Neurofibromatosis and lessons for the war on cancer

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In the war on cancer, a great deal of attention is being paid to knowing the ‘enemy’. It is widely believed that by understanding the driving forces underlying cancer, researchers can develop better ways to target the disease. Currently, large-scale efforts have been undertaken to completely characterize molecular changes in common human cancers (http://cancergenome.nih.gov/) (Collins & Barker, 2007). However, as more is learned about cancer, the debate increases on what exactly the enemy is: cells making up the bulk of the tumour, rare tumour stem cells that can regrow the tumour, tumour microenvironment, the subset of cancer cells with metastatic potential, etc. Studies of the cancers associated with Neurofibromatosis type 1 (NF1) are helping to define the relationship between many of these different cell types. It is still unclear how these different enemies are related to each other and how they interact to wage cancer’s war on the patient.

‘If you know the enemy and know yourself you need not fear the results of a hundred battles.’ – Sun Tzu, The Art of War, c. 500 B.C.

One of the greatest difficulties in fighting cancer is that pathways and mechanisms used by cancer are so closely related to pathways important for development and normal functioning. As an example, Ras signalling is important in a wide variety of normal biological functions, but serves as a key pathway in tumourigenesis. The question then arises how to kill cancer without hurting the patient, and hence the ‘know yourself’ becomes as important a part of winning the war on cancer as ‘know the enemy.’

The familial genetic disease NF1 illustrates the difficulty of defining where self ends and the tumour enemy begins. NF1 patients carry a mutation in the tumour suppressor gene, NF1. NF1 encodes the protein neurofibromin that down-regulates Ras from the active to inactive form.

... for NF1 patients, ‘normal’ cells are not completely normal and may already be along a continuum of tumourigenesis, ...
open question as to whether these two types are distinct tumours with different cells of origin along the SC lineage and different genetic alterations, or whether the differences between these tumours is due to the environmental constraints of where they initiate in the peripheral nervous system. This is particularly interesting to consider in light of their different propensities to progress to malignancy, and could have instructive implications for other cancers where one needs to determine which benign tumours will undergo malignant transformation.

In the article by Miller et al, 2009 (please see page 236 in this issue), the NF1 microarray consortium has addressed the question of the relationship between DNF, PNF and MPNSTs through analysis of the SC compartment. They isolated normal SCs, and SCs from DNFs and PNFs, and MPNSTs cell lines, comparing them using gene expression analysis. In addition, they compared the SC signature to the signature of the whole tumours (DNFs, PNFs and MPNSTs). Interestingly, they have found no significant differences between DNF SCs and PNF SCs, suggesting that these tumours have different characteristics due to the effects of surrounding stromal cells, local environment or developmental timing of tumourigenesis. The comparison between isolated SCs and the neurofibromas, or between cultured MPNST cell lines and MPNSTs, showed different gene expression patterns that could represent the stromal cell signature. Alternatively, as the authors note, the differences between DNFs and PNFs may be due to a very small subpopulation of cells in the tumour (cancer stem cells) that are masked in the microarray analysis. The data demonstrate that the bulk of tumour cells in DNF and PNF are far more similar than would have been predicted by observation of these physically very distinct tumours.

The article also highlights the relationship between normal development and cancer. In analysing gene expression signatures that distinguish normal, benign and malignant cell types, they found links to neurogenesis, morphogenesis, skeletal development and nervous system development. By analysing gene clusters with respect to neural crest and SC development, they found that genes associated with early stages of neural crest migration were associated with tumours, whereas genes activated later in SC development were downregulated. This highlights the importance of understanding ‘self’ and the normal developmental processes to better characterize the state of the tumours.

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Figure 1. Different types of neurofibromas in NF1 patients: DNFs form from smaller nerves near the skin, whereas PNFs form from larger nerve bundles in the body. PNFs can transform into MPNSTs, whereas DNFs do not.

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MPNSTs from other sarcomas is often inconclusive due to a lack of tumour markers. The most commonly used marker, S100, is expressed to varying degrees by other tumour types, and is not expressed by all MPNSTs. Miller et al have found that Sox9 is a promising candidate for distinguishing MPNSTs from other tumour types, and shows differences in the number of positive cells and the degree of nuclear localization in DNFs, PNFs and MPNSTs, suggesting that this marker could aid in grading neurofibromas and MPNSTs. Finally, Miller et al demonstrate that Sox9 is functionally important for tumour cell survival, raising the possibility that Sox9 is an oncogene that could be used as a target for therapy.

In all, Miller et al has provided a detailed look at the similarities and differences between normal and tumour cell types, identifying an important marker and therapeutic target, Sox9. These data provide interesting insights into the relationship between benign quiescent tumours and benign tumours that can progress to malignancy. A better understanding of neurofibromas and MPNSTs has the potential to greatly improve the lives of NF1 patients, as well as serving as a general model for progression to be tested in other more common cancers.

The author declares that she has no conflict of interest.

References