculdade de Ciências da Universidade de Lisboa, Portugal)

- **Ecology, Biodiversity**  
  March 17-21  
  *Organiser:* Mario Dornellas (St. Andrews, UK)  
  *Faculty:* Miguel Barbosa (St. Andrews, UK)

- **Population Genetics and Genomics**  
  March 24-28  
  *Organiser:* Ricardo Beldade (Centre National de la Recherche Scientifique, France)  
  *Faculty:* Luís Chiti (IGC, Portugal), André Levy (Instituto Superior de Psicologia Aplicada, Portugal)

- **Deep Sea and Coastal Ecology**  
  March 31 - April 4  
  *Organiser:* Ana Hilario (Centro de Estudos do Ambiente e do Mar, Portugal)  
  *Faculty:* Ana Paula Mucha (Universidade do Porto, Portugal)

- **Tropical Ecology**  
  April 7-11  
  *Organiser:* JP Voltolini (Universidade Estadual de Santa Paulo, Brazil)  
  *Faculty:* Salomão Bandeira (Universidade Eduardo Mondlane, Mozambique), Eurico Oliveira (Universidade de São Paulo, Brazil), Lilian Krug (Universidade do Algarve, Portugal)

- **Aquatic Plants and Algae**  
  April 21-25  
  *Organiser:* Ester Serrão (Centro de Ciências do Mar, Portugal)  
  *Faculty:* Salomão Bandeira (Universidade Eduardo Mondlane, Mozambique), Eurico Oliveira (Universidade de São Paulo, Brazil), Lilian Krug (Universidade do Algarve, Portugal)

- **Plant Cell Biology and Biochemistry**  
  April 28 - May 2  
  *Organiser:* Paula Duque (IGC, Portugal)  
  *Faculty:* José Feijó (University Maryland, EUA, and IGC, Portugal), Jorge Marques da Silva, Américo Rodrigues (Faculdade de Ciências da Universidade de Lisboa, Portugal)

- **Plant Stress and Physiology**  
  May 5-9  
  *Organiser:* Elena Baena (IGC, Portugal)  
  *Faculty:* José Feliú (University Maryland, EUA, and IGC, Portugal), Jorge Marques da Silva, Américo Rodrigues (Faculdade de Ciências da Universidade de Lisboa, Portugal)

- **Plant Biotechnology**  
  May 19-23  
  *Organiser:* Rita Abranches (Instituto de Tecnologia Química e Biológica, Portugal)  
  *Faculty:* Célia Domingues, Pedro Fevereiro (Instituto de Tecnologia Química e Biológica, Portugal), Carlos Labate (Universidade de São Paulo, Brazil)

- **Immunology and Host-pathogen Interaction**  
  June 2-6  
  *Organiser:* Thiago Carvalho (IGC, Portugal)  
  *Faculty:* Alberto Nobrega (Universidade Federal do Rio de Janeiro, Brazil), Rafaela Cozzelino, Vasco Barreto (IGC, Portugal)

- **Immune and Chronic Diseases**  
  June 9-13  
  *Organiser:* Helena Soares (Institut Pasteur, France)  
  *Faculty:* Margarida Correia-Neves (Universidade da Minho, Portugal), Rogério Amino (Institut Pasteur, France) Patricia Bozza (Fiocruz, Rio de Janeiro, Brazil)
COURSES IN 2014 (cont.)

● Vector-borne Diseases
June 16-20
Organiser: Maria Mota (Instituto de Medicina Molecular, Portugal)
Faculty: Flaminia Catteruccia (Harvard School of Public Health, USA), Luis Teixeira (ICG, Portugal), Silvia Boscardin (Universidade de São Paulo, Brazil), Vanessa Zuzarte Luís (Instituto de Medicina Molecular, Portugal)

● Intestinal Infections
June 23-27
Organiser: Marize Miagostovich (FioCruz, Rio de Janeiro, Brazil)
Faculty: José Paulo Gagliardi, Filipe Carvalho Costa (FioCruz, Rio de Janeiro, Brazil)

● Public Health
June 30 - July 4
Organiser: Susana Nery (University of Queensland, Australia)
Faculty: Cesário Martins (Bandim, Guinea-Bissau), Maria Jesus Trovoada (Centro Cultural Português, São Tomé e Príncipe), Pieter Remes (Development Media International, Burkina-Faso), Inácio Mandomando (Centro de Investigação em Saúde de Manhiça, Mozambique)

● Tropical Medicine and Clinical Microbiology
July 7-11
Organiser: Emilia Valadas (Instituto de Medicina Molecular/Faculdade de Medicina da Universidade de Lisboa, Portugal)
Faculty: Robert Badura, Maria Rebelo (Instituto de Medicina Molecular, Portugal), Thomas Harscheid (Instituto de Medicina Molecular/Faculdade de Medicina da Universidade de Lisboa, Portugal)

● Epidemiology
July 14-18
Organiser: Laura Rodrigues (London School of Hygiene & Tropical Medicine, UK)
Faculty: Mauricio Lima Barreto (Universidade Federal da Bahia, Brazil), Erida Ciri (ICG, Portugal), Nuno Sepúlveda (London School of Hygiene & Tropical Medicine, UK)

● Non-infectious Diseases
July 21-25
Organiser: Marly Cardoso (Universidade de São Paulo, Brazil)
Faculty: Bernardo Lessa Horta (Universidade Federal, Pelotas, Brazil), Suely Cimeno (Universidade Federal de São Paulo, Brazil), Marcia Machado (Universidade Federal do Tocantins, Brazil)

● Science Communication and Management
July 28-30
Organiser: Ana Mena (ICG, Portugal)
Faculty: Ana Godinho (Fundação para a Ciência e a Tecnologia, Portugal), Margarida Trindade (Instituto Superior de Ciências do Trabalho e da Empresa, Portugal), Sheila Vidal (ICG, Portugal)
The GTPB provides practical skills in Bioinformatics. The objective is to deliver those skills with high efficiency and as much autonomy of usage as possible. It consists of short, intensive training courses, held in a specialized training room. The courses are taught and fully documented in English. The very diverse target audiences reflect the variety of the course themes. The majority of the participants are Biologists in the PhD project preparation phase. The courses are self-assessed by the participants through a standardized questionnaire and instant feedback mechanisms. The GTPB runs experiments with innovative training methodologies, aiming at optimizing learning outcomes, increasing the learning rate and ensuring the consolidation of new skills.

**DESCRIPTION**

All courses were organized by Pedro Fernandes (IGC, Portugal).

- **IB14F – Introductory Bioinformatics (first course in 2014)**
  
  April 8-11
  
  Faculty: David P. Judge (Cambridge University, UK), Phil Cunningham (King’s College London, UK) and Pedro L. Fernandes (IGC, Portugal)

- **IBSTAT14 – Introductory Biostatistics**
  
  June 2-6
  
  Faculty: Ana Luisa Papoila (Faculdade de Ciências Médicas, Universidade Nova de Lisboa, Portugal) and Fernanda Diamantino (Faculdade de Ciências da Universidade de Lisboa, Portugal)

- **SMLMC14 – Structural Modeling for Large Macromolecular Complexes**
  
  June 11-13
  
  Faculty: Joanna Kasprzak (Laboratory of Bioinformatics and Protein Engineering, International Institute of Molecular and Cell Biology, Warsaw, Poland, and Institute of Molecular Biology and Biotechnology, Faculty of Biology, Adam Mickiewicz University, Poznani, Poland)

- **ABSTAT14 – Advanced Biostatistics for Bioinformatics Tool Users using R**
  
  September 15-18
  
  Faculty: Lisete Sousa (Faculdade de Ciências da Universidade de Lisboa, Portugal) and Carina Silva Fortes (Escola Superior de Tecnologias da Saúde de Lisboa, Portugal)

- **TA-AFADM14 – Transcriptome Analysis (RNA-seq) and Automatic Function Annotation**
  
  October 6-9
  
  Faculty: Stefan Götz (BioBam Bioinformatics, Valencia, Spain) and Riccardo Avni Cigliano (Sequentia Biotech, Barcelona, Spain)

- **TA-AFADM14 – Transcriptome Analysis (RNA-seq) and Automatic Function Annotation**
  
  October 6-9
  
  Faculty: Lisete Sousa (Faculdade de Ciências da Universidade de Lisboa, Portugal) and Carina Silva Fortes (Escola Superior de Tecnologias da Saúde de Lisboa, Portugal)

- **BPB14 – Bioinformatics using Python for Biologists**
  
  November 3-7
  
  Faculty: Allegra Via (“La Sapienza” Università di Roma, Italy) and Kristian Rother (Academis, Berlin, Germany)

- **CSDM14 – Chromosome structure determination using modelling and Hi-C data**
  
  November 25-28
  
  Faculty: Marc A. Marti-Renom, Davide Basí and François Serra (Centro Nacional de Análisis Genómico and Centro de Regulación Genómica, Barcelona, Spain)

- **IB14S – Introductory Bioinformatics (second course in 2014)**
  
  December 8-12
  
  Faculty: David P. Judge (Cambridge University, UK), Pedro L. Fernandes (IGC, Portugal) and Javier Santoyo-Lopez (Edinburgh Genomics, The University of Edinburgh, Ashworth Laboratories, Scotland, UK)
In 2014, a new internship programme was set up to receive undergraduate students at the IGC laboratories during the summer. The IGC and the University of Oxford established a partnership via the University of Oxford Internship Programme that brought to the IGC six young science undergraduates from the University, for an 8-week lab internship, each fully supported by the University.

GROUPS THAT HOSTED THE INTERNSHIP:
- Bacterial Signalling
- Cell Biology of Viral Infection
- Evolutionary Biology
- Evolution and Development
- Host-Microorganism Interactions
- Inflammation
- Population and Conservation Genetics
- Plant Molecular Biology
- Science and Policy

► FUNDING
University of Oxford

► COORDINATOR
Jonathan Howard
**MSc THESES**

- **Thomas Hermanns**  
  Characterization of Toxoplasma gondii protein GRA7 as the first dense granule-secreted IRG-specific virulence factor.  
  University of Cologne, Germany | March 2014

- **Christina Paparokidou**  
  Unravelling the role of Major Facilitator Superfamily (MFS) transporters in plant abiotic stress tolerance.  
  University of Amsterdam, The Netherlands | August 2014

- **Artur Felipe Rodrigues**  
  Implications of A to I RNA editing in circular RNA biogenesis.  
  Universidade de Aveiro, Portugal | August 2014

- **Marta Lourenço**  
  Evolution of Escherichia coli in the mouse gut.  
  Universidade de Lisboa, Portugal | September 2014

- **Patrícia Soares**  
  Insights into tuberculosis: a survival analysis of time to recurrence.  
  Universidade de Lisboa, Portugal | September 2014

- **Marisa Rodrigues**  
  The effects of macronutrient composition of the larval diet on life history traits and pigmentation in Drosophila viridis.  
  Universidade de Lisboa, Portugal | October 2014

- **Maria Silva Ferreira**  
  Chromosome rearrangements as catalysts of speciation.  
  Universidade de Lisboa, Portugal | October 2014

- **Mariana Batista Santos**  
  Cohesion decay: quantitative analysis of partial sister chromatid cohesion.  
  Universidade Nova de Lisboa, Portugal | November 2014

- **Fábio Faustino**  
  The influence of cortisol and the social environment in adult neurogenesis in zebrafish.  
  Universidade de Lisboa, Portugal | November 2014

**PhD THESES**

- **Rita Valente**  
  Cell-to-cell Communication in Pectobacterium wasabiae.  
  Universidade Nova de Lisboa, Portugal | May 2014

- **Yoan Diekmann**  
  Evolution of function in the Rab family of small GTPases.  
  Universidade Nova de Lisboa, Portugal | June 2014

- **Urs Benedikt Müller**  
  Polymorphism of the IRG resistance system determines virulence of Toxoplasma gondii in mice.  
  University of Cologne, Germany | June 2014

- **Helen Maria Springer-Frauenhoff**  
  The immunity-related GTPase (IRG) resistance system against intracellular parasites.  
  University of Cologne, Germany | June 2014

- **Tom Weber**  
  Optimal Timing of Phase Resolved Cell Cycle Progression.  
  Humboldt University, Germany | June 2014

- **Otilda Almeida**  
  Neuroendocrinology of social behaviour in the African cichlid Oreochromis mossambicus: regulatory mechanisms and social modulation of reproduction.  
  Universidade do Algarve, Portugal | July 2014
● Lurdes Duarte
Unraveling maternal and fetal genetic factors protecting from Pregnancy Associated Malaria in the mouse.
Universidade Nova de Lisboa, Portugal | July 2014

● Marisa Oliveira
Coordinating development: uncovering the mechanisms that coordinate organ growth and patterning with the development of the whole body.
Universidade Nova de Lisboa, Portugal | July 2014

● José Miguel Simões
The Social Brain: How social stimuli are translated into neuroendocrine signals?
Universidade de Lisboa, Portugal | July 2014

● Alexandre Leitão
Hematopoiesis in the Drosophila larva: beyond the lymph gland.
Universidade Nova de Lisboa, Portugal | September 2014

● Sofia Braga
Clinical decisions in breast cancer, a heterogenous disease.
Universidade Nova de Lisboa, Portugal | October 2014

● Ewa Chrostek
Genetic and environmental factors influence Wolbachia-Drosophila symbiosis.
Universidade Nova de Lisboa, Portugal | October 2014

