

# Reports of EACR Sponsored Meetings

*EACR continues its strong tradition of supporting valuable scientific meetings across Europe*

## The MetaBre/BRECOSM Breast Cancer and Metastasis Conference.

CNR - Consigli Nazionale delle Ricerche, Rome

5 -7 December 2007



The MetaBre/BRECOSM Breast Cancer and Metastasis conference took place in Rome from the 5th-7th December 2007. MetaBre and BRECOSM are funded by the European Union under the Framework Program 6, whose aims both relate to developing a better understanding of the mechanisms of organ-specific metastasis in breast cancer. The conference was organised jointly by both consortia as a platform to showcase the results of their research programmes, but also included a world class series of lectures from experts in the field to enhance the occasion. In addition to the main conference, a satellite session was organized for Italian researchers and clinicians covering aspects of bone metastasis. There were approximately 150 registrants, mainly from Europe, but overall representing 17 countries with several delegates from as far afield as Brazil, Puerto Rico and Russia. Sixty seven abstracts were

submitted for free communications. The top scoring 21 were offered oral presentations (these included many of the postdoctoral fellows funded by the consortia) and the remainder were presented as posters.

The presentation of the major findings of the two consortia was an important part of the conference and contributed to the dissemination of FP6 results. Jonathan Sleeman introduced the aims of the BRECOSM consortium, then Gerhard Christofori presented results on the molecular pathway involved in tumour cell invasion, and Peter ten Dijke introduced the role of SMAD4 in TGF- $\beta$  signalling and metastasis. Following Anna Teti's introduction of the aims of the MetaBre consortium, Keltouma Driouch presented the results for the microarray data of gene expression signatures for metastases to the lung, brain and bone and Akeila Bellahcène presented results of the validation of genes of interest at the protein level, focussing on the calcium binding protein S100A4.

The first open session focussed on 'Experimental models'. Jos Jonkers covered the use of sophisticated genetically engineered mouse models (GEMMs) and in particular the development of tissue-specific conditional knockouts of p53. This background could then be combined with other genetic defects such as loss of E-cadherin, which accelerated tumour formation. To model hereditary breast cancer, the

p53-/- genotype was combined with BRCA1 loss. Peter Friedl gave one of his signature lectures full of stunning 3D intravital movies obtained using multiphoton microscopy. He revealed that MMP14 (MT1-MMP) is rate limiting for invasion and that proteolysis occurs just behind the leading edge of a migrating cell. He also showed that tumour cells use blood capillaries as tracks for migration into tissues. Dr De Maria highlighted the significance of cancer initiating (putative stem) cells. These rare, highly tumorigenic cells are thought to express CD133 and to be responsible for drug resistance. Patients with high levels of CD133+ve cells have a poorer prognosis.

This theme was expanded in the second session on "Mechanisms inducing breast cancer" with Matt Smalley describing the evidence for breast cancer stem cells from his own work in mouse mammary gland and from a survey of published work. He suggested that CD44+ stem-like cells could yield progeny that instead expressed CD24 (and that these cells were enriched in metastases). David Lyden followed this up with his highly original observations that tumour cells can generate a "pre-metastatic niche" in distant organs which then provides a favourable environment for circulating tumour cells to lodge and grow. This is perhaps the 21st Century embodiment of Paget's "seed and soil" hypothesis. The third speaker in this session was Carlo Croce who

gave a fascinating and persuasive talk on the importance of microRNAs – small non-coding RNA sequences that seem to have profound effects on protein expression and thus many cellular functions, including metastatic potential. It is likely that microRNA signatures will soon be as widely used (and as informative) as gene expression arrays in cancer research, diagnosis and perhaps even therapy.

In the “New prognostic tools” session, René Bernards described the development of the “Mammaprint” array based on the famous 70 gene signature predictive of poor prognosis in breast cancer. This is now being used in the MINDACT clinical trial to try to spare patients from receiving unnecessary chemotherapy. It is essential that such pioneering trials be done if genetic profiling is to take its place alongside conventional prognostic indicators. He also described attempts to predict which patients would respond to therapies such as herceptin and identified a “PI3K activated pathway” signature (including PTEN loss or PIK3CA mutation) as being particularly powerful. Kent Hunter finished with an illuminating talk on the significant role that host genetic polymorphisms can play in determining metastatic risk (if you like the “climate” in which the metastatic ‘seed’ and environmental niche ‘soil’ reside). These highly original findings emerged from studies in inbred mouse strains, but have now found resonances in man, with some of the key SNPs (such as SipA1) identified.

