



Delineation of Prognostic Markers in Gastric Cancer by Expression Profiling

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Using cDNA microarray technology, it is possible to interrogate the expression of thousands of genes simultaneously in a tissue sample. When linked to survival data, genes whose expression levels correlate with tumour aggressive behaviour can be identified. Using Cox regression analysis, we have prioritized a list of genes that correlates with patient survival in a gene expression profiling experiment involving 90 gastric cancer patients. We have studied in detail two of the prognostic genes that show a high variance in expression levels between different tumours, and validated their prognostic significance using independent cohorts of patients. *PLA2G2A* is expressed at a high level in some gastric cancer cells, and its expression is negatively associated with metastasis and positively associated with prolonged survival. This is consistent with its biological function in suppression of tumour growth in animal model. *CCL18* is a newly identified chemokine that is involved in the generation of primary immune response. We found expression of CCL18 in the tumour-associated macrophages located at the tumour invasion front in gastric cancer. Expression of CCL18 is associated with prolonged overall and disease-free survival, which is stage independent. The finding raises the possibility of involvement of CCL18 in the generation of antitumour immune response, and opens up opportunities for novel therapeutic strategy or risk stratification using CCL18. In conclusion, study of gastric cancer using cDNA microarray technology will lead to identification of many novel elements with therapeutic potential.