● Clara Pereira
Stochasticity and commitment in monoallelic gene activation.
Universidade Nova de Lisboa, Portugal | October 2014

● Sander van Noort
Participatory surveillance and mathematical models in epidemiologic research: successes and challenges.
Universidade Nova de Lisboa, Portugal | October 2014

● Leila Shirai
Morphological diversification through the evolution of developmental hierarchies.
Universidade Nova de Lisboa, Portugal | November 2014

● João Alves
Understanding the impact of chromosomal inversions on the evolution of the human genome.
Universidade do Porto, Portugal | December 2014

● Rui Castanhinha
Developmental and paleontological insights into skull bone homology and evolution.
Universidade Nova de Lisboa, Portugal | December 2014
● Barreto, Vasco
Mechanisms of Somatic Diversification of Antigen Receptor Genes
Graduate Programme in Areas of Basic and Applied Biology (GABBA), Porto, Portugal
April 2014

● Becker, Jörg
Microarrays and deep sequencing as tools to decipher biological processes
BioFIG BioSYS PhD programme, Faculdade de Ciências da Universidade de Lisboa, Portugal
March 2014

● Bettencourt-Dias, Mónica
Graduate Programme in Areas of Basic and Applied Biology (GABBA), Porto, Portugal
January 2014

● Carneiro, Jorge
Statistics for Modern Quantitative Biology
Instituto de Biotechnologia, UNAM, Cuernavaca, Mexico
November 2014

● Castro, Diogo
Transcriptional control of vertebrate neurogenesis
Graduate Programme in Areas of Basic and Applied Biology (GABBA), Porto, Portugal
March 2014

● Chaouiya, Claudine
Introduction to Systems Biology - Qualitative modelling of regulatory networks
ITQB PhD Programme MolBioS, Oeiras, Portugal
February 2014

● Chelo, Ivo
Experimental evolution: theory and current practices
International graduate programme in life sciences and Interdisciplinary master in life sciences, Institut de Biologie de l'Ecole Normale Supérieure (BENS), Paris, France
November 2014

● Duque, Paula
Alternative splicing of a novel Arabidopsis membrane transporter enhances translation to promote plant zinc tolerance
BioFIG BioSYS PhD programme, Faculdade de Ciências da Universidade de Lisboa, Portugal
January 2014

● Ferreira, Álvaro Gil
Building an African Biomedical Research Community using Drosophila
Kampala International University, Uganda
September 2014

● Ferreira Moita, Luís
Sepsis
PhD programme in Health Sciences, Faculdade de Medicina da Universidade de Coimbra, Coimbra, Portugal
November 2014

● Gardner, Rui
Basic Training in Flow Cytometry
Karolinska Institute, Stockholm, Sweden
January 2014

● Martins, Gabriel
Intro to Microscopy
ITQB PhD programme MolBioS, Oeiras, Portugal
January 2014

● Oliveira, Rui
Research Seminar (course)
University of Saint Joseph, Macau, China
April 2014

● Social Neuroscience
PhD Programme in Neuroscience, Faculdade de Medicina da Universidade de Lisboa, Lisbon, Portugal
October 2014
Rebelo, Manuel
Biotério e regulamentação para experimentação animal
PhD Programme in Health Sciences, Faculdade de Medicina da Universidade de Coimbra, Coimbra, Portugal
January and October 2014

Rocha, Luís M.
Introduction to Informatics
PhD Programme in Informatics, Indiana University, USA
March 2014

Advanced Seminar in Complex Systems
PhD Programme in Informatics, Indiana University, USA
September 2014

Silva, Pedro
Statistics for Modern Quantitative Biology
Instituto de Biotecnologia, UNAM, Cuernavaca, Mexico
November 2014

Soares, Miguel
Inflammation (Immunology module)
- Graduate Programme in Areas of Basic and Applied Biology (CABBA), Porto, Portugal
  April 2014
- Programa de Doutoramento em Ciências da Saúde, Faculdade de Medicina da Universidade de Coimbra, Coimbra, Portugal
  November 2014

Advanced Immunology
Institut Pasteur, Paris, France
December 2014

Sobral, Daniel
High Throughput Sequencing Sequence Data Generation and Analysis
ITQB PhD Programme MolBioS, Oeiras, Portugal
February 2014

Tranfield, Erin
Methods in Biosciences I: Introduction to Electron Microscopy
ITQB PhD Programme MolBioS, Oeiras, Portugal
January 2014

Vidal, Sheila
Research Skills in a Medical Career: management, communication and funding – Scientific Writing
PhD Programme in Medicine and Life Sciences, Faculdade de Ciências Médicas da Universidade Nova de Lisboa, Lisboa, Portugal
October 2014

Research Skills in a Medical Career: management, communication and funding – The writing of the PhD thesis, papers and grants: Structure II
PhD Programme in Medicine and Life Sciences, Faculdade de Ciências Médicas da Universidade Nova de Lisboa, Lisboa, Portugal
November 2014

Xavier, Karina
Signalling in bacterial communities
ITQB MolBioS PhD Programme, Oeiras, Portugal
March 2014
## Seminars & Meetings

### January 2014

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<th>Date</th>
<th>Speaker</th>
<th>Affiliation</th>
<th>Title</th>
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<tbody>
<tr>
<td>07.01</td>
<td>Vasco Barreto</td>
<td>IGC</td>
<td>Genome protection, DNA repair and Activation Induction Cytidine Deaminase</td>
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<tr>
<td>07.01</td>
<td>Tiago Dantas</td>
<td>Columbia University</td>
<td>Analysing the role of centrosomes in genomic stability and cell proliferation</td>
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<td>14.01</td>
<td>Raquel Oliveira</td>
<td>IGC</td>
<td>Sister chromatid cohesion not too little, not too much</td>
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<td>17.01</td>
<td>Luísa V. Lopes</td>
<td>IGC</td>
<td>Coffee and adenosine receptors of memory deficits related to aging</td>
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<tr>
<td>17.01</td>
<td>William Bynum</td>
<td>University College London, UK</td>
<td>A PP1/PP2A protein phosphatase relay regulates progression through mitosis</td>
</tr>
<tr>
<td>17.01</td>
<td>Iain Hogan</td>
<td>Cancer Research UK, Manchester Institute, Manchester, UK</td>
<td>A PP1/PP2A protein phosphatase relay regulates progression through mitosis</td>
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<tr>
<td>21.01</td>
<td>Ana Mera</td>
<td>IGC</td>
<td>A tour of the Science Communication and Outreach activities at the IGC</td>
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<tr>
<td>22.01</td>
<td>Lívia Perfeito</td>
<td>IGC (Post-Doc Seminars)</td>
<td>Evolution and Genome Structure</td>
</tr>
<tr>
<td>22.01</td>
<td>Alexandre Leitão</td>
<td>IGC (PhD Seminars)</td>
<td>Where, when and (a little bit of) hematopoiesis occurs in Drosophila larva</td>
</tr>
<tr>
<td>24.01</td>
<td>Luís Fereira Costa</td>
<td>Institute of Biomedicine and Immunology, Lisbon</td>
<td>Anthracnysin-Induced DNA Damage Response Mediated Protection against Severe Sepsis</td>
</tr>
<tr>
<td>27.01</td>
<td>Katri Franke</td>
<td>Welsch Ries Group, Institute of Clinical Pathobiotechnology, Medical Faculty Technical University, Dresden, Germany</td>
<td>The oxygen sensor PHD2 has important in vivo functions in erythropoiesis and inflammation</td>
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<tr>
<td>27.01</td>
<td>Anna Akmanova</td>
<td>Utrecht University, The Netherlands</td>
<td>Microtubule Dynamics: a tale of two ends</td>
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<td>28.01</td>
<td>Constantin Tselis</td>
<td>IGC</td>
<td>Deficient T cell regulation in an autoimmune condition involves two components</td>
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<tr>
<td>30.01</td>
<td>Gonçalo Bernardes</td>
<td>Department of Chemistry, University of Cambridge, UK, Instituto de Medicina Molecular, IPML, Lisbon</td>
<td>Chemoselective Transformations for Bioimaging and Targeted Therapeutics</td>
</tr>
<tr>
<td>31.01</td>
<td>Sandra de Macedo Ribeiro</td>
<td>Instituto de Biologia Molecular e Celular, Porto</td>
<td>Sex or Leu: Structural impact of genetic code ambiguity in Candida albicans</td>
</tr>
</tbody>
</table>