Pat Steeg focussed on brain metastasis in her talk in the “Metastatic disease” symposium. This site seems to be increasing in prevalence in breast cancer, perhaps because many drugs (and certainly antibodies such as herceptin) fail to cross the blood brain barrier. She has developed an experimental xenograft tumour model and found that the cells are highly motile and overexpress activated EGFR and AKT. Max Wicha continued a discussion on breast cancer stem cells. His group was one of the first to isolate and characterise these cells using a floating culture ‘mammasphere’ model, based on a similar technique

used to culture neural stem cells. Although highly clonogenic, the cells in the mammaspheres require fibroblast support to grow in mice (again highlighting the need for a permissive environment). He also identified ALDH1 as a key marker of stem cells which enables their rapid identification and isolation. Finally, Toshiyuki Yoneda discussed bone metastasis, again very common in breast cancer with an incidence of around 83%. Using a mouse model, he described key features of bone-colonising breast cancer cells and their propensity for osteomimicry, enabling them to thrive in this specialised site. TGFβ signalling seems to be one of the key pathways involved, but hypoxia is also important. He speculated that acidosis (due to the release of protons by osteoclasts) may be responsible for bone pain and suggested that the proton pump may be a good therapeutic target, for which he presented some preclinical supporting data.

A further plenary session was on “Lymphangiogenesis”. Unfortunately, Michael Detmar was unable to attend, but his place was taken at short notice by Jonathan Sleeman who gave an excellent overview of lymphatic metastasis and its significance in breast cancer. He was followed by

Douglas Noonan who suggested that angiogenesis may be a good target for chemoprevention and early intervention. It is interesting that many agents (especially dietary factors such as green tea polyphenols) that have been found to reduce cancer incidence or progression in animal models, turn out to have strong antiangiogenic activity. However, it may be that endothelial cells are not the primary (or only) target, since in some cases there is an anti-inflammatory component which indirectly prevents angiogenesis, thus implicating leukocytes and possibly the innate immune system.

In “Genetic and epigenetic regulators” Howard Chang identified a “wound response signature” which predicts worse survival in patients. Although this includes around 500 genes, he identified MYC and CSNS (the catalytic unit of a signalosome) as master regulators. Both are linked to processes involving the proteasome and he found that bortezomib (a proteasome inhibitor) selectively killed tumour cells expressing the ‘wound signature’ – which are presumptively the rogue cells that are most likely to kill the host. Dan Welch discussed BRMS-1, a key metastasis suppressor gene that his group identified. It encodes a protein that seems to have



*“Friends, Romans and countrymen: lend me your ears!” Three of our illustrious speakers go native (the central three, from left to right: Dan Welch, Pat Steeg and Kent Hunter), flanked by centurions*

multiple functions, but Dan's main hypothesis is that it (and possibly other suppressors) regulate cellular responses to exogenous signals in secondary sites.

Finally, in the "Targeted therapy" session, there were three lectures covering different potential therapeutic strategies. Peter Carmeliet summarised the possibilities of antiangiogenic therapy, noting that most current agents targeted VEGF or its receptor. He considers that there is a great opportunity for complementary approaches, and proposed that PIGF and/or FGFR might be promising targets. The former, unlike VEGF, doesn't induce compensatory angiogenic factors when targeted and also induces less hypoxia (which could be counterproductive by encouraging proangiogenic macrophage infiltration). He also described an unconventional inhibitor of FGFR which doesn't target the kinase domain, but rather the FGF binding pocket. Paolo Comoglio focussed on the MET pathway as a master switch and promising drug target. He emphasised the parallels between homeostasis and invasion and suggested that both are regulated by similar genetic programmes. He described new approaches to therapy using lentiviral vectors to deliver genes encoding anti-MET antibodies.

