Amalio Telenti - MD, PhD
Director Institute of Microbiology - University of Lausanne
A. Telenti, MD (Infectious Diseases) and PhD (Microbiology) trained in internal medicine and infectious diseases at the Mayo Clinic, Rochester, Minnesota, in microbiology research at the university of Berne, Switzerland and at the Albert Einstein College of Medicine, New York.
Dr. Telenti primary scientific interest is in the field of host genetics and pharmacogenetics in HIV disease. He is member of the Swiss HIV CohortStudy, and member of the scientific executive board of SystemsX.ch, the Swiss national program for Systems Biology.

Interview by
Stefano Rusconi
Ospedale Luigi Sacco– Milano

Prof. Amalio Telenti
ICAR: Italian Conference on Aids and Retrovirus- TORINO
May 12-14, 2013

Stefano Rusconi:
When does genomics meet HIV?

Prof. Telenti:
This was the title of a Perspective paper I co-authored with the geneticist David Goldstein. It was intended to highlight the opportunity to study HIV biology and pathogenesis using a new set of tools that became available around 2007.
In fact genetics (as opposed to genomics) had been important to the discovery of CCR5 deletions (in 1996), and showing the relevance of different HLA class I alleles on disease progression toward the end of the 90s.

Stefano Rusconi:
Are there feasible measurements to prevent drug toxicity?

Prof. Telenti:
From the pharmacogenetic standpoint we have some tools that could help limit some of the toxicities observed. One test, measurement of HLA-B*57.01, is in clinical use for the prevention of abacavir hypersensitivity. Other tests are possible but have not been used routinely to prevent high drug levels of efavirenz and consequent toxicity, to avoid Gilbert's syndrome associated with atazanavir, and to identify a genetic predisposition to cardiovascular risk and metabolic complications in an HIV treatment setting.

Stefano Rusconi:
What about HIV eradication and genomics?

Prof. Telenti:
Genomic analyses have been identified by the HIV Cure Research Agenda published in 2012 in Nature Reviews in Immunology as a priority approach towards understanding the transcriptional features of the process of latency, identification of biomarkers and chromatin status at HIV integration sites. Several groups are using these approaches, and I expect their investigations will contribute to the field.