### February 2014

<table>
<thead>
<tr>
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<th>Speaker</th>
<th>Affiliation</th>
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<td>04.02</td>
<td>Patricia Belkadi</td>
<td>IGC</td>
<td>The genetic and developmental bases of variation and diversity</td>
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<tr>
<td>05.02</td>
<td>Duarte Mesquita</td>
<td>CEDOC (Post-Doc Seminar)</td>
<td>c-Myc - a key factor for zebralos caulid fin regeneration?</td>
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<tr>
<td>05.02</td>
<td>Ewa Chrostek</td>
<td>IGC (PhD Seminar)</td>
<td>Mutational breakdown in Wolbachia - Drosophila system</td>
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<tr>
<td>05.02</td>
<td>Camilla Söger</td>
<td>Karolinska Institute, Stockholm, Sweden</td>
<td>The SMC complexes - connecting transcription and replication to chromosome segregation</td>
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<td>06.02</td>
<td>Seamus J. Martin</td>
<td>Molecular Cell Biology Laboratory, Dept of Genetics, The Smurfit Institute, Trinity College, Dublin, Ireland</td>
<td>Career paths in Science for Postdocs</td>
</tr>
<tr>
<td>07.02</td>
<td>Seamus J. Martin</td>
<td>Molecular Cell Biology Laboratory, Dept of Genetics, The Smurfit Institute, Trinity College, Dublin, Ireland</td>
<td>Surprising Outcomes from “Death Receptor” Engagement</td>
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<tr>
<td>10.02</td>
<td>Zvonimir Marelja</td>
<td>Department of Molecular Enzymology, Institute of Biochemistry and Biology, University of Potsdam, Germany</td>
<td>The L-cysteine desulphurase NFS1 is additionally localized in the cytosol of human cells where it provides the sulfur for molybdenum cofactor biosynthesis</td>
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<tr>
<td>10.02</td>
<td>Manuel Theri</td>
<td>LPC/IVRST/DSV/CCEA - Hospital Saint-Louis, Unite de Therapie Cellulaire Paris, France</td>
<td>Centrosome Positioning during Morphogenesis</td>
</tr>
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<td>11.02</td>
<td>Lívia Perfeito</td>
<td>IGC</td>
<td>Genetic determinants of evolution</td>
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<td>11.02</td>
<td>Eva Paluch</td>
<td>MRC-VERS Us College London, United Kingdom</td>
<td>Apical constriction mechanisms in axonal cell morphogenesis</td>
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<td>12.02</td>
<td>Raquel Santos</td>
<td>IGC (PhD Seminar)</td>
<td>Novel functions of the cohesion accessory factor dRSS uncover a new mitotic checkpoint</td>
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<td>14.02</td>
<td>Thomas Locat</td>
<td>Developmental Biology Institute of Marseille Luminy (IBDM), CNRS &amp; Av Mas重重 Universite, Luminy, France</td>
<td>Biomechanical regulation of tissue morphogenesis</td>
</tr>
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<td>18.02</td>
<td>Daniel Sabral</td>
<td>IGC</td>
<td>The Bioinformatics Unit @ IGC</td>
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<tr>
<td>19.02</td>
<td>Alexandre Raposo</td>
<td>IGC (Post-Doc Seminar)</td>
<td>A genome wide study of Ascl1 function in vertebrate neurogenesis uncovers a novel role in regulating chromatin accessibility</td>
</tr>
<tr>
<td>DATE</td>
<td>SPEAKER</td>
<td>AFFILIATION</td>
<td>TITLE</td>
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<tr>
<td>19.02</td>
<td>Rita Mateus</td>
<td>CEDOC (PhD Seminars)</td>
<td>Tissue growth regulation of zebrafish caudal fin regeneration through cell density dependent mechanotransduction of Yap</td>
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<td>19.02</td>
<td>Val Wilson</td>
<td>MRC Centre for Regenerative Medicine, The University of Edinburgh, UK</td>
<td>Specifying and maintaining neurohaematodermal axial progenitors for anterioposterior axis elongation</td>
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<td>20.02</td>
<td>Benedikt Berninger</td>
<td>Institute of Physiological Chemistry, University Medical Center, Johannes Gutenberg, University Mainz, Germany</td>
<td>Direct reprogramming of brain resident cells into induced neurons</td>
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<td>21.02</td>
<td>Anne Grantham Bottom</td>
<td>The Danish Stem Cell Center, University of Copenhagen, Denmark</td>
<td>Cells developing as communities during pancreas development</td>
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<td>25.02</td>
<td>Alekos Athanassiadis</td>
<td>IGC</td>
<td>To B or not to B? Dynamics of helical conformation in DNA and RNA: emerging functions in RNA editing, innate immunity and genomic instability</td>
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<tr>
<td>26.02</td>
<td>Catarina Bias-Pereira</td>
<td>IGC (Post-Doc Seminars)</td>
<td>The retinal determination gene dachshund restricts cell proliferation by limiting the activity of the Homothorax Yorkie complex</td>
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<td>26.02</td>
<td>Zeina Gouveia</td>
<td>IGC (PhD Seminars)</td>
<td>Targeting heme with single domain antibodies</td>
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<td>28.02</td>
<td>Jochen Cuck</td>
<td>Cellular Machines, Biotechnology Center, Technical University of Dresden, Germany</td>
<td>Do cells care about physics?</td>
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<td>03.03</td>
<td>Catarina Homem</td>
<td>Institute of Molecular Biotechnology, Austrian Academy of Science, Austria</td>
<td>Ecdysone and Mediator trigger a metabolic switch uncoupling cell cycle from cell growth to end proliferation in Drosophila neural stem cells</td>
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<td>03.03</td>
<td>Didier Gonze</td>
<td>Université Libre de Bruxelles, Bruxelles, France</td>
<td>Modeling circadian clocks: Molecular mechanism, robustness to noise, and intercellular synchronization</td>
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<td>04.03</td>
<td>Edita Schulte</td>
<td>Institut Curie, Paris, France</td>
<td>The role of X chromosome dosage and dosage compensation in pluripotency and differentiation</td>
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<td>05.03</td>
<td>Rita Valente</td>
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<td>Cell to cell Communication Systems Controlling Virulence in a Plant Pathogen</td>
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<td>05.03</td>
<td>Ricardo Leite</td>
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<td>Exploring an uncommon host parasite interaction</td>
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<td>06.03</td>
<td>Yannick Schwab</td>
<td>Electron Microscopy Core Facility - EMBL, Heidelberg, Germany</td>
<td>Correlative Light and Electron Microscopy: taking snapshots of the living at the ultrastructural level</td>
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<td>06.03</td>
<td>Attilla Cikás Nagy</td>
<td>Fondazione Edmund Mach and King's College London</td>
<td>Models and experiments to understand cell size control</td>
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<td>07.03</td>
<td>Nils Böhgen</td>
<td>Institute of Pathology, Charite and Institute for Theoretical Biology, Humboldt University Berlin, Germany</td>
<td>Modelling cancer signalling from perturbation data</td>
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<td>10.03</td>
<td>Patricia Bastos Amado</td>
<td>Laboratori di Immunobiologia i Diagnostic Molecola (URAD), Universitat Autonoma de Barcelona, Institut de Investigacio Germans Trias i Pujol, Barcelona, Spain</td>
<td>Induction of Tolerance in Transplantation: Evaluation of Eosomes and Tolerogenic Dendritic Cells</td>
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<td>Søren Tvorup Christensen</td>
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<td>Primary cilia and ciliary pockets: hot spots for cellular signaling</td>
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<td>Trafficking of Influenza A virus components</td>
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<td>Margarida Santos</td>
<td>Experimental Immunology Branch, National Cancer Institute, National Institutes of Health (NIH), USA</td>
<td>DNA damage induced differentiation of leukemic cells as an anti-cancer barrier</td>
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<td>14.03</td>
<td>Gáspár Jékely</td>
<td>Max Planck Institute for Developmental Biology, Neurobiology of Marine Zooplankton, Tübingen, Germany</td>
<td>Neuronal connectome of a sensory motor circuit for visual navigation</td>
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<td>NBR1 and RLP kinase signalling in inflammation</td>
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<td>Sylvain Gandon</td>
<td>Équipe Ecologie et Epidemiologie Evolutive, Centre d’Ecologie Fonctionnelle et Evolutive (CEFE), Montpellier, France</td>
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<td>22.04</td>
<td>Jörg Becker</td>
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<td>A NOT so simple change of fate: NOT1 as a key regulator of gametophyte maturation</td>
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<td>José Pereira-Leal</td>
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<td>Size matters (in the cell)</td>
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<td>30.04</td>
<td>Félia Bono</td>
<td>Max Planck Institute for Developmental Biology, Tübingen, Germany</td>
<td>Mechanistic studies of gene expression, transport and localization?</td>
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<td>02.05</td>
<td>Paulo J. Fonseca</td>
<td>Dpto. Biologia Animal, Centro de Biologia Ambiental, Fac. Ciências, Univ Lisboa, Portugal</td>
<td>Neuroethology of acoustic communication in cicadas: from hearing to finding the right mate</td>
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<td>06.05</td>
<td>Miguel Godinho Ferreira</td>
<td>IGC</td>
<td>The role of telomeres in cancer and ageing</td>
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<td>06.05</td>
<td>Nicola Brownlow</td>
<td>Protein Phosphorylation Laboratory, Cancer Research UK London Research Institute and King's College London, London, UK</td>
<td>Catenation in metaphase engages distinctive SAC silencing requiring PKC theta revealing a unique therapeutic window</td>
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<td>07.05</td>
<td>Batthyány Yilmaz</td>
<td>IGC (PhD Seminars)</td>
<td>Natural Occurring Antibodies Combat Protection Against Plasmodium Infection</td>
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<td>07.05</td>
<td>Oscar Ruiz</td>
<td>IGC (Post-Doc Seminars)</td>
<td>Dissecting the genetic basis for Wolbachia induced resistance to viral infections in Drosophila melanogaster</td>
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<td>09.05</td>
<td>João Mosca Cabral</td>
<td>Instituto de Biologia Molecular e Celular, Porto</td>
<td>A molecular study of a component of the bacterial machinery involved in hyperosmotic adaptation</td>
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<td>Joana Gonçalves-Sá</td>
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<td>Can (big) data help us solve real world problems?</td>
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<td>Francisco Vasconcelos</td>
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<td>Transcriptional control of the onset of neurogenesis: the interaction of MyT1 with Proneural and Notch transcriptional networks</td>
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<td>Mariana Lince Pafa</td>
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<td>Microtubule regulators control centrosome size</td>
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<td>Gustavo Ramos</td>
<td>Translational Myocardial Infarction Research Lab, Universitätsklinikum, Würzburg, Germany</td>
<td>Immunological phenomena in cardiac physiology</td>
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<td>16.05</td>
<td>Tom Mignot</td>
<td>CNRS, Marseille, France</td>
<td>Evolution and core structure of a modular signaling pathway governing multicellularity in a bacterium</td>
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<td>16.05</td>
<td>Matthias Haury</td>
<td>Max Planck Florida Institute for Neuroscience, Florida, United States</td>
<td>Alternative Careers for Young Scientists</td>
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<td>20.05</td>
<td>Mónica Bettencourt-Dias</td>
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<td>Control of Centrosome Biogenesis in Development, Cancer and Evolution</td>
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<td>22.05</td>
<td>Kalet Leon</td>
<td>Molecular Immunology Center, Havana, Cuba</td>
<td>Mutant cytokines for cancer immunotherapy at CMI: An informal update</td>
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<td>Carl-Philipp Heisenberg</td>
<td>Technology Austria, Klosterneuburg, Austria</td>
<td>Cell and tissue mechanics in zebrafish gastrulation</td>
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<td>Daniel Muñoz</td>
<td>Rockefeller University, NY, USA</td>
<td>T-cell plasticity in the gut</td>
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<td>Ivo Chelo</td>
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<td>The eco-evolutionary genetics lab</td>
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<td>Darren Cilmour</td>
<td>EMBL, Heidelberg, Germany</td>
<td>The collective cell biology of organ formation</td>
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<td>30.05</td>
<td>Francesca Peri</td>
<td>EMBL, Heidelberg, Germany</td>
<td>Neuronal cell death goes live: how do microglia find and engulf dying neurons</td>
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<td>04.06</td>
<td>Mariola R. Chacón</td>
<td>Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany</td>
<td>Meiotic Nuclear oscillations are necessary to avoid excessive chromosome associations</td>
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<td>05.06</td>
<td>Silvia Gruhn</td>
<td>Zoological Institute, University of Cologne, Cologne, Germany</td>
<td>Mathematical modeling of the neural control of insect locomotion</td>
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<td>Alfonso Valencia</td>
<td>Spanish National Cancer Research Centre, Madrid, Spain</td>
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<td>Lori Bargar</td>
<td>Univ. of Cologne, Germany</td>
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<td>Answers to the last questions</td>
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<td>Pavel Tomancak</td>
<td>Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany</td>
<td>Patterns of gene expression in development and evolution</td>
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<td>Rita Sinka</td>
<td>University of Szeged, Faculty of Science and Informatics, Department of Genetics, Szeged, Hungary</td>
<td>The role of lipid metabolism during the Drosophila spermatogenesis</td>
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<td>27.06</td>
<td>Mauricio Cente</td>
<td>B Cell Biology Unit, Fundacion IMI PRBB, Barcelona, Spain</td>
<td>Innate signaling networks in splenic and mucosal immunity</td>
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<td>11.07</td>
<td>Nikitas Tavernaridis</td>
<td>Institute of Molecular Biology and Biotechnology, Foundation for Research and Technology-Hellas, Heraklion, Crete, Greece</td>
<td>Intrinsic mechanisms protecting against neurodegeneration: the heat stroke paradigm</td>
</tr>
<tr>
<td>11.07</td>
<td>Prof. Jorge Guimaraes</td>
<td>CAPES, Brazil</td>
<td>Funding opportunities for young scientists in Brazil</td>
</tr>
<tr>
<td>11.07</td>
<td>Alfredo Mayor</td>
<td>Barcelona Centre for International Health Research (ICB-CSIC), Hospital Clinic-Universitat de Barcelona, Spain</td>
<td>Targeting pregnant women to assess malaria transmission</td>
</tr>
<tr>
<td>15.07</td>
<td>Jorge Cameiro</td>
<td>IGC</td>
<td>Better than your eye: successful application of rnasynthetic models of cells in quantitative imaging</td>
</tr>
<tr>
<td>16.07</td>
<td>Marc Kirschner</td>
<td>Harvard Medical School, USA</td>
<td>On being the right cell size</td>
</tr>
<tr>
<td>18.07</td>
<td>Marc Kirschner</td>
<td>Department of Systems Biology, Harvard Medical School, USA</td>
<td>The nature of biological specificity: decoding ubiquitination, proteasome mediated degradation and maybe other things</td>
</tr>
<tr>
<td>22.07</td>
<td>Carlos Penha Goncalves</td>
<td>IGC</td>
<td>Malacia, placenta insufficiency and poor pregnancy outcomes</td>
</tr>
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</table>
### JULY 2014 (cont.)

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<th>DATE</th>
<th>SPEAKER</th>
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<tbody>
<tr>
<td>23.07</td>
<td>Filipe Castro Soeiro</td>
<td>Universidade Europeia, Nova School of Business and Economics, Univ Nova de Libra and the Faculty of Creative Industries, Univ. of St. Joseph, Macau</td>
<td>Executive Master’s in Entrepreneurship and Innovation</td>
</tr>
<tr>
<td>24.07</td>
<td>Andrew Isman</td>
<td>Centre for Integrative Physiology, School of Biomedical Sciences, University of Edinburgh, Edinburgh, UK</td>
<td>Drosophila as a model for understanding mechanosensory cilium formation and human ciliopathy</td>
</tr>
<tr>
<td>25.07</td>
<td>Judith Campisi</td>
<td>Buck Institute for Research on Aging and Lawrence Berkeley National Laboratory, CA, USA</td>
<td>Cancer and aging: Rival demons?</td>
</tr>
<tr>
<td>29.07</td>
<td>Jordi Garcia Oslavo</td>
<td>Universitat Pompeu Fabra, Spain</td>
<td>Pulsatile dynamics in gene regulation circuits</td>
</tr>
<tr>
<td>29.07</td>
<td>Jocelyne Demengeot</td>
<td>IGC</td>
<td>Two shorts on biological togetherness</td>
</tr>
<tr>
<td>30.07</td>
<td>Miguel Coelho</td>
<td>Harvard University, USA</td>
<td>Experimental evolution of genetic instability during a yeast model of cancer</td>
</tr>
<tr>
<td>31.07</td>
<td>Brian Trench</td>
<td>Dublin City University, Ireland</td>
<td>Ten Reasons to do Public Communication of Science and the Main reason is You</td>
</tr>
</tbody>
</table>

### AUGUST 2014

<table>
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<th>DATE</th>
<th>SPEAKER</th>
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</thead>
<tbody>
<tr>
<td>27.08</td>
<td>Nuno Martins</td>
<td>Wellcome Trust Centre for Cell Biology, Edinburgh, Scotland, UK</td>
<td>HACing centromeres: manipulating transcription silencing at the centromere using an Human Artificial Chromosome</td>
</tr>
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### SEPTEMBER 2014

