J. Cell. Mol. Med. Vol 13, No 10, 2009 pp. 4089

Impact of tumour genotyping on cancer management

Gianni Bussolati *

Department of Biomedical Science and Human Oncology, University of Turin, Turino, Italy

Genetic, epigenetic and transcriptomic analyses, hastily conduced for over 20 years, have greatly improved our understanding and classification of tumours and the bulk of accrued information is really overwhelming, since more than 118,000 articles appear in an online search focused on 'genetic and neoplasms'.

The interest of tumour genotyping was originally linked to disclosure of causes of tumours development and evolution, but slowly evidence emerged of how genomic sub-classifications could be established, and of their prognostic and therapeutic interest, particularly in the subset of tailored therapies.

The holistic concept of cancer has been subsidized and characterization of genetic features of single cases is gradually emerging as the area of interest both, for research and clinical application. This evolution involved the development of several techniques, such as microarray-based gene expression profiling and comparative genomic hybridization technologies, translational silencing, gene sequencing and transfer, microRNA profiling and epigenetic silencing of tumour suppressor genes.

A crucial point of this field of genetic studies on cancer can be referred to the seminal study on breast cancer by the Stanford group [1], which led to the identification of five molecular groups. The related classification is now widely accepted and show definite clinical implications [2].

A similar approach has now been applied to tumours of different sites, particularly of soft tissues, lung, colon, brain and haematopoietic system [3–6].

Time is ripe for affording the question of the present role and impact of molecular genotyping on the clinical management of tumours, and so the present Review Series is aiming to provide the status of the art. Well-known experts will give our update on the impact of tumour genotyping on the management of different tumours, understandably starting from the breast. Further reviews will follow, dedicated to tumour from other sites.

Clinical management of cancer patients is still mainly based on a morphological basis, that is histopathological typing and staging supported with additional data from morphology-based procedure as immunohistochemistry and fluorescent *in situ* hybridization. It is an easy prediction that genetic analysis will not substitute, but complement pathological data and open new prospects. For pathologists, this should represent a challenge and a stimulus [7].

References

1. **Perou CM, Sorlie T, Eisen MB, *et al.*** Molecular portraits of human breast tumours. *Nature.* 2000; 406: 747–52.
2. **Sotiriou C, Pusztai L.** Gene-expression signatures in breast cancer. *N Engl J Med.* 2009; 360: 790–800.
3. **Kanu OO, Mehta A, Di C, *et al.*** Glioblastoma multiforme: a review of therapeutic targets. *Expert Opin Ther Targets.* 2009; 13: 701–18.
4. **Osuna D, de Alava E.** Molecular pathology of sarcomas. *Rev Recent Clin Trials.* 2009; 4: 12–26.
5. **Swanton C, Caldas C.** Molecular classification of solid tumours: towards pathway-driven therapeutics. *Br J Cancer.* 2009; 100: 1517–22.
6. **Walther A, Johnstone E, Swanton C, *et al.*** Genetic prognostic and predictive markers in colorectal cancer. *Nat Rev Cancer.* 2009; 9: 489–99.
7. **Walk EE.** The role of pathologists in the era of personalized medicine. *Arch Pathol Lab Med.* 2009; 133: 605–10.

*Correspondence to: Prof. Gianni BUSSOLATI,
University of Turin, Biomedical Science and Human Oncology
Via Santena, 7 Turin, 10126 Italy

Tel.: +39-011-6334274
Fax: +39-011-6635267
E-mail: gianni.bussolati@unito.it

doi:10.1111/j.1582-4934.2009.00883.x