Overall, this was a timely and exciting meeting, with presenters willing to share unpublished data and to discuss novel areas of work. It undoubtedly enabled many new collaborations and interactive links to be fostered, and it is good to know that one doesn't always have to travel to the US for excellence: European science is alive and well! The organisers would sincerely like to thank the EACR for their support which contributed to the success of the meeting.

*Sue Eccles*

For further information on MetaBre and BRECOSM, please see the respective websites:

<http://www.metabre.org> and [http://itgmv1.fzk.de/www/brecosm/home\\_e.html](http://itgmv1.fzk.de/www/brecosm/home_e.html)

## The 4th International Conference on Tumour Microenvironment: Progression, Therapy and Prevention Florence, Italy 6 October 2006

The concept that the tumour microenvironment plays a crucial role in cancer development and especially in its progression is now widely accepted. From less than 90 publications with the key word "Tumour Microenvironment" or "Cancer Microenvironment" in 1995, the number of publications with these key words rose, in 2006, to almost 600.

The Tumour Microenvironment is a multifactorial arena in which tumour cells engage in an active cross-talk with many different cells and molecules. A comprehensive understanding of the significance of such interplays requires an active interaction between researchers engaged in multidisciplinary Tumour Microenvironment research.

In an effort to promote such interactions, we took it upon ourselves to organize multidisciplinary international conferences on the Tumour Microenvironment.

The fourth "Tumour Microenvironment" Conference was held in the Palazzo dei Congressi Florence, Italy from March 6 to March 10, 2007.

The opening session was held at the Palazzo Vecchio. Greetings by Isaac Witz, President, International Cancer Microenvironment Society, Margaret Foti CEO, American Association for Cancer Research and Raffaella Giavazzi, President, Italian Cancer Society, were followed by the opening lecture delivered by Alberto Mantovani on "Molecular Links between Inflammation and Cancer". This high priority topic was also addressed in a plenary and a symposium session. The Florence conference was unique in three parameters: First it was a joint venture between the International Cancer Microenvironment Society and the American Association for



Cancer Research. Second it was the largest Tumour Microenvironment Conference ever, and third it had a very large percentage of young researchers.

The conference was a truly multidisciplinary event where the Tumour Microenvironment was approached and discussed thoroughly by specialists from a wide spectrum of biomedical sciences. The conference met, in full, the intentions of the organizers to create a friendly forum that promotes a critical review of novel basic findings and of innovative clinical studies pertaining to the cancer microenvironment.

Over 400 scientists from 37 nations took part in this conference that dealt with cutting-edge issues in cancer biology and treatment.

There were 39 plenary lectures in 9 sessions, 58 symposium lectures presented in 7 concurrent sessions, and 153 posters. Six posters were selected to be presented in a special plenary poster session. The authors of these posters presented their results and were awarded "best poster" prizes.

The full programme as well as a picture gallery of the Florence conference can be viewed at the web site: <http://cancermicroenvironment.tau.ac.il>

# Cancer Research at Nottingham (CRN) Summer School and EACR/BACR Symposium

## University of Nottingham, UK

20 - 22 June 2007

The fourth annual CRN Summer School "New Developments in Translational Research" and the equally popular EACR-BACR Symposium which follows took place from June 20<sup>th</sup>-22<sup>nd</sup> 2007. Sponsorship and support for the events from the British Association for Cancer Research (BACR), European Association for Cancer Research (EACR), Cancer Research U.K and the Association for International Cancer Research (AICR), along with ALMAC and Merck Biosciences is gratefully acknowledged.

### CRN Summer School: 'New Developments in Translational Research'

The Summer School followed the format of the previous year, mixing teaching (overview) presentations on contemporary topics with practical demonstrations of cutting-edge technology and equipment.

The first day focused on the design

and therapeutic assessment of new cancer modalities. Charlie Laughton surveyed the pros and cons of a number of alternative approaches to drug discovery, then Tracey Bradshaw gave an overview of target-directed drug discovery, the predominant approach now used by the pharmaceutical industry. Sue Watson completed the morning session describing a number of in vivo models currently used in cancer research, and the increasingly sophisticated imaging technology available to support them.