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<tr>
<th>DATE</th>
<th>SPEAKER</th>
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</thead>
<tbody>
<tr>
<td>01.09</td>
<td>Miguel A. S. Cavadas</td>
<td>Systems Biology Ireland &amp; Conway Institute of Biomedical and Molecular Biology, School of Medicine and Medical Sciences, University College of Dublin, Ireland</td>
<td>Cross talk between REST and HIF 1 reveals the basic mechanisms for gene repression in hypoxia</td>
</tr>
<tr>
<td>02.09</td>
<td>Colin Adrain</td>
<td>IGC</td>
<td>Control of signaling by membrane trafficking</td>
</tr>
<tr>
<td>04.09</td>
<td>Arun Prakash</td>
<td>Department of Anesthesia and Surgery, University of California, San Francisco, USA</td>
<td>Role of Intra Innate Cells, Receptors and the Microbiome in Sterile Lung Inflammation after Trauma</td>
</tr>
<tr>
<td>05.09</td>
<td>Upol Baranesie</td>
<td>Molecular, Cell and Developmental Biology, University of California, Los Angeles, USA</td>
<td>Metabolic Control of growth and overweight in Drosophila models</td>
</tr>
<tr>
<td>09.09</td>
<td>Catalina Romero</td>
<td>Harvard Medical School, USA</td>
<td>Spatial and temporal organization of redox potential in live C. elegans</td>
</tr>
<tr>
<td>12.09</td>
<td>Eicke Latz</td>
<td>Institute of Intra Innate Immunity, University of Bonn, Germany, USA and University of Massachusetts Medical School, Division of Infectious Diseases &amp; Immunology, USA</td>
<td>The role of inflammasome activation in chronic inflammatory diseases</td>
</tr>
<tr>
<td>15.09</td>
<td>Wista Siewie</td>
<td>International Institute of Molecular and Cell Biology, Warsaw, Poland</td>
<td>The mechanism of action of N6 methyladenine dependent restriction endonuclease R.A-n</td>
</tr>
<tr>
<td>16.09</td>
<td>Rui Oliveira</td>
<td>IGC</td>
<td>Behavioural flexibility as phenotypic plasticity using fish to ask why and how questions</td>
</tr>
<tr>
<td>18.09</td>
<td>Sreyoshi Mika</td>
<td>IITCAS, Bangalore, India</td>
<td>Role of DNA replication and repair in epigenetic maintenance of Candida albicans centromeres</td>
</tr>
<tr>
<td>19.09</td>
<td>Thomas S. Murray</td>
<td>London Research Institute, UK</td>
<td>The molecular mechanisms of microtubule nucleation and dynamics</td>
</tr>
<tr>
<td>23.09</td>
<td>Florence Janody</td>
<td>IGC</td>
<td>When the actin cytoskeleton goes away: Role in cancer initiation and progression</td>
</tr>
<tr>
<td>23.09</td>
<td>Giovanni Maroni</td>
<td>University of Milan, Italy</td>
<td>Functional cooperation of Nks and Sox, regulates fiber specification during post natal muscle development</td>
</tr>
<tr>
<td>24.09</td>
<td>Erida Gini</td>
<td>IGC (Post-doc Seminar)</td>
<td>Dynamics at the edge of neutrality: insights on multi type pathogens</td>
</tr>
</tbody>
</table>
### SEMINARS & MEETINGS

#### SEPTMBER 2014 (cont.)

<table>
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<tr>
<th>DATE</th>
<th>SPEAKER</th>
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</thead>
<tbody>
<tr>
<td>24.09</td>
<td>Rita Fior</td>
<td>ICC (Post-Doc Seminars)</td>
<td>Establishing a xenograft assay in zebrafish for personalized cancer therapy</td>
</tr>
<tr>
<td>26.09</td>
<td>Luca Scorrano</td>
<td>Venetian Institute of Molecular Medicine, Dept. of Biology, University of Padua, Italy</td>
<td>Keeping mitochondria in shape, a matter of life and death</td>
</tr>
<tr>
<td>30.09</td>
<td>Jose Feio</td>
<td>ICC</td>
<td>Not supplied by the speaker</td>
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#### OCTOBER 2014

<table>
<thead>
<tr>
<th>DATE</th>
<th>SPEAKER</th>
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</thead>
<tbody>
<tr>
<td>01.10</td>
<td>Maria Serrano Correia</td>
<td>CEDOC (PhD Seminars)</td>
<td>Melanosome transfer between melanocytes and keratinocytes</td>
</tr>
<tr>
<td>01.10</td>
<td>Claudia Mendes</td>
<td>ICC (PhD Seminars)</td>
<td>Not supplied by the speaker</td>
</tr>
<tr>
<td>03.10</td>
<td>Nicolas Buchon</td>
<td>Department of Entomology, Cornell University, Ithaca, New York, USA</td>
<td>Gut check in Drosophila tissue homeostasis in a microbial world</td>
</tr>
<tr>
<td>07.10</td>
<td>Isabel Gordo</td>
<td>ICC</td>
<td>Adaptive immunity increases the speed and predictability of evolution of commensal E. coli in the mouse gut</td>
</tr>
<tr>
<td>08.10</td>
<td>Marc Gouw</td>
<td>ICC (PhD Seminars)</td>
<td>Variation and ancestral state reconstructions of MTOCs and cilia across the eukaryotic kingdom</td>
</tr>
<tr>
<td>08.10</td>
<td>Patrícia Gonçalves</td>
<td>ICC (PhD Seminars)</td>
<td>Pollen Tube Growth and Guidance - A Critical Anion Gap</td>
</tr>
<tr>
<td>09.10</td>
<td>Wolfgang L. Miller</td>
<td>Laboratories of Genome Dynamics, Center of Anatomy and Cell Biology, Medical University of Vienna, Vienna, Austria</td>
<td>Symbiont triggered speciation: concepts, causes and consequences</td>
</tr>
<tr>
<td>10.10</td>
<td>Nancy A. Moran</td>
<td>Department of Integrative Biology, University of Texas at Austin, USA</td>
<td>Tiny genomes in insect symbionts</td>
</tr>
<tr>
<td>13.10</td>
<td>Julia Gog</td>
<td>Department of Mathematics and Theoretical Physics, University of Cambridge, UK</td>
<td>Capturing the spread and evolution of influenza A</td>
</tr>
<tr>
<td>14.10</td>
<td>Diogo Castro</td>
<td>ICC</td>
<td>Gene Regulatory Networks in Neurogenesis</td>
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#### OCTOBER 2014 (cont.)

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<tr>
<th>DATE</th>
<th>SPEAKER</th>
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<tbody>
<tr>
<td>15.10</td>
<td>Marc Lipsitch</td>
<td>Center for Communicable Disease Dynamics, Harvard School of Public Health, USA</td>
<td>Ethical alternatives to experiments to create potential pandemic pathogens</td>
</tr>
<tr>
<td>17.10</td>
<td>Paul Lehner</td>
<td>Cambridge Institute for Medical Research, UK</td>
<td>Novel genetic and proteomic approaches to viral evasion</td>
</tr>
<tr>
<td>21.10</td>
<td>Lounès Chikhi</td>
<td>ICC</td>
<td>Social structure matters: on some genetic consequences of social and population structure</td>
</tr>
<tr>
<td>22.10</td>
<td>Ana Portelinha</td>
<td>CEDOC (PhD Seminars)</td>
<td>A novel internalization pathway followed by the Sonic Hedgehog signaling receptor Patched</td>
</tr>
<tr>
<td>22.10</td>
<td>Catarina Camo</td>
<td>ICC (Post-Doc Seminars)</td>
<td>Identification of Wolbachia effector proteins</td>
</tr>
<tr>
<td>24.10</td>
<td>Jonathan Jones</td>
<td>John Innes Center, Sainsbury Lab, Norwich, UK</td>
<td>It takes two to tango</td>
</tr>
<tr>
<td>24.10</td>
<td>Caroline Dean</td>
<td>John Innes Centre, Cell and Developmental Biology Department, Norwich, UK</td>
<td>Chromatin and antisense transcript dynamics in seasonal timing</td>
</tr>
<tr>
<td>30.10</td>
<td>Lieve Ongena</td>
<td>VIB, Ghent, Belgium (EU-LIFE Partner)</td>
<td>Horizon 2020 for beginners</td>
</tr>
<tr>
<td>31.10</td>
<td>Arjan de Visser</td>
<td>Laboratory of Genetics, Wageningen University, Wageningen, The Netherlands</td>
<td>Exploring the evolvability of an antibiotic resistance enzyme</td>
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### NOVEMBER 2014

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<th>DATE</th>
<th>SPEAKER</th>
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<tbody>
<tr>
<td>04.11</td>
<td>Ivo Telley</td>
<td>IGC</td>
<td>Simple questions on nuclear positioning</td>
</tr>
<tr>
<td>05.11</td>
<td>Jorge André B. Sousa</td>
<td>IGC (PhD Seminars)</td>
<td>The Long and Winding (and Crowded) Road: Clonal Interference and interactions in evolution</td>
</tr>
<tr>
<td>05.11</td>
<td>Tasashi Kayano</td>
<td>IGC (Post-Doc Seminars)</td>
<td>Coordinating the nutritional regulating of systemic growth</td>
</tr>
<tr>
<td>07.11</td>
<td>Laila Ramakrishnan</td>
<td>Department of Internal Medicine University of Cambridge, Wellcome Trust, UK</td>
<td>Insights into tuberculosis pathogenesis and treatment from the zebrafish</td>
</tr>
<tr>
<td>10.11</td>
<td>Goenter Weiss</td>
<td></td>
<td>Linkage of iron homoeostasis to immune control of infections</td>
</tr>
<tr>
<td></td>
<td>Elena Baena Gonzalez</td>
<td>IGC</td>
<td>Regulation of plant growth and development by nutrient signals understanding the regulators</td>
</tr>
<tr>
<td>12.11</td>
<td>Krysztof Kus</td>
<td>IGC (PhD Seminars)</td>
<td>Binding a saga: Zfp106a domains</td>
</tr>
<tr>
<td>12.11</td>
<td>Marica Rosa Rosa</td>
<td>CEDOC (Post-Doc Seminars)</td>
<td>Study of the crosstalk between Poyasyl 2 and CFTR - step towards the understanding of the Autosomal Dominant Polycystic Kidney Disease</td>
</tr>
<tr>
<td>13.11</td>
<td>Juan Laliffe</td>
<td>NYU Langone Medical Center, USA</td>
<td>Regulatory T-cells in obesity related disease</td>
</tr>
<tr>
<td>14.11</td>
<td>Shahnaaz Tabakhah</td>
<td>Stem Cells &amp; Development, CMR UR 2578 Dept of Developmental &amp; Stem Cell Biology, Institut Pasteur Paris, France</td>
<td>Skeletal muscle stem cell properties in development and regeneration</td>
</tr>
<tr>
<td>18.11</td>
<td>Christen Mirth</td>
<td>IGC</td>
<td>The ecology and the evolution of nutrient dependent choice in Drosophila</td>
</tr>
<tr>
<td>18.11</td>
<td>David W. Scott</td>
<td>University of Maryland School of Medicine, Baltimore, USA</td>
<td>From Fusion IgG Tolerogens to Engineered Human T Regulatory Cells: A Life of Tolerance</td>
</tr>
<tr>
<td>19.11</td>
<td>Joana Cardoso Vaz</td>
<td>IGC (Post-Doc Seminars)</td>
<td>New insights on how to “kill a tricky cancer”: synthesis of centrosome biology and bioinformatics</td>
</tr>
<tr>
<td>21.11</td>
<td>Joda Barata</td>
<td>Instituto de Medicina Molecular, Lisbon</td>
<td>Mifly exposed Interleukin 7 signaling in T-cell leukemia</td>
</tr>
<tr>
<td>25.11</td>
<td>Gabriela Cores</td>
<td>IGC</td>
<td>The mathematics of study design and global health policy</td>
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### NOVEMBER 2014 (cont.)

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<tbody>
<tr>
<td>26.11</td>
<td>Pedro Romaininho</td>
<td>IGC (PhD Seminars)</td>
<td>Characterizing the Zeb2 L function in glioblastoma cancer stem cells</td>
</tr>
<tr>
<td>26.11</td>
<td>Paulo Navario Costa</td>
<td>IGC (Post-Doc Seminars)</td>
<td>Histone methylation in the female germline regulates the reactivation of acetylase transcription and dictates the onset of embryogenesis</td>
</tr>
<tr>
<td>27.11</td>
<td>Lotte Sagaard Andersen</td>
<td>Max Planck Institute for Terrestrial Microbiology, Marburg, Germany</td>
<td>Regulation of cell division in bacteria</td>
</tr>
<tr>
<td>28.11</td>
<td>Thomas Boehm</td>
<td>Max Planck Institute of Immunobiology and Epigenetics, Freiburg, Germany</td>
<td>Life and times of the Thymus</td>
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### DECEMBER 2014

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<tbody>
<tr>
<td>02.12</td>
<td>Paula Duque</td>
<td>IGC</td>
<td>The Arabidopsis SR45 splicing factor, a negative regulator of sugar signaling, modulates stability of the energy sensing SnRK1 protein kinase</td>
</tr>
<tr>
<td>05.12</td>
<td>Simon Frost</td>
<td>Dept. of Veterinary Medicine, University of Cambridge, UK</td>
<td>Integrating pathogen evolution into epidemiological models of RNA viruses</td>
</tr>
<tr>
<td>09.12</td>
<td>Vasco Baneto</td>
<td>IGC</td>
<td>AD as a guardian of the genome</td>
</tr>
<tr>
<td>10.12</td>
<td>Macies Zylcz</td>
<td>Institute of Moleculer Cell Biology, Warsaw, Poland</td>
<td>HSP70-dependent formation of a structural mutant p53-TAP73A-MDM2 complex</td>
</tr>
<tr>
<td>12.12</td>
<td>Hans Larson</td>
<td>McGill University, Montreal, Canada</td>
<td>Developmental influences at the fish-tetrapod and dinosaur-bird macroevolutionary transitions</td>
</tr>
<tr>
<td>16.12</td>
<td>Elia Sucea</td>
<td>IGC</td>
<td>New insights into the evolution and development of immunity in arthropods</td>
</tr>
<tr>
<td>17.12</td>
<td>Carlos Ramirez</td>
<td>IGC (PhD Seminars)</td>
<td>Generation of a Phycomitrella patens transcriptome atlas and identification of Cc genes as crucial mediators of reproduction in early land plants</td>
</tr>
<tr>
<td>17.12</td>
<td>Dasuki To</td>
<td>IGC (Post-Doc Seminars)</td>
<td>Fusion yeast as a paradigm to study centrosome evolution and biogenesis</td>
</tr>
<tr>
<td>18.12</td>
<td>Joana Bernardes</td>
<td>Craig Lab, Max Planck Institute for Evolutionary Biology, Germany</td>
<td>Heterosis in yeast increases with parental divergence and environmental stress</td>
</tr>
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</table>
● Traffic Club
Organiser: Maria João Amorim (IGC)
Traffic Club comprises monthly meetings with IGC groups and groups from other institutes.

