
The Pezcoller Foundation Symposia

13th Pezcoller Symposium:

Focusing Analytical Tools on Complexity in Cancer

May 31 – June 2, 2000 Rovereto, Italy

Co-chairs:

E. Mihich, Jean Feunteun and Stephen Friend

Program Committee:

David Livingston, Giorgio Parisi, Lee Hartwell

This Symposium will be held in Rovereto, Italy, from May 31 to June 2, 2001; the program has been organized by the Co.Chairmen, J.Feunteun, S.Friend and E. Mihich, with the aid of Program Committee Members, L. Hartwell, D.Livingston and G. Parisi.

It is becoming increasingly evident that the physiopathology of cancer cells is the result of very complex signaling networks which represent in many cases distortions of the orderly networks regulating the physiology of normal cells. Basically these networks are the consequence of the expression of, or the lack of expression of, genes, mutated or not, which represent the genomic profile of different types of, or of individual cancers. The complex signaling pathways, the cross-talk among them and the redundancies existing for several of them mediate not only the transmission of signals from the cell environment to the nucleus but also that from the nucleus to the other cellular components whose function is involved in cell proliferation, apoptosis or differentiation.

Modern approaches to cancer therapy and also prevention are aimed at identifying new molecular targets, pivotal to the life of the cancer cell, which would provide for specific sites of intervention. In the face of the enormous complexity of the phenomena mentioned above on which the life of cancer cells is based, it is both difficult to identify unique specific targets for intervention and important to develop analytical tools and approaches capable to identify them for further exploitation. This will be the main all-encompassing subject of the Symposium.

Specific consideration will be given to: 1) Expression array analysis by which to identify determinants of specific characteristics of the cancer cell; 2) Tumor genotype analysis to identify expression profiles affecting cell regulations; 3) Approaches to visualize profitable new targets for antitumor action; 4) Multifactorial analysis of the complex interactions regulating cancer cells and their responses to endogenous and/or exogenous stimuli, and 5) Methods to comprehend the complexities of molecular models and validate their functional relevance. As the Program will include 30 minute talks each followed by a 30 minute discussion, it is expected that ample opportunities will be available for cross-stimulation and synergistic interaction among participants.

Program

May 31

- 8:30 Registration
- 9:00 Pezcoller Foundation Officers *Welcome & Introductory Remarks*
9:15 Enrico Mihich *Focus & Goals*

AM, Session I, Expression Array Analysis

Co-Chairs: Marco Pierotti and Jean Feunteun

- 9:30 Joe Gray *Genoma Evolution in Breast Cancer-thoughts on mechanisms and interventions*
10:00 Discussion
- 10:30 Coffee Break
- 11:00 Tood Golub *Transcriptional Profiling in Cancer*
11:30 Discussion
- 12:00 Olli P. Kallioniemi *Microarray Analysis of Cancer Progression*
12:30 Discussion
- 13:00 Lunch

PM, Session II, Tumor Genotype Analysis

Co-Chairs: Thomas Tursz and Carlo Croce

- 14:00 Raju Kucherlapati *Genetic Analysis of Tumors from Mouse Models of Colorectal Cancer*
14:30 Discussion
- 15:00 Anne-Lise Borresen-Dale *Tumor Genotype Analysis from Studies of Breast Cancer*
15:30 Discussion
- 16:00 Coffee Break
- 16:30 Michael Stratton* *Genome-wide searches for mutations in cancer*
17:00 Discussion
- 17:30 General Discussion
- 18:00 Adjourn

June 1

AM, Session III, Deciding anti-tumor targets

Co-Chairs: David Livingston, Alex Matter

- 8:30 Steve Friend *Genomic Sensor Pads and Pattern Recognition: Impacting both the discovery and development of drugs.*
- 9:00 Discussion
- 9:30 Charles Sawyers *Signal Transduction Abnormalities in Prostate Cancer: Therapeutic Implications*
10:00 Discussion

10:30 *Coffee Break*

11:00 Pier Paolo Pandolfi* *Modeling Cancer in the Mouse and its Therapeutic Implications*

11:30 *Discussion*

12:00 *General Discussion*

13:00 *Lunch*

14:00 **Poster Session**

PM, Session IV, Multifactorial Analysis

Co-Chairs: Pablo Tamayo, John Weinstein

15:00 Eric Shadt *Microarray-measured Transcript Abundances Considered as Quantitative Traits in Genetic Studies*

15:30 *Discussion*

16:00 *Coffee Break*

16:30 Mark Lathrop *Genetic Epidemiology of Human Disease*

16:30 *Discussion*

17:30 Carol Kovac *Perspectives and future directions*

18:00 *Discussion*

18:30 *General Discussion*

19:00 *Adjourn*

June 2

AM, Session V, Understanding Models Complexity

Co-Chairs: Giorgio Parisi, Roberto Di Lauro

8:00 Anton Berns *New Conditional Mouse Models for Sporadic Cancer*

8:30 *Discussion*

9:00 Lucio Luzzatto *Paroxysmal Nocturnal Hemoglobinuria (PNH): a Clonal Disorder and a Model for Darwinian Selection of Mutant Somatic Cells*

10:00 *Discussion*

10:00 *Coffee Break*

10:30 Sydney Brenner *Is Complexity in the Mind of the Beholder ?*

11:00 *Discussion*

11:30 Sydney Brenner *Concluding Remarks*

12:00 *Lunch*

14:00 *Adjourn*