The afternoon session began with a talk from Fred Sablitzky on transgenic mouse, embryonic stem cell, and gene targeting technologies, then Cliff Murray illustrated the realities of diagnostics developments – commercial and practical considerations may be at least as important as 'clever' science in getting a diagnostic test accepted. The afternoon tours and demonstrations covered computational methods in drug discovery and development, medicinal chemistry and structural

biology. To wrap up, the major themes of the day were summarised in a review lecture given by Alan Perkins.

The second day focused on new target discovery and validation, and began with an overview of microarray (post genomic) technologies by Paddy Tighe. Peter Shaw then discussed proteomics, providing an overview of the principles, practicalities and perspectives involved in the rapid identification of proteins within biological samples. Next, Anna Grabowska presented a review of molecular technologies for target validation, focusing on methodologies for manipulating gene expression levels and for measuring protein expression. A wide-ranging discussion of the use of tissue microarrays, immunocytochemistry and image analysis was presented by Ian Ellis. The afternoon began with a talk from Stewart Martin, who overviewed the assessment of in vitro systems, encompassing cell proliferation, cytotoxicity, apoptosis and angiogenesis assays. Tim Gant then discussed how the varying genomics techniques discussed earlier in the day found practical applications in Cancer Research. The afternoon demonstration sessions featured a range of biological techniques, including flow cytometry, microarray technologies and confocal microscopy, then the events of the day and the theme of target discovery and validation were encapsulated in a summary presentation by Anne Willis.

All the speakers and demonstrators should be congratulated for their expertise in providing broad overviews of important themes in contemporary translational cancer research. The feedback from delegates was overwhelmingly positive, and it is clear that this annual event fulfils a valuable role in the education and training of cancer researchers.



## EACR / BACR Symposium: 'Cancer Drug Discovery, Development and Evaluation'

For the last three years, the 1-day symposium on cancer drug discovery, development and evaluation that follows the summer school has provided an important opportunity to showcase the translation of recent advances in our understanding of the cellular and molecular biology of cancer into targeted therapeutic products providing real clinical benefit over existing therapies. This year's event, on the 22<sup>nd</sup> June, continued this theme and proved the most popular so far, being attended by about 100 delegates from the U.K. and overseas.

The morning session, chaired by Richard Marais (Institute for Cancer Research, Sutton, UK), started with two talks dealing with innovative treatment approaches in radiation oncology. Verena Jendrossek (Institute for Cell Biology, University of Duisburg-Essen, Germany) introduced the field in a talk entitled "Molecular radiation oncology: Targeting cell death pathways to overcome treatment resistance". She first described signalling pathways of radiation-induced cell death and associated resistance mechanisms of tumour cells and then gave several examples of molecularly targeted drugs which are actually tested in preclinical investigations and clinical trials in combination with ionising radiation.

Next, Kaye Williams (University of Manchester) in her talk "Therapeutic opportunities targeting hypoxia and HIF" discussed how hypoxia in tumours is associated with aggressive disease and treatment resistance. However, a number of therapeutic approaches are being developed that can selectively target this tumour specific phenomenon. The presentation centred the exploitation of the transcription factor HIF-1 (hypoxia-inducible factor-1) in cancer therapy. HIF-1 plays a crucial role in the adaptation of cells to low oxygen tension. It is activated under hypoxic conditions



*Left to right: John Hickman, Kaye Williams, Peter Fischer, Stephen Neidle, Malcolm Stevens, Richard Marais and Verena Jendrossek*

and induces the expression of over 70 proteins associated with survival, angiogenesis, proliferation and metabolism, amongst others. HIF-1 can be targeted in two ways in cancer therapy- it can be used to drive the expression of exogenous cytotoxic and/or drug activating proteins specifically in hypoxic cells or it can be inhibited to alter how cells respond to the hypoxic environment. Data presented demonstrated that both approaches are therapeutically effective in pre-clinical studies, especially when combined with standard chemo- or radiotherapy were hypoxia and/or HIF-1 expression are associated with poor therapeutic response.

Joan Seoane (Vall d'Hebron Research Institute, Spain) then described his research on the oncogenic role of TGF-beta in glioma. The TGF-beta oncogenic response has prompted the design of several compounds to be used as anti-TGF-beta therapies in cancer. However, it is crucial that the molecular pathways implicated in the malignant role of TGF-beta in oncogenesis are properly understood in order to select the patient population that may benefit from an anti-TGF-beta therapy.