● Assessment of training methods in NGS data analysis
March 17 - 18
Organiser: Pedro L. Fernandes (IGC)
The workshop aims at discussing training methods in NGS data analysis, their measurable effectiveness and their adaptation to a diversity of research interests.

● Institutional funding opportunities: H2020 Widening and Spreading Excellence Programme and AXA Chairs
April 28
Organiser: Research Funding Affairs Unit (Speaker: Sheila Vidal)
The aim of this session is to present to a smaller number of IGC members two institutional funding opportunities that the IGC may profit in the near future. The presentation focused on the H2020 Spreading Excellence and Widening Participation Action and the AXA Research Funds Chairs programme. A total of 6 IGC members attended this session, including the director and deputy-director for science.

● Imaris Open Day
May 1-4
Organisers: Gabriel Martins, Nuno Martins, Ana S. Gonçalves
Sponsor: Bitplane-Andor
Theoretical and practical workshop on image analysis with Imaris and ImageJ/FIJI.

● AMeeGus
May 24-28
Organiser: IGC PhD students Committee
The IGC PhD students retreat took place in Mina de São Domingos, Mértola. Organised by and for the PhD students of the IGC, this meeting aims to promote the scientific discussion about the research projects being developed by the students, in an inspiring atmosphere.

● Distance and e-Learning Technologies Workshop
July 3-4
Organisers: Pedro L. Fernandes (IGC), Amâlindo Costeira (UP Training Center, Portugal), Mario Macedo (Universidade Atlântica, Portugal), David P Judge, (Cambridge University, UK), Ovídio Costa (Faculdade de Medicina da Universidade do Porto, Portugal).
The 2014 edition focuses on the following main themes: usage of learning objectives and outcomes, engaging techniques in training, distance learning in medical education, mind mapping and critical thinking, and ontology-based concept extraction.

● EMBO course on 3D developmental imaging
July 4-12
Organisers: Gabriel Martins, Nuno Moreira, José Fito
Sponsors: EMBO and multiple vendors
The 2014 EMBO Practical Course on 3D Developmental Imaging is aimed at young developmental biologists, interested in answering specific questions that require 3D imaging of tissue architecture, cell movement and tissue morphogenesis in whole embryos and which cannot rely on conventional imaging techniques.

● Funding Opportunities for Postdoctoral Fellowships
July 9
Organiser: Research Funding Affairs Unit (Speaker: Sheila Vidal)
The aim of this seminar is to guide potential postdoctoral applicants to the insights of the most well known international funding opportunities sponsoring high quality postdoctoral research. On the other hand, it also intends to provide some tips to search for additional funding opportunities and to get a better understanding of the present international research funding environment.

● bioPSmed-2014
July 14 – 15
Organiser: Pedro L. Fernandes (IGC).
This unconventional workshop focuses on the emergence of new ideas about medical provision that are springing-up from bringing together biological information, bioinformatics, systems biology, clinical practice, patient intervention, and modelling.

● Marie-Curie Fellowships Informative Session
July 18
Organiser: Research Funding Affairs Unit (Speaker: Teresa Costa)
This informative session aims at guiding the IGC candidates to the insights of the application procedure of the 2014 Marie S. Curie Individual Fellowships. We went through the application form, answered specific questions and concerns regarding this call and provide some tips to improve chances to write a successful application. A total of 6 Marie Curie applicants attended this session.

● Bioinformatics activities for High Schools: what can we offer you?
July
Organiser: Isabel Marques
Informal Discussion with High School Teachers regarding the potential future of the project Bioinformatics @ Schools.

● How to apply to the 2014 FCT Call for Individual Fellowships
September 1
Organiser: Research Funding Affairs Unit (Speaker: Teresa Costa)
Annually FCT opens calls to fund PhD or Post-doc fellowships. This session aims to inform and guide potential applicants on how to apply to the 2014 FCT Call
for Doctoral (BD) and Post-Doctoral fellowship (BPD) hopefully providing advice for future success. We intent to clarify questions and help to solve specific regarding procedures, online-forms, rules and give some tips and numbers to help potential candidates to be more successful. A total of 28 potential applicants attended this session.

- **Funding Opportunities for LIA?**
  September 17
  Organiser: Lounès Chikhi (Speaker: Sheila Vidal)
  The aim of this short presentation is to present potential funding opportunities that may be used by the IGC and the laboratory Evolution & Diversité Biologique from Toulouse under the LIA (Laboratoire International Associé) collaborative framework that intent to favour research collaborations and student/post-doc/PI visits between the two institutions.

- **EMBO Meeting on Centrosomes and Spindle Pole Bodies**
  September 30 – October 3
  Organiser: Mónica Bettencourt-Dias
  Sponsors: EMBO, EMBO YIP, eLife
  This meeting occurs every 3 years. The centrosome and centrosome-related organelles are major microtubule organizing centers and play diverse roles in polarity, signaling, cell division and cell movement. In addition, the core structures that make the centrosomes, the centrioles, are essential for cilia and flagella formation. In this EMBO Conference we discussed the structure and function of centrosomes as well as their role in diseases such as cancer and ciliopathies. This meeting was held at the Calouste Gulbenkian Foundation.

- **IGC/CEDOC/IMM Post-doc Retreat**
  October 29 – 31
  Organisers: Paulo Navarro-Costa, Catarina Henriques, Inês Castro and Nicole Walczyk (from IGC) and Maria Caglardi, Raquel Lourenco and Florent Ubelmann (from CEDOC).
  The Post-doc retreat took place in Praia Grande, Sintra. This retreat aims to promote interactions among post-docs of this institution and to be a forum for the discussion of their issues. This year there were Art&Science activities, science communication workshops and talks about science and scientific careers.

- **PathProt-7**
  October 16 - 18
  Organisers: Pedro L. Fernandes (IGC), Alexander Kel (genExplain GmbH, Germany), Roman Zubarev (Karolinska Institutet, Sweden), Carlos Cordeiro (Universidade de Lisboa, Portugal).
  PathProt is the international forum for Pathway Analysis in Proteomics. We are an informal discussion group that meets annually to brainstorm, since 2008. Our annual workshop is an ideal setting for open-minded, unbiased opinion-making.

- **Focus on Autoimmune Diseases**
  November 29
  Organisers: Francisca Fontes (IGC and Hospital Curry Cabral), Nuno Riso and Antonio Panarra (Hospital Curry Cabral)
  The aim of this symposium was to allow students, clinicians and scientists, to learn about the most recent advances in autoimmunity. This meeting celebrated the 21st Anniversary of the ‘Unidade de Doenças Autoimunes’ from Hospital Curry Cabral and its recent partnership with the IGC.
Adaptive developmental plasticity; combining ecology, evolution, and developmental biology
3rd TULIP Summer School: Biotic interactions: from genes to ecosystems
Pyrénées, France | July 2014

Evolution and Development of Pigmentation Patterns
Institut Jacques-Monod
Paris, France | October 2014

Eco-evo-devo and the mechanisms underlying variation and diversification in pigmentation
Université Pierre et Marie Curie
Paris, France | October 2014

Bettencourt-Dias, Mónica
Centrosome Biogenesis
College of Life Sciences, University of Dundee
Dundee, UK | January 2014

Centrosomes in Cancer
National Institutes of Health, NIH
Washington, USA | February 2014

Centrosomes in Evolution
Department of Organismic Evolution, Harvard University
Boston, USA | February 2014

Centrosomes in Cancer
Cambridge Cancer Institute
Cambridge, UK | April 2014

Centrosomes in Cancer
Barts Institute
London, UK | April 2014

Centrosome and Cilia Biogenesis and Evolution
EMBL European Bioinformatics Institute, EBI
Cambridgeshire, UK | April 2014

Centrosomes and Disease
Workshop in Bayreuth
Bayreuth, Germany | June 2014

Centrosome and Cilia Biogenesis and Evolution
EMBL
Heidelberg, Germany | July 2014

Centrosomes in Cancer
FEBS-EMBO Meeting
Paris, France | September 2014

Reshaping Microtubule Organising Centers
EMBO Centrosome Meeting
Porto, Portugal | September 2014
Architectural diversity of cilia
Cilia Meeting
Paris, France | November 2014

● Boavida, Leonor
Intercellular interactions within the male germ unit: functional relevance in double fertilization
23rd International Congress on Sexual Plant Reproduction
Porto, Portugal | July 2014

● Carneiro, Jorge
Decision making in unicellular and multicellular systems
Nonlinearity and Stochasticity in Emergent Phenomena II, Centro Internacional de Ciencias
Cuernavaca, Mexico | November 2014

● Carvalho, Thiago
Heads up: skulls, brains and the evidence before our eyes
University of the Arts
London, UK | February 2014

● Castro, Diogo
Transcriptional control of vertebrate neurogenesis by the Proneural factor Ascl1/Mash1
Brain and Spine Institute (ICM)
Paris, France | September 2014

Synergistic and antagonistic interactions between Ascl1 and Notch transcriptional programs during vertebrate neurogenesis
Notch Meeting VII: Notch Signaling in the Nervous System
Athens, Greece | September 2014

Transcriptional control of vertebrate neurogenesis by the Proneural factor Ascl1/Mash1
University of Mainz
Mainz, Germany | November 2014

● Chaouiya, Claudine
A Discrete Model of Drosophila Eggshell Patterning
3rd CoLoMoTo meeting (Consortium for Logical Models and Tools)
Lausanne, Switzerland | April 2014

Computational Tools to Define and Analyse Logical Models of Cellular Networks (Tutorial with T. Helikar and J. Saez-Rodriguez)
13th Eur. Conf. on Computational Biology
Strasbourg, France | July 2014

Logical modelling of pattern formation
Workshop Regulatory Logic of Developmental Systems, X Meeting Spanish Society for Developmental Biology SEBD
Madrid, Spain | October 2014

● Chela, Ivo
Phenotypic plasticity in experimentally adapted C. elegans populations
Revisiting the role of phenotypic plasticity in evolution using Caenorhabditis nematodes as model organisms
Les Tisselles, France | August 2014

● Chikhi, Lounès
Some things I read about the Neolithic transition in Europe
EMBO meeting Human Evolution in the Genomic Era
Leicester, UK | April 2014

Spatial structure and genetic data for demographic inference
International Primatological Society Meeting
Hanoi, Vietnam | August 2014

From conservation genetics to conservation genomics: a primate perspective (with Jordi Salmona)
International Primatological Society Meeting
Hanoi, Vietnam | August 2014

Conservation genomics of primates: where are we, where can we go? (with Jordi Salmona and G. Perry)
International Primatological Society Meeting
Hanoi, Vietnam | August 2014

Genome biology and endangered species management: getting out of neutral (with Benoit Goossens)
International Primatological Society Meeting
Hanoi, Vietnam | August 2014

● Chrostek, Ewa
Mutualism breakdown by amplification of Wolbachia genes
8th International Wolbachia meeting
Innsbruck, Austria | June 2014

● Costa, Sílvia
Alterations to the recycling endosome during influenza A virus infection
American Society of Virology Conference
Colorado, USA | June 2014

● Demengeot, Jocelyne
A unique organ for natural and induced Foxp3 regulatory T cells: a fourth function for the thymus
Symposium: Immunological phenomena in cardiac diseases, Clinical University Wurzburg, Germany | October 2014
● Domingos, Ana
Lean on circuits or Lean for sugar
Dutch Annual Neuroscience meeting (ENP 2014)
Lunteren, The Netherlands | May 2014

Lean on Leptin or Lean for sugar
University of Utrecht Seminae series
Utrecht, The Netherlands | May 2014

Lean on circuits or Lean for sugar
EMBO Workshop on Decoding neural circuit structure and function
Istanbul, Turkey | September 2014

Obesity and the Consilience between neurons and immunity
University of Texas Southwestern Medical School Seminar Series
Dallas, USA | November 2014

● Duque, Paula
Alternative splicing controls translation of a novel Arabidopsis transporter to promote plant zinc tolerance
Post-transcriptional Gene Expression Regulation in Plants Symposium
Poznan, Poland | June 2014

On the physiological significance of alternative splicing in plants: translational regulation of a membrane transporter to control zinc tolerance
CRC Seminar Series, Martin Luther University of Halle-Wittenberg
Halle, Germany | July 2014

● Ferreira Moita, Luís
Anthracyclines induce DNA damage response-mediated protection against severe sepsis
VIB
Ghent, Belgium | May 2014

Anthracyclines induce DNA damage response-mediated protection against severe sepsis
Leibniz Institute for Molecular Pharmacology
Berlin, Germany | September 2014

Anthracyclines induce DNA damage response-mediated protection against severe sepsis
European Workshop on Immune - Mediated Inflammatory Diseases
Funchal, Portugal | November 2014

