Scientific Programme – Details

Tuesday 18 November 2014

Opening Ceremony **Auditorium**

13:00–13:15 Opening Remarks

13:00	*J.C. Soria (France)*	EORTC
13:05	*L.J. Helman (USA)*	NCI
13:10	*J.A. Engelman (USA)*	AACR

13:15–14:00 **Michel Clavel Lecture** **Auditorium**
Chair: J.C. Soria (France)

13:15 Rational combination therapies for cancer
R. Bernards (Netherlands)

14:00–14:45 **Keynote Lecture** **Auditorium**
Chair: A.M.M. Eggermont (France)

14:00 Immunocheckpoints – Gateway to Immunotherapy
D. Chen (USA)

Objectives:
1. Understand how cancer immunotherapy works, the cancer-immunity cycle and what makes it different from other forms of cancer therapy.
2. Understand what rationale approaches can be taken to monotherapy and combination therapy involving cancer immunotherapy.
3. Understand the role for biomarkers in understanding emerging immune biology, interpreting clinical results and identifying optimal treatment decisions.

Key Messages:
1. Our understanding of how the immune system interacts with cancer is rapidly evolving.
2. Cancer immunotherapy approaches may be able to generate durable responses in patients with metastatic cancer.
3. Emerging biomarkers may be able to help us understand biology, define combination approaches and choose between therapeutic options.

Plenary Session 1 **Auditorium**

15:15–17:30 **Is the Genomic Landscape Changing the Outcome for Cancer Patients?** Abstract number
Chairs: R. Stupp (Switzerland) and J. Tabernero (Spain)

15:15 Overview of academic precision medicine trials
P. Bedard (Canada)

15:35 Lessons from SAFIR01 trial
F. Andre (France)

Main objectives:
1. Understand the pillars of personalised medicine.
2. Understand the main reasons of failures to deliver personalised medicine.
3. Understand what are the possible solutions to address these limitations.

Key messages:
1. There is a need for randomised trials before implementing multigene tools for personalised medicine.
2. Drug availability and rules to interpret genome data are mandatory.
3. Genome analysis will not provide all the informations needed to deliver personalised medicine.

15:55 Translating gene expression signatures into clinical practice: prospects and challenges in the context of 'next-generation medicine'
R. Dienstmann (USA)

Key messages:
1. There are unique issues with high-dimensional data that represent obstacles to generating performant genomic signature classifiers and translating initial research findings into robust diagnostics.
2. Better understanding of the intrinsic gene expression-based subtypes of a histopathologically defined cancer, independent of their prognostic and predictive values, may also lead to new biological insights and eventually to development of novel therapies directed toward homogeneous molecular subsets.
3. A rational and focused approach to the evaluation of genomic markers is needed, whereby analytically validated assays are prospectively investigated in clinical trials with adaptive designs that take into consideration primary–metastatic site tumour heterogeneity and clonal evolution in the decision-making process.

16:15 Genomic characterisation of cancer: Case studies
E.R. Mardis (USA)

Key objectives:
1. Provide detailed description of the molecular assays being used to characterise the cancer mutations and their expression in RNA for individual patients.
2. Describe the analytical approaches that permit integrated analysis of mutations and RNA expression toward two therapeutic ends: (1) identification of small molecule therapies that may provide relief of tumour burden, (2) identification of immunoepitopes that may contribute toward a personalised vaccine strategy for individual patients.
3. Illustrate the two aforementioned objectives by detailed descriptions of specific case studies from our work in this area of applied cancer genomics.

16:35 Screening Patients for Efficient Clinical Trial Access (SPECTA)
D. Lacombe (Belgium)

Key messages:
1. Cancer drug development is undergoing profound changes and the path to registration will be substantially altered due to challenges of big data (omics).
2. The forms and the methods of cancer clinical research are evolving with the need to integrate new technologies to understand biology early on in development. New efficient platforms for patient access (molecularly defined subgroups) are needed.
3. Clinical oncology will need to take into account new type of guidelines for treatment decision with an increased role played by molecular advisory boards.

16:55 ORAL PRESENTATION: Feasibility of large-scale genomic testing to facilitate enrollment on genomically-matched clinical trials 1
F. Meric-Bernstam, L. Brusco, S. Kopetz, M. Davies, M.J. Routbort, S.A. Piha-Paul, R. Alvarez, S. Khose, J. DeGroot, V. Ravi, F. Janku, D. Hong, Y. Li, R. Luthra, K.P. Patel, R. Broaddus, K. Shaw, J. Mendelsohn, G.B. Mills

17:10 General discussion
J. Tabernero (Spain)

17:15 Faster execution of clinical trials – has bioinformatics the solution?
G. McVie (Italy)