Joan's group has demonstrated

that high TGF-beta-Smad activity is present in aggressive, highly proliferative gliomas and confers poor prognosis in patients with glioma. His work has also revealed that human glioma stem cell self renewal is regulated by TGF-beta. Glioma stem cells are considered to be responsible for glioma initiation, maintenance and recurrence, and hence are optimal therapeutic targets against this deadly disease.

The morning finished with a talk from John Hickman (Institut de Recherches Servier, France) on targetting cancer cell survival mechanisms with small molecules. Suppression of apoptosis is one of the Hallmarks of cancer. Tumour-associated evasion of apoptosis stimulated by drug treatment, of either targeted therapies or antiproliferative cytotoxics may in addition be a major contributor to drug resistance. Targeting the increased "survival potential" of cancer cells permits selective tumour cell killing by coupling tumour-associated stimuli for the activation of apoptosis (genomic damage, aberrant expression of oncogenes) to cell death: these "drivers" of apoptosis are not present in normal cells, where there is no genomic instability nor aberrant oncogene expression. BCL-2 binds to and

inhibits the pro-apoptotic activity of BAX through the binding of the alpha-helical BH3 domain of BAX to a hydrophobic pocket in BCL-2. Guided by structural biology (nmr and X-ray crystallography), elegant drug discovery programmes to generate BH3 mimetics – effectively small molecule inhibitors of this key protein-protein interaction – are providing potent and selective inducers of apoptosis in some tumours. These molecules are powerful cytotoxics but have a wide therapeutic margins in animal models. They are also able to potently synergise with minimally toxic targeted therapies, such as kinase inhibitors, since kinase inhibition initiates the canonical apoptosis pathways, inhibited by BCL-2 family members. Clinical trials of BCL-2 inhibitors are now in progress.

In the afternoon session, chaired by Peter Fischer (Nottingham), Stephen Neidle (School of Pharmacy, London) presented his recent work on “Structure-based design of small molecules targeting G-quadruplexes”.

DNA is the oldest therapeutic target in cancer. Descendants of the original mustard alkylators are still in clinical use, and have been joined by many other covalent and non-covalent DNA binding small molecules, some of which (such as cisplatin in testicular cancer), have been of major clinical benefit. However, it is also clear that cytotoxic therapy is unable to produce further significant improvements. The large amount of knowledge that we currently have about the molecular basis of cancer has resulted in a fundamental change of emphasis, so that (small molecule) cancer drug discovery is now almost entirely concerned with targeting proteins and enzymes that are directly involved in initiating or maintaining the malignant phenotype.

In his talk Stephen emphasised that this does not mean DNA is no longer a valid target. Cancer-selective proteins can be targeted either at the protein level – the preferred approach in industry at present – or at the individual gene level. Specific DNA sequences, for example in promoter regions, can be induced to

form high-order guanine quadruplex structures. These structures may be stabilised by new types of DNA-binding ligands, which as a result modulate expression. He has recently characterised the unique fold of a quadruplex in the c-kit promoter sequence, which presents novel opportunities for small-molecule based selective inhibitors of this important target. Quadruplexes are also of significance in eukaryotic telomeres; their induction by small molecules can inhibit the action of the key immortalisation enzyme telomerase. Approaches to the design and development of these small-molecule quadruplex-binding agents were also discussed.

The day finished with a talk from Malcolm Stevens (University of Nottingham), who very kindly stepped in at short notice for Ivan Dikic, who was unavoidably unable to attend. Malcolm provided a ‘chemist’s eye view’ of the process of translational research, in a wide-ranging and entertaining review of his own contributions to this area over a long and distinguished career. In an era when drug design and development is sometimes seen as a rather subsidiary activity to the investigation of cancer biology, his talk emphasised the many pitfalls and potholes along the road from “a target wannabe” to a drug molecule that really makes it in the clinic, and provided strong support for a higher profile for chemistry in the future, an aspiration that now seems to be gaining support in the guise of chemical biology and chemical genomics focussed initiatives.

The day provided the audience with a fascinating insight into cancer drug discovery and development from the bench to the clinic, and the speakers should be congratulated on the quality and breadth of their presentations, which will serve as an inspiration to researchers to more effectively translate basic research findings into therapeutic products that ultimately benefit the cancer patient.