● Fesel, Constantin
T-regulatory cells in SLE
German Lupus Day
Freiburg, Germany | May 2014

● Garcês, Sandra
The Clinical Impact of Drug Immunogenicity
European Immunogenicity Platform Meeting
Lisbon, Portugal | March 2014

The Impact of Immunogenicity on Drug Safety Profile
9th International Congress on Autoimmunity
Nice, France | March 2014

The Immunogenicity of anti-TNF alpha Therapy in Immune-Mediated Inflammatory Diseases
9th International Congress on Autoimmunity
Nice, France | March 2014

Monitoring Immunogenicity in Clinical Practice and Outcomes
Annual European Congress of Rheumatology (EULAR)
Paris, France | June 2014

Biologic Therapy: How to decide?
Colombian Rheumatology Congress
Bogota, Colombia | August 2014

Clinical Relevance of Drug Immunogenicity
2014 Tokyo Westin Immunogenicity Seminar
Tokyo, Japan | September 2014

Considerations in RA management: Immunogenicity
Abu Dhabi Advanced Rheumatology course
Abu Dhabi, UAE | September 2014

Immunogenicity of biologics: can we control or predict the treatment results?
Russian Rheumatologic Conference
Moscow, Russia | October 2014

Clinical Relevance of Immunogenicity: case studies from daily practice
Immunocorvention 2014
Berlin, Germany | October 2014

How to set up an immunogenicity testing in hospital and testing experience
Immunocorvention 2014
Berlin, Germany | October 2014

Immunogenicity of biologics: Pharmacokinetics/Pharmacogenomics
IX Immune/Biological Therapeutic Course in Dermatology
Barcelona, Spain | October 2014
The Immunogenicity and the Impact on the Treatment Outcomes in RA
American Congress of Rheumatology (ACR)
Boston, USA | November 2014

Gardner, Rui
Purity Yields to Recovery
Annual Meeting of the Irish Cytometry Society (ICyS 2014)
Dublin, Ireland | February 2014

Telling Ain’t Teaching: a guide to effective training
XXIX Congress of the International Society for Advancement of Cytometry (CYTO2014)
Fort Lauderdale, Florida, USA | May 2014

Core Technology Facility staff and career development
CTLS
Paris, France | June 2014

Cell Biology Techniques in Flow Cytometry
ESCCA2014
Lisbon, Portugal | September 2014

Flow Cytometry: Fundamentals and Applications
Modern Solutions for Study of Natural, Synthetic and Biological Materials
St. Petersburg, Russia | October 2014

Role of the Core Manager in the Modern SRL
ACS
Gold Coast, Australia | November 2014

Sorting out Performance
ACS
Gold Coast, Australia | November 2014

Gjini, Erida
Pneumococcal dynamics pre- and post-vaccination, the interplay between serotype competition and vaccine efficacy
International Symposium on Pneumococci and Pneumococcal Diseases 2014
Hyderabad, India | March 2014

An organizing centre for competition and coexistence in multi-type pathogens: insights on Pneumococcus
Models in Population Dynamics and Ecology
Trento, Italy | August 2014

Godinho Ferreira, Miguel
Telomere protection in cancer and ageing
HHMI Science Meeting
Washington, USA | March 2014

Telomere protection in cancer and ageing
Telomeres, telomerase and disease
Brussels, Belgium | April 2014

The role of telomere protection
EMBO Practical Course on Molecular Genetics with fission yeast Schizosaccharomyces pombe
Paris, France | July 2014

The role for telomeres in cancer and ageing
CIMA Annual Meeting – Zebrafish Ageing Models
Sheffield, UK | September 2014

Telomere protection in cancer and ageing
XII Congress of the Italian Federation of Life Sciences (FISV)
Pisa, Italy | September 2014

Diversity in Telomere Dynamics
Glasgow Ageing Research Network
Glasgow, UK | November 2014

Concelves-Sá, Joana
Graduate education in the Portuguese-speaking African countries:
Campus Africa, Universidad de La Laguna
Spain | October 2014

Scientific Mobility in the Portuguese-Speaking African countries
Congresso Iberoamericano de Ciencia, Tecnología, Innovación y Educación
Buenos Aires, Argentina | November 2014

Cardo, Isabel
Evolution in E. coli within ecosystems
Evolution of Drug resistance: Superbugs 14, KITP
Santa Barbara, California | July 2014

Transition between commensalism and pathogenesis: an experimental evolution study of pathoadaptation in E. coli
Mathematics and Genetics of Selection and Adaptation
Aarhus, Denmark | October 2014
● Gualda, Emílio
Open Spin Microscopy & Functional imaging in Zebrafish through light sheet microscopy
Lightsheet Fluorescence Microscopy Workshop, Institute for Medical Biology (IMB)
Biopolis, Singapore | April 2014
Open Spin Microscopy and functional imaging in Zebrafish through light sheet microscopy
Bitplane webinar series | June 2014
Open Spin Microscopy
EMBO practical course on Developmental Biology
Oeiras, Portugal | July 2014
Open Spin Microscopy
EMBO practical course on Light sheet microscopy
Dresden, Germany | August 2014
Functional imaging on zebrafish using digital scanned light sheet microscopy
Light sheet Fluorescence Microscopy Congress LSFM2014
Barcelona, Spain | September 2014

● Janody, Florence
Microarray profiling of breast tumours identified key regulators of cytoskeletal-based structures
EU-LIFE
Barcelona, Spain | May 2014

When the actin cytoskeleton goes awry: Role in cancer development and progression
JEDI
Cary Le Rouet, France | September 2014

When the actin cytoskeleton goes awry: Role in cancer development and progression
TAGC
Marseille, France | September 2014

Zyxin antagonizes the FERM protein Expanded to regulate tissue growth
28th Annual French Drosophila Conference
Set, France | October 2014

● Jansen, Lars
Chromatin-based epigenetic inheritance: The centromere and beyond
EMBO workshop “Epigenetic plasticity: Implications in neural (dys)function”
Braga, Portugal | October 2014
Chromatin-based epigenetic inheritance: The centromere and beyond
University of Pennsylvania
Pennsylvania, USA | December 2014
Cell cycle control mechanisms of mammalian centromere assembly
The American Society for Cell Biology, Annual Meeting
Philadelphia, USA | December 2014

● Mallo, Moisés
Of trunk and tails: creating shape diversity among vertebrates
Faculty of Human and Medical Sciences, The University of Manchester
Manchester, UK | March 2014
Trunk or tail: the changing lives of axial progenitors
37th Annual Meeting of the Molecular Biology Society of Japan
Yokohama, Japan | November 2014
Shaping the vertebrate body
Kyoto University
Kyoto, Japan | November 2014
The control of anatomic diversity in vertebrates
V Galician meeting of young researchers abroad, Barrie Foundation
La Coruña, Spain | December 2014

● Martell, Caillé
Centrosome Clustering in Cancer
American Society for Cell Biology, ASCB
Philadelphia, USA | December 2014
Screening the NCI60 panel for centrosome changes in cancer
American Society for Cell Biology, ASCB
Philadelphia, USA | December 2014

● Martins, Gabriel
Optical tomography in Developmental Biology - an Open-source approach
International Symposium in Applied Bioimaging
Porto, Portugal | October 2014
Mesoscopic OpenSource imaging
MicroSpectroscopy Workshop
Wageningen, The Netherlands | September 2014
“Haeckaliens” and OPeNT - Open source mesoscopic imaging for developmental biologists
Bitplane webinar series | May 2014
● Mena, Ana
Using animated videos for science engagement and science learning
13th International Public Communication of Science and Technology Conference (PCST) Salvador, Brazil | May 2014

The amazing world of living things: a short story about evolution (video session)
13th International Public Communication of Science and Technology Conference (PCST) Salvador, Brazil | May 2014

Me and my body (video session)
13th International Public Communication of Science and Technology Conference (PCST) Salvador, Brazil | May 2014

● Mirth, Christen
The ecology of macronutrient balancing in Drosophila species
Behavioral Neurogenetics of Larval Drosophila: Molecules, Circuits, Computation & Robotics
Atami, Japan | March 2014

Nutritional plasticity and the physiology of organ size
Size and Shape Symposium
Coetlingen, Germany | April 2014

Eco-Evo-Devo Summer school
Oxford Brookes University
Oxford, UK | August 2014

Drosophila neurobiology summer school
Teaching and Research in Neuroscience for Development (TReND) in Africa
Dar es Salaam, Tanzania | August 2014

Coordinating organ and whole-body development in a varied environment
Institute of Functional Genomics, Ecole Normale Supérieure de Lyon
Lyon, France | September 2014

Life history traits mould nutrient-dependent choice in Drosophila melanogaster
European Fly Neurobiology Meeting
Hersonissos, Greece | October 2014

Coordinating organ and whole-body development in a varied environment
Faculty of Life Sciences, University of Manchester
Manchester, United Kingdom | October 2014

Genetic mechanisms of plasticity: integrating environmental conditions and developmental programs
School of Biological Sciences, Monash University
Melbourne, Australia | November 2014

The ecology and the evolution of nutrient-dependent choice in Drosophila
Flies, Worms and Robots: Combining Perspectives on Minibrains and Behaviour
Barcelona, Spain | November 2014

● Mohr, Elodie
Exploring the paths towards the diversity of B cells and immunoglobulins in the jungle of the lymphoid organs
Deutsche Rheumaforschungszentrum
Berlin, Germany | April 2014

● Monteiro, Pedro
Attractors identification and quantification
3rd ColMoTo meeting (Consortium for Logical Models and Tools)
Lausanne, Switzerland | April 2014

Model Checking Logical Regulatory Networks
12th IFAC - IEEE International Workshop on Discrete Event Systems (WODES’14)
Cachan, France | May 2014

● Moreno, Nuno
Super-resolution in a facility
Congress of the Spanish Network of Advance Microscopy-REMOA
Madrid, Spain | October 2014

● Oliveira, Raquel
Packing and Chuing DNA molecules for mitosis
Annual Young Investigator Programme meeting (YP)
Heidelberg, Germany | June 2014

Sister chromatid cohesion: not too little, not too much
Karolinska Institute
Stockhol, Sweden | June 2014

● Oliveira, Rui
Socially driven genetic mechanisms underlying neural and behavioural plasticity in fish
The Journal of Experimental Biology 2014 Symposium “Epigenetics in Comparative Physiology”
Banff, Canada | March 2014

Rapid neuromolecular responses to social interactions mediate socially driven behavioural flexibility in zebrafish
Impact of animal aggression and dominance on neurobiology and stress
Symposium at the Society for Experimental Biology (SEB) Annual Meeting 2014
Manchester, UK | July 2014
Simple minds living in complex social worlds: zebrafish as a model to study social cognition and behavior
4th CoGevo - Rovereto Workshop on Cognition and Evolution, Università degli Studi di Trento
Rovereto, Italy | July 2014

Neurogenomics of social behaviour and cognition in (zebra)fish.
Champalimaud Workshop “One, Two, Many Brains”
Estoril, Portugal | September 2014

Plasticity of reproductive behavior in fish: why and how?
International Conference on “Sex Determination and Differentiation in Fishes: Genes, Environment and Behaviour”
University of Lisbon, Portugal | September 2014

Neuromolecular mechanisms of socially driven behavioral plasticity in zebrafish
Janelia Conference “Life in the Aggregate: Mechanisms and Features of Social Dynamics”, Howard Hughes Medical Institute; Janelia Farm Research Campus
Virginia, USA | October 2014

Pereira-Leal, José
Variation and Ancestral States in Centrosome Evolution
EMBO Centrosome Meeting
Lisbon, Portugal | October 2014

Perfeito, Lilia
Forces driving the evolution of genome structure
56th WE-Heraeus-Seminar Mechanisms, Strategies and Evolution of Microbial Systems
Bad Honnef, Germany | June 2014

New mutations seen through the eyes of natural selection
Workshop on quantitative evolutionary biology
Izmir, Turkey | September 2014

The impact of genetic background on evolvability
Collège de France
Paris, France | December 2014

Rocha, Luis M.
Redundancy, control and collective computation in network dynamics
European Conference on Complex Systems 2014, Dynamics on and of Complex Networks VII Workshop
Lucca, Italy | September 2014

Redundancy, control and collective computation in network dynamics
Networks and Complex Systems Talk Series, Indiana University
Bloomington, USA | October 2014

Emergence of organism as a collective behavior
12th Annual National Academies Keck Futures Initiative (Nakfi) Conference: Collective Behavior from Cells To Societies
Irvine, USA | November 2014

Salmona, Jordi
Towards conservation genomics of northern Madagascar lemurs
International Primatological Society Meeting
Hanoi, Vietnam | August 2014

From conservation genetics to conservation genomics: a primate perspective (with Lounès Chikhi)
International Primatological Society Meeting
Hanoi, Vietnam | August 2014

Conservation genomics of primates: where are we, where can we go? (with Lounès Chikhi and G. Perry)
International Primatological Society Meeting
Hanoi, Vietnam | August 2014

Silva, Vanina
A Role for Neuro-Induced Cardiac Stress in Autoimmunity
Symposium: Immunological phenomena in cardiac diseases, Clinical University Würzburg, Germany | October 2014

Soares, Helena
Regulated vesicle fusion generates signaling nanoterritories that control T cell activation
EMBO conference: Lymphocyte Signaling
Bertinoro, Italy | May 2014

Soares, Miguel
Frankfurt Institute for Advanced Studies (FIAS)
Frankfurt, Germany | January 2014

