

P018 Profiling non-Hodgkin's lymphoma cell lines using translation cDNA microarray

P.J. Goodrem, M. Bushell and A.E. Willis

Nottingham University

Several studies have been carried out using cDNA microarrays to construct gene profiles of Non Hodgkin's Lymphoma (NHL) cell lines and tumours. These transcription array studies have identified disease subtypes, and classified existing conditions into tighter boundaries. However, using translational profiling, we have been able to construct new profiles in a number of NHL cell lines that may open avenues for the identification of possible novel therapeutic targets. Using sucrose density gradients to fractionate highly translated messages from the less translated messages; and cDNA microarrays, we have been able to identify genes highly expressed at the protein level. Furthermore, they display high levels of translational control that has been shown to be important in a number of other cancer-associated genes, most notably the *myc* genes. We have initially chosen to examine a panel of NHL cell lines, all of which derive from the low grade tumour follicular lymphoma (FL), or the more aggressive diffuse large B-cell lymphoma (DLBCL). Both these tumours often contain the t(14;18) that leads to the deregulation of the Bcl-2 gene (FL \approx 90%, DLBCL \approx 40%), and the cell lines chosen in the screen contain this translocation, along with others. The results have shown a number of potential oncogenes that have not previously been associated with the disease.