*Stewart Martin and Charlie Laughton*

**Please see Page 48 for information about the 2008 Summer School and Symposium**

**The EACR  
University of Nottingham  
School of Pharmacy**

**Second Annual Lecture**

Professor Peter Parker

Protein Phosphorylation  
Laboratory,  
London Research Institute,  
UK



“Protein Kinase C – dividing and migrating”

Wednesday May 7th 2008

1.00 pm

Boots Science Building B34

For further details please contact  
[kathryn.wass@nottingham.ac.uk](mailto:kathryn.wass@nottingham.ac.uk)

**The EACR  
University of Nottingham  
School of Pharmacy**

**Inaugural Annual Lecture  
2007**

Heike Allgayer



Differential regulation  
of the u-PAR- from the  
bench to new prognostic  
high-risk groups and  
molecular  
staging models

# The Genes and Cancer Meeting

## University of Warwick

### Warwick

### UK

### 10 - 12 December 2007

As with previous meetings, the 2007 Genes and Cancer meeting proved to be an excellent conference, with a high calibre lineup of speakers who gave a series of outstanding talks. This year there was a record number of posters which created a vibrant poster session. The quality of the posters was very high making judging for the poster prize particularly difficult.

The conference was split into four sessions, loosely based around common topics. The first session was centred on various aspects of gene expression in cancer. Barbara Graves opened the conference with a talk on the ETS family of transcription factors. These are associated with various tumourigenic processes, but it is currently unclear how different family members give specific effects. By using ChIP-chip analysis Barbara nicely demonstrated that both the normal ETS transcription factors and oncogenic fusion proteins regulate overlapping and distinct sets of target genes. Subsequent talks focussed on the NF- $\kappa$ B pathway (by Vishva Dixit and Michael Hottiger) and highlighted the importance of post-translational modifications such as acetylation in controlling transcription factor activity and polyubiquitin chains in promoting the assembly of signalling complexes. The theme of acetylation and ubiquitination was maintained through structural insights into histone acetyl transferases (Ronen Marmorstein) and the role of the E3 ligase arcadia in Smad pathway signalling (Caroline Hill). Insights into the control of p63 by ubiquitin-dependent proteolysis were provided by Gerry Melino. The last talk in this session by Bob White presented the incredible finding that overexpression of a tRNA molecule, and hence an increase in protein synthesis, is sufficient to cause cancer.

Steve West gave a fantastic keynote lecture focussing on defects in DNA repair and recombination in human

diseases, and in particular nicely dissected the molecular mechanisms underlying neurodegeneration due to impaired repair of damaged DNA resulting from defective APTX function. Subsequent talks extended this theme of DNA repair defects in cancer with initial focus on the role of ubiquitination of RNA polymerase II in controlling the fate of polymerase stalled at DNA damage sites (Jesper Svejstrup). Ashok Venkitaraman discussed the interplay between BRCA2 and the Rad51 recombinase and demonstrated that Rad51 has an important role after the completion of S phase and hence DNA replication. Further studies on DNA replication demonstrated how cyclin-dependent kinases can control replication origin firing through promoting regulatory protein complex assembly (John Diffley). Further talks illustrated how double strand breaks initiate signalling events in the cell (John Rouse) and how kinetochores are controlled through microtubule attachment during the normal cell cycle (Tomo Tanaka).

The third session was on signalling and metastasis and Peter Friedl gave a fantastic talk with excellent movies that illustrated how tumour cells can metastasise by either amoeboid or mesenchymal like migration mechanisms. Interestingly, when adopting amoeboid like movement in dense matrices, the strain on the nucleus generated stress that gave rise to DNA damage foci, which is likely to be important in the context of cancer development. Further insights into metastatic mechanisms were provided by Anne Ridley in her discussion of RhoE and its activation. Owen Samson illustrated the importance of myc upregulation in response to Wnt signalling in colon cancer. Finally, we got a glimpse of the power of mass spectrometry applied to phosphoproteomics (Forest White). Studies focussed on the HER2 and EGFR receptors and how differing amounts could give rise

to different signalling responses. This in turn could be used to predict key nodes for therapeutic intervention.