34th European Workshop for Rheumatology Research
Lisbon, Portugal | February 2014

Exploratory seminar on “The Use of Animal Models to Study Diseases in Humans”, Radcliffe Institute
Boston, USA | April 2014

Marion KochHand Symposium, University of Chicago
Chicago, USA | June 2014

Cordon Research Conference - Thiol Based Redox Regulation & Signaling
Girona, Spain | July 2014

XXXX Congress of the Brazilian Society for Immunology
Buzios, Brazil | October 2014
AABB Annual Meeting
Philadelphia, USA | October 2014

Keystone Symposium: Cell Death Signaling in Cancer and the Immune System* (S2)
São Paulo, Brazil | October 2014

- Soosa, Ana
  The repeatability of Escherichia coli evolution in its natural environment
  Mathematics and Genetics of Selection and Adaptation
  Aarhus, Denmark | October 2014

- Sousa Maior, Caetano
  Quantitative descriptions of Wolbachia impact in disease-vectors; computing the bits and finding the pieces
  ETH
  Zürich, Switzerland | October 2014

- Stankovic, Ana
  Cell cycle control mechanisms of mammalian centromere assembly
  Gordon Conference on Centromere Biology
  Boston, USA | July 2014

  Cell cycle control mechanisms of mammalian centromere assembly
  Roscoff Cell Cycle Meeting
  Brittany, France | October 2014

- Teixeira, Luis
  Phylogenomics and evolution of symbiont-mediated protection to pathogens
  8th International Wolbachia meeting
  Innsbruck, Austria | June 2014

  Linking genotype to phenotype in Wolbachia
  10th European Congress of Entomology
  York, UK | August 2014

- Bacterial symbionts of Drosophila
  4th Junior European Drosophila Investigator Meeting
  Marseille, France | September 2014

  Natural host-microbe interactions in Drosophila; from defensive endosymbionts to gut microbiota
  Max Planck Institute for Developmental Biology
  Tübingen, Germany | October 2014

- Tranfield, Erin
  Three Dimensional Imaging in Electron Microscopy
  EMBO Practical Course on 3D Developmental imaging
  Oeiras, Portugal | July 2014

- Vidal, Sheila
  Strategies to look for funding to develop a research project
  Praia, Cape Verde | July 2014

- Xavier, Karina
  Manipulating interspecies quorum sensing in bacterial consortia
  Max Planck Institute for Infection Biology
  Berlin, Germany | March 2014

  Manipulating interspecies quorum sensing in bacterial consortia
  College of Life Sciences, University of Dundee
  Dundee, Scotland | April 2014

  Manipulating interspecies quorum sensing in the mouse gut
  3rd Mol Micro Meeting
  Würzburg, Germany | May 2014

  Small RNAs are central in integrating quorum-sensing signals in plant associated pathogens
  RNA Workshop: Post-Transcriptional Control of Microbial Gene Expression at ITQB
  Oeiras, Portugal | May 2014

- Zitouni, Sihem
  Centrosomes in Xenopus Extracts
  PRIME XS meeting
  Ávila, Spain | October 2014
At National Meetings & Seminars

- Amorim, Maria João
  How does progeny RNA reaches the plasma membrane during influenza A virus infection
  Universidade de Aveiro
  Aveiro, Portugal | October 2014

- Baena-González, Elena
  Energy signaling: connecting environmental stress and plant growth
  XVII Congress of the Portuguese Biochemical Society
  Coimbra, Portugal | December 2014

- Becker, Jörg
  How microarrays and deep sequencing transform today’s biology
  1st Jornadas de Biotecnologia, Escola Superior de Tecnologia do Barreiro
  Lavradio, Portugal | May 2014

  Highs and Lows of One Year MiSeq at IGC
  1st Illumina User Group Meeting Portugal
  Coimbra, Portugal | October 2014

  Restraining (the epigenetic) landscape of Arabidopsis pollen for genome stability and transgenerational inheritance
  XVII Congress of the Portuguese Biochemical Society
  Coimbra, Portugal | December 2014

- Bergman, Marie Louise
  Novel role for TEC in Treg selection: TEC present self-antigens through a mechanism of cross-presentation
  XL Annual Meeting, Sociedade Portuguesa de Imunologia, SPI’40, From immune responses to immunotherapy
  Lisbon, Portugal | October 2014

- Bispo, Cláudia
  Aplicações de Citometria de Fluxo na Área de Investigação
  Universidade Atlântica
  Barcarena, Portugal | May 2014

- Borges, Vanessa
  LabEscolas
  Sci Comm PT 2014
  Porto, Portugal | June 2014

- Carneiro, Jorge
  Deconvolution of the multi-threaded concept of self tolerance in contemporary immunological literature
  Notions of Self: Exploring theories of immunity, ICBAS
  Porto, Portugal | September 2014

  A Brief History of the Portuguese Society of Immunology
  SPI40-40º Annual Meeting of the Portuguese Society of Immunology, Instituto de Medicina Molecular
  Lisboa, Portugal | October 2014

- Carneiro, Tiago
  Uma viagem artística pelas células
  Espaços Abertos entre Arte e Ciência, APECV, FIL
  Lisbon, Portugal | March 2014

  How I choose an alternate career: from research to biosafety
  IMM/CAML PhD students meeting, Instituto de Medicina Molecular
  Lisboa, Portugal | March 2014

- Chaouiya, Claudine
  Logical modelling of regulatory networks: Advances and challenges
  3rd Workshop in Bio-Optimization, Instituto Superior de Agronomia
  Lisboa, Portugal | November 2014

- Correia, Ana Catarina
  Microwave Processing for Electron Microscopy: A Comparison with Conventional Processing in Zebrafish Tissues
  XVIII Congress of the Portuguese Microscopy Society
  Porto, Portugal | November 2014

- Costa, Teresa
  How to write a successful CV
  5th Annual International Medical Students Meetings (AIMS), Faculdade de Medicina, Universidade de Lisboa
  Lisboa, Portugal | March 2015

- Demengeot, Jocelyne
  The pathogenesis of autoimmune disease
  Focus on Autoimmune Diseases, Caboite Gulbenkian Foundation
  Lisbon, Portugal | November 2014

- Duque, Paula
  Quando um gene vale por dois: “splicing” alternativo de um transportador de membrana de Arabidopsis
  XV Jornadas de Biologia Aplicada, Universidade do Minho
  Braga, Portugal | February 2014
Saccharomyces cerevisiae as a pivotal tool for the functional characterization of plant membrane transporters
XX Jornadas de Leveduras Professor Nicolau Van Uden, Instituto Superior Técnico
Lisbon, Portugal | July 2014

• Ferreira, Álvaro Gil
The Toll pathway is necessary for resistance to viral infection in Drosophila
Annual Portuguese Drosophila Meeting 2014
Tomar, Portugal | September 2014

• Ferreira Moita, Luís
Anthracyclines induce DNA damage response-mediated protection against severe sepsis
UC-Biotechnology
Cantarinheda, Portugal | October 2014

Anthracyclines induce DNA damage response-mediated protection against severe sepsis
Center for Neurosciences & Cell Biology, Universidade de Coimbra
Coimbra, Portugal | November 2014

• Franco, Ana
Dos golfinhos aos confins da Etiópia
Encontro Anual da Associação dos Antigos Alunos da Faculdade de Medicina Veterinária
Lisbon, Portugal | April 2014

• Gardner, Rui
Aplicações de Citometria de Fluxo na Área de Investigação
Universidade Atlântica, Barcarena, Portugal | May 2014

• Gomes, Gabriela
Unfolding Infectious Disease Studies
Encontro Nacional da Sociedade Portuguesa de Matemática, Faculdade de Ciências e Tecnologia, Universidade Nova de Lisboa
Lisboa, Portugal | July 2014

• Gonçalves-Sá, Joana
Understanding public fears in the 2009 flu epidemic context
Workshop ISCTE
Lisbon, Portugal | September 2014

Graduate education in the Portuguese-speaking African countries
IV Workshop for International Affairs in Medicine, Faculdade de Medicina da Universidade do Porto
Porto, Portugal | May 2014

• Cordo, Isabel
Evolution in E. coli within ecosystems
XVI Portugaliae Geentérica
Porto, Portugal | March 2014

• Gualda, Emílio
OpenSPIN microscopy project
IMARS Open Day
Oeiras, Portugal | May 2014

• Júlio, Catarina
A descoberta a começar nos mais novos: um programa inovador para o ensino da ciência nas escolas
Sci Comm PT 2014
Porto, Portugal | June 2014

Eu e o meu corpo! À descoberta das células (with Ana Mena)
II Encontro Internacional da Casa das Ciências
Porto, Portugal | July 2014

• Martins, Gabriel
Mesoscopy & Haeckoliens
BIORG Seminar series, Faculty of Sciences, Universidade de Lisboa
Lisbon, Portugal | April 2014

Capture & Visualization of 3D Images
Natural History Collections course, MNHNC
Lisbon, Portugal | June 2014

• Martins, Nelson
Adaptation of Drosophila melanogaster to DCV relies on few genes with different cross-resistance properties
Annual Portuguese Drosophila Meeting 2014
Tomar, Portugal | September 2014

• Martins, Nuno
Intro to Macros in ImageJ
IMARS Open Day Oeiras | May 2014

Eu e o meu corpo! À descoberta das células (with Catarina Júlio)
II Encontro Internacional da Casa das Ciências
Porto, Portugal | July 2014

• Mena, Ana
Separating the sisters: Mitosis without cohesion
Annual Portuguese Drosophila Meeting 2014
Tomar, Portugal | September 2014
● Oliveira, Raquel
Pericentric heterochromatin gets sticky when misplaced at chromosome arms
Annual Portuguese Drosophila Meeting 2014
Tomar, Portugal | September 2014

Sister chromatid cohesion: not too little, not too much
Instituto de Biologia Molecular e Celular (IBMC)
Porto, Portugal | June 2014

Mitosis and Cancer (Cell Cycle Checkpoints)
Oncologia molecular: Biologia do Cancro e Terapias Emergentes, Instituto Português de Oncologia Francisco Gentil
Coimbra, Portugal | October 2014

● Pais, Inês
Characterization of stable bacterial communities associated with laboratory and wild Drosophila populations
Annual Portuguese Drosophila Meeting 2014
Tomar, Portugal | September 2014

● Perfeito, Lilia
Forces driving the evolution of genome structure
CIBIO Seminar Series
Vairão, Portugal | February 2014

Forces driving the evolution of genome structure
16th Portugalete Genética
Porto, Portugal | March 2014

Experimental evolution of chromosome structure in yeast
XX Jornadas de Biologia de Leveduras “Professor Nicolau van Uden”
Lisbon, Portugal | July 2014

● Pinho, Julia
Different mechanisms involved in fear learning in zebrafish
XI Congress of the Portuguese Ethological Society, CIBIO
Vairão, Portugal | October 2014

● Rocha, Luis M.
Collective behavior and control of network dynamics
Champalimaud Foundation
Lisbon, Portugal | October 2014

Collective decision in the global brain: science and policy
Deliberation Day Conference, Champalimaud Foundation
Lisbon, Portugal | October 2014

● Silva, Vânia
A Role for Neuro-Induced Cardiac Stress in Autoimmunity
SPIRO-40° Annual Meeting of the Portuguese Society of Immunology, Instituto de Medicina Molecular
Lisbon, Portugal | October 2014

● Simas, Tiago
Complex networks and the epidemiology of Influenza
Workshop ISCTE
Lisbon, Portugal | September 2014

● Soares, Helena
HIV alters the nanoarchitecture of TCR signaling to prevent activation-induced cell death
SPIRO: From Immune Responses to Immunotherapy
Lisbon, Portugal | October 2014

● Sobral, Daniel
The Bioinformatics Unit @ IGC
Instituto de Medicina Molecular
Lisbon, Portugal | March 2014

Bioinformatics Algorithms
ITQB, Masters Course on Advanced Topics in Bioinformatics
Oeiras, Portugal | May 2014

● Sousa, Ana Laura
Comparison of Mouse Kidney Ultrastructure using PHEM, Phosphate, Cacodylate, PIPES and H2O
XLVIII Congress of the Portuguese Microscopy Society
Porto, Portugal | November 2014

● Sousa, Jorge
Resistance is not futile: Evolutionary potential and the fates of antibiotic resistant bacteria
X Encontro Nacional de Biologia Evolutiva
Lisbon, Portugal | December 2014

● Élio Sucena
Portugalete genética
Porto, Portugal | March 2014

Instituto Superior de Agronomia
Lisbon, Portugal | November 2014

Instituto de Medicina Molecular
Lisbon, Portugal | November 2014
● Teixeira, Luís  
Mutualism breakdown by amplification of Wolbachia genes  
Annual Portuguese Drosophila Meeting 2014  
Tomar, Portugal | September 2014

● Teles, Magda  
Cognitive appraisal drives neural and behavioural plasticity in zebrafish  
XI Congress of the Portuguese Ethological Society, CIBIO  
Vairão, Portugal | October 2014

● Telley, Ivo  
An ex vivo approach to study the mechanics of nuclear positioning in syncytial embryos  
Instituto de Medicina Molecular, Faculdade de Medicina da Universidade de Lisboa  
Lisbon, Portugal | November 2014

● Tranfield, Erin  
Improvements in Ultrastructure Preservation by Cryo-Immobilization  
Course on Electron Microscopy, Instituto Nacional de Saúde Dr. Ricardo Jorge (INSA)  
Lisbon, Portugal | May 2014

● Varela, Pedro  
The legislation of fear- influenza as a case study  
Workshop ISCTE  
Lisbon, Portugal | September 2014

● Vasconcelos, Francisca  
Function of the zinc finger protein Myt1 in vertebrate neurogenesis  
Development In Action meeting (Portuguese Society for Developmental Biology)  
Faro, Portugal | July 2014

● Xavier, Karina  
Cell-cell communication in multispecies bacterial communities  
Faculdade de Ciencias, Universidade de Lisboa  
Lisbon, Portugal | January 2014

Manipulating interspecies quorum sensing in bacterial consortia  
Universidade de Coimbra  
Coimbra, Portugal | June 2014
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public engagement in science
The IGC runs a dedicated science communication and outreach programme, which actively engages IGC researchers, staff and PhD students in a dialogue with the society. We aim at promoting the values in science, namely, critical thinking, honesty and ethics, and openness to share and discuss new knowledge, encouraging public engagement in science. We also aim to raise the profile of the IGC and its research, both nationally and internationally. Our programme involves a broad range of audiences: the media, students, teachers, the general public, artists and policy makers.

