

also promotes cell proliferation and oncogenic transformation [1]. The tumour suppressors RB and p53 keep tRNA expression under tight control by binding and directly repressing the pol III-specific transcription factor TFIIB [2,3]. Inactivation of RB and/or p53 in cancer cells releases TFIIB from restraint, allowing tRNA expression to rise. The situation is aggravated by several oncogene products that further stimulate tRNA production. For example, c-Myc binds directly to TFIIB and raises pol III transcription [4]. Furthermore, mTOR associates with tRNA genes and stimulates their expression in response to signaling from Ras, Akt and PI3 kinases [5]. Combinations of these molecular events ensure elevated tRNA levels in most if not all tumours [6].

## References

- [1] Marshall et al. (2008) *Cell* 133, 78–89.
- [2] White et al. (1996) *Nature* 382, 88–90.
- [3] Cairns & White (1998) *EMBO J* 17, 3112–3123.
- [4] Gomez-Roman et al. (2003) *Nature* 421, 290–294.
- [5] Kantidakis et al. (2010) *PNAS* 107, 11823–11828.
- [6] Marshall & White (2008) *Nature Rev Cancer* 8, 911–914.

## 15

INVITED

### Small RNA Regulators of Gene Expression

P. Sharp<sup>1</sup>. <sup>1</sup>Massachusetts Institute of Technology, Koch Institute and Department of Biology, Cambridge, USA

About fifty years ago the central role of RNA in life sciences was recognized with the discovery of t-RNA, ribosomal RNA and mRNA. A little over ten years ago with the discovery of RNA interference (RNAi), the generality of regulation of gene expression by RNA became apparent. Since then, the biology and biochemistry of small RNAs such as siRNAs, miRNAs and piRNAs have been investigated in many model systems. Over half of all mRNAs in mammalian cells are targets of miRNA and changes in miRNA activity are important in differentiation, growth and control of cell death. Although some miRNAs function as oncogenes where increases in expression promote tumour formation, it is much more common to find loss of miRNA activity as an important event in the development of a tumour. In this mode, miRNAs act as tumour suppressors. In fact, even though miRNAs are critical for normal development and differentiation, many cell lines are viable when the synthesis of all miRNAs is blocked by deletion of a gene essential for their production, Dicer. This puzzling finding suggests that miRNAs have a general role of providing robustness to systems so that transitions between cell states are balanced through the interactions of feed forward and feed backward systems. The small degree of change in gene expression upon loss of miRNAs indicates that they fine-tune protein expression in cells under steady state conditions. As part of the cellular system, the synthesis of miRNAs is regulated at levels of transcription, processing and stability. Developing an integrated concept of the roles of miRNAs will also require understanding their ability to buffer the response of cells to stress.

Deep sequencing of RNA from mammalian cells has revealed classes of small and large non-coding RNAs that are present at approximately one copy per cell. The functions of these RNAs in normal or disease states are not well established. However, there is growing confidence that RNAs can bridge between sequence-specific DNA recognition processes and regulator complexes. One example of this is the recognition of splicing signals in nascent RNA and control of elongation by RNA polymerase.

## Scientific Symposium (Sat, 24 Sep, 11:15–13:15) Molecular Imaging of Hypoxia

## 16

INVITED

### Imaging of Hypoxia With PET Radiotracers, Including, Ca-IX Antibodies

H. Schöder<sup>1</sup>. <sup>1</sup>Memorial Sloan-Kettering Cancer Center, Nuclear Medicine Service, New York NY, USA

Hypoxia in tumours occurs when cell proliferation exceeds the rate of angiogenesis; tumour cells are then pushed beyond the boundaries for oxygen diffusion. In cancers, hypoxia is an indicator of poor prognosis, regardless of the treatment modality employed. It is probably one of the leading causes of radio- and chemotherapy failure. Hypoxia imaging with positron emission tomography (PET) is a non-invasive way of measuring regions of low partial oxygen pressure within the tumour tissue. A number of compounds are available for hypoxia imaging. In the past, most studies have used <sup>18</sup>F FMISO; other agents in clinical trials include <sup>18</sup>F EF5, <sup>60/64</sup>Cu-ATSM, <sup>18</sup>F-FETNIM and <sup>18</sup>F-FAZA. The ideal hypoxia