The final day revolved around senescence and apoptosis. Eyal Gottlieb illustrated how phospholipids and their aberrant metabolism could disrupt apoptotic mechanisms. The apoptotic theme was continued by Pascal Meier who used a Drosophila system to demonstrate the importance of IAP as a ubiquitin E3 ligase which causes polyubiquitination of caspase and hence its inactivation. An alternative form of death, mediated by lysosomes was also discussed and the importance of upregulation of Hsp70 proteins in promoting cancer cell survival by stopping lysosomal permeabilisation was illustrated (Marja Jaattela). Finally, two talks focussed on senescent pathways and their disruption in cancer cells. Two important findings were that PKC $\downarrow$  plays an important role in oncogene-mediated senescence through blocking cells in G2 (Eiji Hara) and that senescent cells are associated with a persistent DNA damage response (Fabrizio d'Adda di Fagnagna).

Overall, the meeting was uniformly excellent and addressed many of the important key molecular questions in the cancer research field. We look forward in anticipation to another excellent meeting next year which will be the 25th consecutive annual meeting that has followed cancer research developments since people first began to begin to apply molecular biology to address this important area.

*Andy Sharrocks (Chair of the organising committee, 2007)*

**The  
Genes and Cancer  
meeting  
2008**

*will be announced in the  
EACR e-news  
bulletin to members  
and on the  
EACR website*

# SENECA 2007: From Cellular Senescence and Cell Death to Cancer and Ageing Warsaw, Poland 4 - 6 October 2007

The main goal of the conference was to provide a forum for scientific exchange among leading scientists working in the fields of ageing and cancer as well as to stimulate cooperation aimed at redefining molecular targets and improving cancer prevention and therapeutics in the ageing population. The discussion focused around such issues as DNA damage, telomeres and telomerase in cancer and ageing, effects of tissue environment in tumour formation, impact of the ageing immune system on cancer, immunosurveillance and immunotherapy, links between stem cells, cancer and ageing, links between tumour suppression and cellular senescence, and cellular senescence as a new target in anticancer therapy.



*Beatrice Lucaroni*

The SENECA Conference was one of the most exciting and important meetings in cancer and ageing research in 2007. It brought together a diverse group of outstanding scientists at the forefront of those two areas of research. Over 30 outstanding researchers from around the world gave excellent and inspiring lectures in 6 thematic sessions, including Biodemography moderated by Prof. Anatoly Yashin from the Duke University (USA), Maintenance of Genomic Integrity moderated by Prof. Jan H. J. Hoeijmakers from the Erasmus Medical Centre (The Netherlands), Cell Death and



*Julio Celis*

Cellular Senescence moderated by Prof. Judith Campisi from the Buck Institute (USA), Immunosenescence and Immunotherapy moderated by Prof. Graham Pawelec from the University of Tuebingen (Germany), Stem Cells session moderated by Dr Derrick Rossi from the Stanford University (USA) and the Host-Tumour Relationship session moderated by Prof. Vladimir Anisimov from N.N. Petrov Research Institute of Oncology (Russian Fed.)

The organizers supported active participation in the Conference of young scientists and students, granting 31 fellowships for Early Stage and Early Career Researchers. Overall the conference gathered participants representing eighteen countries who gave oral and poster presentations on a variety of topics related to the conference theme and an audience of over 120 people from 22 countries. Summary publications of scientific results presented at the conference will appear in the EMBO journal as a Conference Summary Report and as a collection of thematic articles in Mechanisms of Ageing and Development journal.

*Marcin Szumowski*

*EACR greatly appreciated the invitation to this important meeting and the opportunity to introduce the Association to delegates in the opening session*



*EACR Secretary General, Richard Marais and President Elect Anne-Lise Borresen-Dale study the programme at the EACR stand during ECCO-14 in Barcelona*



*Andrew Binns, EACR's Administrator (Member Services) and Kathryn Wass, EACR's Senior Administrator, took charge of the EACR information stand at a number of European Meetings this year. Numerous colleagues took the opportunity to join EACR while attending a meeting in 2007*



*Sponsored Meetings: EACR is able to support a number of important scientific meetings each year and organisers who are seeking sponsorship, and wish to work in partnership with EACR, should contact Kathryn Wass for further information and guidance*