### DESCRIPTION

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### PROJECTS WITH SCHOOLS

**'Aqui há Ciência' – training programme for teachers**

This collaborative project aims to develop in-class laboratory activities and teacher training for pre- and primary schools, using methodologies in inquiry-based learning. The project involves teacher-training sessions, followed by in-class activities with the students. The third year of this project occurred from January until July 2014, with 38 participating teachers from 6 local schools, and a total of 8 training sessions and 6 experimental activities completed. Experimental protocols are available online. ‘Aqui há Ciência’ was credited for teachers’ continuous professional development by the national ‘Conselho Científico-Pedagógico da Formação Contínua’.

**‘Inspirar Ciência 2014 – Evolução’ – Workshop for teachers**

‘Inspirar Ciência’ is a workshop targeted at high school biology teachers. The 2014 edition was dedicated to Evolution and combined informal lectures by IGC researchers, laboratory sessions and group work to produce a final project. Four IGC groups participated and 16 teachers (out of 25 applications) were admitted. This workshop lasted four days and was credited for teachers’ continuous professional development by the national Conselho Científico-Pedagógico da Formação Contínua.

### MAJOR PROJECTS & ACCOMPLISHMENTS

#### PRESS OFFICE AND NEW MEDIA

In 2014, 20 press releases were sent out announcing research developments and awards accomplished by IGC scientists. On average, 22.4 news items were generated per release; 573 news clippings mentioning the IGC were registered, in Portuguese (56%) and international (44%) media outlets (values are underestimates). Social networks as Facebook (26,801 fans) and Twitter (2,058 followers) have been used to provide regular updates on research developments, seminars and outreach to broad audiences. In the YouTube channel we have 27 movies uploaded, with a total of 124,972 views. In addition, the IGC website received a total of 196,503 visits (average of 538.3 visits per day).

### STAFF

- Vanessa Borges (Post-doc) | Started in January
- Inês Domingues (Post-doc)
- Carolina Júlio (Project Officer)

### COLLABORATORS

- Maria de Assis (DESCOBIR - Programa Gulbenkian Educação para a Cultura e Ciência, Portugal)
- Simão Costa (LabMóvel, Portugal)
- Fundação para a Computação Científica Nacional (Portugal)
- Mafalda Lapa (Escola Secundária da Cidadela, Portugal)
- Maria João Leão and Sofia Rodrigues (Maratona da Saúde)
- Élia Morais (Centro de Formação das Escolas de Torres Vedras e Lourinhã, Portugal)
- Alexandra Paio, Maria João de Oliveira and Sancho Oliveira (Vitruvius FabLab, ISCTE-IUL, Portugal)

### PhD in Cell Biology

Universidade Nova de Lisboa, 2008

Other position at IGC:

- Member of the Ethics Committee

- Mena, Ana

Head of Unit since 2012

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This website joins resources developed at the IGC for the life sciences teaching and learning. It is dedicated to teachers from primary to high school, educators, science communicators and all enthusiasts of life sciences. The resources available include experimental activities suitable for the classroom and divided by school years, videos illustrating biological processes and articles focusing areas of cutting-edge research. During 2014, the website received 5,637 total views, and at the end of the year had 635 registered users. A total of 313 downloads were done.

**LabEscolas (LabSchools)**

This project aimed at promoting knowledge, interest and engagement of students in the latest advances in life science research. During 2014, 25 students from the 12th grade conducted experimental activities in the classroom, and worked in group to write a scientific proposal on a biological problem. On 5 June, the students presented and discussed their proposals with the IGC scientific community, in a forum that took place at the IGC. The authors of the three best proposals did a one-week internship at the IGC. This project was run at Escola Secundária de Cidadela (Cascais) during the 2013-2014 school year.

**FUNDING**

- Agência Nacional para a Cultura e Tecnologia - Ciência Viva, Portugal

**RESEARCH GROUPS AND FACILITIES HOSTING THE INTERNSHIP**

- Cell Biology of Viral Infection
- Chromosome Dynamics
- Development, Evolution and the Environment
- Evolutionary Biology
- Flow Cytometry
- Genomics
- Host-Microorganism Interactions
- Integrative Behavioural Biology
- Obesity
- Plant Molecular Biology
- Population and Conservation Genetics

**COORDINATION**

- Ana Franco (Collective Dynamics group)

**INSTITUTIONAL VIDEOS**

Two institutional videos were produced in 2014; one addressing the PhD programmes, the other addressing what makes the IGC "a special place to be." Both videos were uploaded in the IGC YouTube channel:

- "IGC | A special place to be" – 1,672 views (since June 2014)
- "Doing a PhD at Instituto Gulbenkian de Ciência" – 4,060 views (since February 2014).

**GRIPENET**

(Since 2009, part of the FP7-funded project, Epiwork)

Gripenet is a syndromic surveillance system that monitors the activity of influenza-like-illness (ILI), in near-real-time, with the help of volunteers, via the internet. In 2014, over 2,200 citizens participated in this project, with approximately 28,300 online weekly symptoms questionnaires being collected and analysed (https://www.influenzanet.eu/en/results). The system includes a broad range of science communication and education activities. Notably, Gripenet Kids (http://kids.gripenet.pt/) is an online multimedia application dedicated to children from 6 to 12 years old that was developed by Gripenet for Portugal and is being implemented also in Mexico. In 2014, Gripenet celebrated its 10th anniversary, and started an official collaboration with the Portuguese National Health Institute (Instituto Nacional de Saude Doutor Ricardo Jorge), that coordinates the traditional national influenza surveillance system based on data from health services.

Gripenet is a co-founder of the European consortium Influenzanet, that standardizes the digital epidemiologic surveillance of influenza-like-illness in Europe. Research groups from 10 European countries currently participate in this consortium.

**SCHOOL’S OUTREACH**

In 2014, 175 students from 6 high schools (from Barcelos, Cartaxo, Cascais, Lisbon, Oeiras and Vila Real) and 15 students from one university (Instituto Superior de Psicologia Aplicada) visited the IGC. In addition, one of our scientists went to a high school to lecture on genetics (in Lisbon), and two other scientists gave webinars, one within the scope of LabChat (the IGC programme that uses videoconference to bring together scientists and students) and the other within the scope of inGenious (a programme from the European Schoolnet). The latter reached 30 teachers and their students from across Europe. In total, we received 26 requests either to visit the IGC, to bring scientists to schools, to participate in webinars, or to provide material or assistance in the development of experiments.

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PUBLIC EVENTS

IGC presence at NOS Alive 14 | 10-12 July, 2014

Science, Music and Art came together for the seventh year running, during NOS Alive 14 music festival. During the three days of this major music and art event the main activities at the IGC corner were: speed dating with scientists, a biodiversity game, a game testing the evolution of hosts and parasites, a photo exhibition of the Optimus Alive fellows, and molecular cooking (in partnership with the Cooking Lab). This year, we had a wheel of fortune indicating which activity visitors should take, and a publicity spot in the main screens of the Festival. Fifty-two IGC volunteers made these activities possible for about 1500 young people who visited the IGC corner.

Open Day – ‘Ciência em Construção’ (Science in Progress)

The 7th edition of the IGC Open Day brought 1500 visitors to the IGC. Over 100 researchers and staff took part in this event, organizing several activities amongst which: hands-on experiments, a Top Model room showing the model organisms used at the IGC, a fluorescent room with GFP-organisms, and several talks with scientists and a final debate on where is science taking us. This year, a group of sketchers from the Portuguese Urban Sketchers, came to the Open Day to picture some of our science.

ART AND SCIENCE PROJECTS

Musical Morphogenesis

Musical Morphogenesis is an interactive installation that traduces in sound, light and movement the development of a flower, unveiling the role of genetic networks during that process. During 2014, work has been done to ameliorate and implement new features in this installation.

INVITATIONS AND OTHER COLLABORATIONS

In 2014, IGC scientists participated in a series of events organised by Maratona da Saúde, to fundraise for cancer research, including TV programmes and interviews, as well as a football game with former football players and sympathizers of Benfica. The IGC hosted the visit of several delegations, including the Ambassadors of Israel and Poland, The Minister of Science and Technology of Argentina, representatives of MERCK, the president of CAPES (Brazil) and the European Commissioner for Science and Research. The IGC also hosted an informal meeting to promote the gathering and exchange of information between members of the Bioprocess Engineering Group at Wageningen University, PhD students working at AlgaeParc (The Netherlands) and the IGC PhD students.

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The IGC develops an in-house programme aimed at raising private funds for science through fundraising initiatives with private companies, charities and the general public. The IGC is under the Scientific Sponsorship Law. This law provides tax benefits for science-related donations by either individuals or companies.

**MAJOR PROJECTS AND ACCOMPLISHMENTS**

- **THE IGC – EVERYTHING IS NEW (EIN) PARTNERSHIP**
  
  This partnership was established in 2007 between the Instituto Gulbenkian de Ciência (IGC) and Everything is New, promoter of the NOS Alive music festival (former Optimus Alive). Its main aim is to bring Science closer to the Portuguese society and to raise funds for scientific research. This unique partnership established between a Research Institute in Biomedicine and a music promoter is a strong example of how the private sector and Society in general may contribute to the progress of research and therefore to the future wellbeing of all.

  **NOS Alive – IGC research fellowships**

  This partnership resulted in research fellowships that give the opportunity to young graduates to start their scientific careers, funded by Everything is New. Since 2009, over 400 young graduates around the country have applied to these fellowships.

  In 2014, Gonçalo Matos and Tiago Maié received a fellowship to develop one-year research projects in Biodiversity and Evolution, at the Population and Conservation Genetics, and Evolution and Development research groups, respectively. These projects were carried out at the IGC with practical works in France and Switzerland.

- **COLEÇÃO CIÊNCIA – A PARTNERSHIP BETWEEN THE IGC AND VISTA ALEGRE**

  A collection of porcelain products, Coleção Ciência, results from a partnership between the IGC and Vista Alegre, a prestigious and market leader Portuguese porcelain manufacturer. Young scientists obtained the original images of this collection, as part of their research at the IGC. Part of the money raised by selling this collection has been used in scientific meetings organised by the PhD students and post-docs from the IGC.

  In 2014, the porcelain Coleção Ciência was available at the IGC and at the Calouste Gulbenkian Foundation.

- **FUNDRAISING ACTIVITIES ORGANISED BY THE IGC PHD DELEGATES AND POST-DOCTORAL COMMITTEE**

  Several fundraising activities (beer hours, wine hours, thematic parties, etc.) were organised in 2014 to raise funds for the 8th PhD AMeeGuS meeting and for the Post-Doctoral retreat, via donations from attendees at the events, both from IGC staff and the general public.
Several partnerships and sponsorships have been established to support, financially or in goods, scientific research, education and outreach activities at IGC. We thank all our partners and sponsors:

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CAMÕES INSTITUTO DA COOPERAÇÃO E DA LÍNGUA PORTUGAL
CAPES - COORDENAÇÃO DE APERFEIÇOAMENTO DE PESSOAL DE NÍVEL SUPERIOR
CELEXPLORER LABS
CENTRO DE BIOLOGIA AMBIENTAL
CENTRO DE FORMAÇÃO DAS ESCOLAS DE TORRES VEDRAS E LOURINHÃ
CIÊNCIA VIVA - ESCOLHER CIÊNCIA
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EU-LIFE
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FUNDACAO CHAMPLAUM
FUNDACÃO PARA A CIÊNCIA E A TECNOLOGIA
GOVERNO DE PORTUGAL, MINISTÉRIO DA EDUCAÇÃO E CIÊNCIA
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UNIVERSITY OF OXFORD
VALCHROMAT - INVESTWOOD
VISTA ALEGRE
VWR
ZEISS
We are grateful to everyone at the IGC - researchers, students and staff - who supplied information, text and images used in this report.

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The Instituto Gulbenkian de Ciência (IGC) Annual Report is available to download from the IGC website at www.igc.gulbenkian.pt.

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The IGC was set up by the Calouste Gulbenkian Foundation, a Portuguese private institution of public utility whose statutory aims are in the fields of arts, charity, education and science. Created by a clause in Calouste Sarkis Gulbenkian’s will, the Foundation’s statutes were approved in 1956. The head-office is located in Lisbon.
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