tracer should show high specific uptake and irreversible retention in hypoxic cells, low background activity in normoxic tissues, chemical stability against enzymatic cleavage in blood, rapid blood clearance enabling early imaging, and scan findings should be reproducible. None of the currently available agents meets all of these requirements. Current clinical trials are investigating the utility of hypoxia tracers for prognostication, radiotherapy target volume planning, and response prediction. For instance, a current multicenter trial with <sup>64</sup>Cu ATSM is investigating the prognostic value of hypoxia imaging in cervical cancer. Similar studies are ongoing with <sup>18</sup>F FMISO and <sup>18</sup>F FAZA in head and neck and rectal cancer. Ultimately, this should lead to changes in therapy regimens for hypoxic cancers (which are resistant to standard therapy). For instance, one clinical trial will investigate if therapy with the VEGF antibody bevacizumab can decrease tumour hypoxia in lung cancer and thus improve treatment response (as compared to chemotherapy alone) and patient outcome. Carbonic anhydrase IX (Ca-IX) is an enzyme that is overexpressed in many hypoxic tumours because it is a downstream target of HIF-1 $\alpha$ ; it is involved in pH regulation. Ca-IX expression can be imaged with the chimeric antibody cG250 labelled with <sup>124</sup>Iodine or <sup>89</sup>Zr. Whereas full antibodies may be suboptimal for clinical imaging (long blood circulation time; large size limits tissue penetration), smaller molecules including antibody fragments relying on the same principle, may be more suitable. In hypoxic tumour xenografts, the antibody fragment <sup>89</sup>Zr-cG250-F(ab')<sub>2</sub> showed good correlation with tissue expression of Ca-IX, thus providing the rationale for future clinical trials.

## 17

INVITED

### Interest of Functional Imaging to Guide Stereotactic Radiotherapy

E. Lartigau<sup>1</sup>. <sup>1</sup>Centre Oscar Lambret, Radiotherapy Department, Lille, France

Stereotactic Body Radiotherapy (SBRT) is used for the treatment of patients with early stage non-small cell lung cancer (T1-T2 N0M0), liver or prostate cancer.

The definition of treatment target and the evaluation of the treatment's efficacy remains a challenge and, for follow up, it is often difficult to distinguish progression and therapeutic response.

As an example, the target definition for lung tumours is based on PET CT images, CT slices remaining the main informative tool. For liver and prostate, the role of MRI is increasing and the place of functional MRI starts to be crucial in case of partial treatments (prostate boost).

Some issues are specific of SBRT and radiographic features after lung SBRT are significantly different from the images found after standard conformal three-dimensional radiation therapy, in both patterns and chronology. Early (lung injury) and late (lung fibrosis) toxicity must be known in order to differentiate progression from therapeutic response.

The role of functional imaging (PET and MRI) will be described in various clinical situations.

## 18

INVITED

### Imaging of Hypoxia (HIF-1 $\alpha$ ) With Genetically Encoded Reporter Genes

I. Serganova<sup>1</sup>, R. Blasberg<sup>1</sup>. <sup>1</sup>Memorial Sloan Kettering Cancer Center (MSKCC), Departments of Neurology and Radiology, Molecular Pharmacology & Chemistry Program, SKI, New York, USA

Hypoxia is an important factor involved in the progression of solid tumours, and alters tumour metabolism, angiogenesis and metastasis. Adaptation to hypoxia at the cellular or organism level is predominantly regulated by hypoxia inducible factors 1 and 2. HIF-1 $\alpha$ , the most studied factor, is frequently activated by genetic alterations and by oncogenic pathway activation (e.g., cMYC, PI3K, MAPK, HSF1), in addition to physical hypoxia. HIF-2 $\alpha$  expression has been linked to poor patient outcome in several tumour types, and was detected in tumour stem cells, but not in non-stem tumour cells or normal progenitor cells. The precise role of HIF-2 $\alpha$ , in comparison to that of HIF-1 $\alpha$ , in target gene activation and in tumour progression remains unclear.

The mechanisms of hypoxia-dependent stabilization of the HIF-1 $\alpha$  and HIF-2 $\alpha$  proteins and their mode of transcriptional activation are thought to be similar. The oxygen sensing mechanism controlling protein stability of the HIF- $\alpha$  subunits occurs through a post-translational modification within the oxygen-dependent degradation domain (ODDD), and is carried out by HIF-specific prolyl hydroxylase-domain proteins (PHDs). The PHDs hydroxylate two conserved proline residues; the prolyl hydroxylated HIF- $\alpha$  subunits are recognized by the von-Hippel Lindau (VHL) tumour suppressor protein which is part of a multiprotein E3 ubiquitin-ligase that polyubiquitylates and targets HIF- $\alpha$  for proteasomal degradation. The O<sub>2</sub>-independent degradation of HIF-1 $\alpha$  occurs by the competitive binding to either heat shock protein 90 (HSP90), which stabilizes the protein,