PublisherInfo		
PublisherName	:	BioMed Central
PublisherLocation	:	London
PublisherImprintName	:	BioMed Central

Signatures of tumor origin

ArticleInfo		
ArticleID	:	4291
ArticleDOI	:	10.1186/gb-2001-3-1-reports0005
ArticleCitationID	:	reports0005
ArticleSequenceNumber	:	23
ArticleCategory	:	Paper report
ArticleFirstPage	:	1
ArticleLastPage	:	3
ArticleHistory	:	RegistrationDate : 2001–11–6 Received : 2001–11–6 OnlineDate : 2001–12–20
ArticleCopyright	:	BioMed Central Ltd2001
ArticleGrants	:	
ArticleContext	:	130593311

John C Rockett

Abstract

Gene-expression profiling can distinguish the anatomical origin of over 90% of samples of ten different types of solid cancer

Significance and context

Early commentators on the practical applications of gene-expression profiling speculated that the development of disease induces unique gene-expression profiles or 'fingerprints' that can be identified and used as a diagnostic tool for determining details such as disease type, grade and stage. Various groups have already discerned fingerprints associated with subclasses of various cancers, including leukemia, lymphoma and breast cancer. Su *et al.* have taken these studies a step further by showing that expression profiling can also be used to predict the tissue of origin for samples of various types of cancer. The fact that they have done this with a limited gene set, comprising only about one-third of the human genome, suggests that expression profiling has the potential to become an accurate and useful tool to assist the diagnosis of certain diseases.

Key results

Using a panel of 12,533 genes, Su *et al*. identified subsets of genes with tumor-specific expression for ten distinct classes of solid tumor. They found they were able to predict the anatomical origin of over 90% and 80% of the training and blinded tumor samples, respectively, by tracking the expression of as few as 11 genes.

Links

Supplementary data to *Cancer Research* **61:**7388-7393 including the complete list of genes comprising the multiclass predictor, is available from the authors' website at the Genomics Institute of the Novartis Research Foundation.

Conclusions

The authors conclude that custom-built DNA microarrays are discriminatory enough to be used for the molecular classification of solid tumors, and that they could become a useful tool to augment the current site-specific and histopathological classifications used to evaluate stage, grade and treatment regimes.

Reporter's comments

The 90% prediction rate will undoubtedly improve as larger sets of tumor samples are examined, expression profiling becomes more sensitive and reproducible, the gene sets being interrogated become larger or more representative, and statistical analysis becomes more refined. In the longer term, it should be possible to use just a small panel of highly predictive genes (such as the 11 reported by the authors) to assess the origin, type and grade of different tumors. The ten tumor classes examined account for approximately 70% of all cancer deaths in the US. As others have already shown that expression profiling can differentiate different cancer subtypes, this technique should soon provide a useful contribution to the management of a high percentage of cancer patients. One problem not addressed in this paper is the relationship between the predictive power of expression profiling and the stage or grade of tumor. This needs to be addressed so as to define the boundaries within which expression profiling can be usefully applied. Expression profiling seems well suited to assisting the diagnosis of cancer and other pathologically definable diseases such as microbial infection. A much greater challenge will be to apply it to elucidating and classifying less definable conditions such as depression and behavioral disorders. But given the increasing evidence that such diseases can have genetic causes, expression profiling might eventually be used to probe all sorts of maladies.

Table of links

Cancer Research

Supplementary data to *Cancer Research* **61:**7388-7393

Genomics Institute of the Novartis Research Foundation

References

1. Su AI, Welsh JB, Sapinoso LM, Kern SG, Dimitrov P, Lapp H, Schultz PG, Powell SM, Moskaluk CA, Jr HF Frierson, Hampton GM: Molecular classification of human carcinomas by use of geneexpression signatures. Cancer Res. 2001, 61: 7388-7393.