provided proof-of-principle data identifying fusion genes from a set of 6 leukaemia and prostate cancer samples. The aim is now to establish this as a robust tool that can be used to test for an extended set of known and candidate fusion genes in both a research and clinical diagnostic setting.
Materials and Methods: A combination of measurements of chimeric transcript junctions with exon-wise measurements of individual fusion partners is used. We have now gone through various literature and database sources, and our database of fusion genes now contains 559 previously reported fusion genes. A second-generation of the fusion gene microarray has been designed where about 500,000 oligos are used to interrogate each sample (NimbleGen HD2 technology, 3-plex microarrays).
Results and Conclusions: The new version of the fusion gene microarray have so far been successfully picking up known fusion genes from leukaemia cell lines, and we are currently moving into analyses of diagnostic cancer samples from leukaemia and sarcomas, as well as cell lines of various origins in search for known fusion genes in new cancer types. The method bears promise of an important complement to currently used diagnostic and research tools for the detection of fusion genes in neoplastic diseases.

1331 POSTER

Identifying the primary site using gene expression profiling in patients with carcinoma of an unknown primary (CUP): a feasibility study from the GEFCAPI

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Background: CUP are an heterogeneous family of neoplasms with a dismal prognosis, with empiric chemotherapy as the recommended treatment. The aim of this study was to evaluate the feasibility of a 500-mRNA microarray to identify the tissue of origin in patients with CUP.
Patients and Methods: Diagnostic biopsy formalin-fixed, paraffin-embedded (FFPE) specimens from 22 patients with CUP were prospectively collected. Gene expression profiling was performed using oligonucleotide microarray that contains 495 genes selected as highly differentially expressed between 49 tumor types (CupPrint®).
Results: The assay was successfully performed on specimens from 18 of the 22 patients (82%). It could not be performed because of a low RNA preservation in the remaining 4 cases. The median age was 57 years (range: 29−70 years). The median delay from tissue shipping to receipt of CupPrint® result was 11 days (range: 1−26 days). The most common tissues of origin identified were lung cancer (22%) and colorectal cancer (17%). Of note, a primary cancer which would not be adequately treated by an empiric chemotherapy regimen currently recommended in CUP (like cisplatin-gemcitabine or carboplatin-paclitaxel) was identified in about half patients: kidney cancer (1), hepatocarcinoma (1), colorectal cancer (3), head and neck cancer (2) and cholangiocarcinoma (1).
Conclusion: Gene expression profiling of FFPE biopsy specimens from patients with CUP is feasible in a reasonable delay, making it feasible in clinical practice. A phase III randomized trial is planned to compare therapy based on gene expression-suspected primary cancer versus empiric chemotherapy.

1332 POSTER

The distribution of recurrence scores in Europe and Middle East (EME) compared with the US

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Background: The Recurrence Score (RS), derived from the quantitative RT-PCR analysis of 21 individual genes, quantifies the likelihood of distant recurrence in hormonal-treated patients with estrogen receptor (ER)-positive breast cancer. We examined whether there are differences in the RS distribution between EME and the US.
Material and Methods: 2,676 tumor specimens successfully examined in the Genomic Health laboratory from January 2004 through April 2009 that were submitted by physicians from EME were included in the analyses. Quantitative expression of 16 individual cancer related genes was measured by the pre-specified 21 gene Recurrence Score assay (Oncotype DX®) on a scale from 0 to 15 (relative to reference genes), where a one unit increment is associated with a 2-fold change in expression. RS is calculated from a published equation (Paik et al, NEJM 2004) using the quantitative expression of five proliferation-related genes (CCNB1, Ki-67, MYBL2, STK15 and Survivin), four ER-related genes (ER, PR, Bcl2 and SCUBE2), two HER2-related genes (HER2 and GRB7), two invasion-related genes (CTSL2 and STMY3), and three single genes, BAG1, CD68 and GSTM1. Based on the observed distribution of expression among the tumors for each individual gene and group, we determined the range in RSs for low, intermediate and high risk patients and compared these results to those submitted by physicians in the US.
Results: The distribution of the results from EME and the US were consistent. The table shows the distribution of RSs that may be observed for low, intermediate or high risk patients between these two regions.

	EMEA (n = 2676)	US (>90,000)
RS 0−17	51%	52%
RS 18−30	37%	35%
RS >31	12%	13%

Conclusions: The distribution of the RSs in EME is similar to that in the US even though there are differences in practice pattern management of early stage breast cancer. The 21 gene Recurrence Score assay (Oncotype DX®) Oncotype DX breast cancer assay consistently identifies >50% of patients who have a RS <18. This finding is consistent with the results from the validation (Paik et al., NEJM 2004) and confirmatory studies (Habel, BC Res. 2006; Dowsett et al., SABCS 2008). Patients with a RS < 18 have been shown to have minimal, if any, chemotherapy benefit, so this assay has potential clinical utility in EME as it does in the US (Paik et al., JCO, 2006; Albain et al., SABCS 2007).

1333 POSTER

Aberrant expression of ZDHHC14 gene in human tongue squamous cell carcinoma

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Background: Molecular alterations in a number of oncogenes and tumor suppressor genes associated with metastasis of cancer could be important clues to predicting and suppressing metastasis. The aim of this study was to identify differentially expressed gene(s) among lymph node-positive (pN(+)) cases and lymph node-negative (pN(−)) cases in tongue squamous cell carcinoma (TSCC).
Patients and Methods: In this study, genetic aberrations and gene expression profiles were examined in 20 cases of primary TSCCs, paired normal oral tissues, 6 TSCC-derived cell lines, and 2 normal oral keratinocytes (NOKs). Whole genome profiling using the Affymetrix 10K SNP Mapping Array was performed on 3 pN(+) cases, 2 pN(−) cases of TSCCs and correspondence to normal tissues. In addition, we also examined mRNA expression level of the candidate gene product identified.
Results: We found that DNA copy number abnormality of chromosome 6q region is associated with metastasis of TSCCs. *ZDHHC14* is on 6q25.3, a region gained in pN(+) cases of TSCCs when compared with pN(−) cases. Quantitative real-time reverse-transcription polymerase chain reaction (RT-PCR) showed that *ZDHHC14* was over expressed in all TSCC derived-cell lines when compared with primary cultured NOKs at the mRNA level. Similar to TSCC-derived cell lines, high frequencies of *ZDHHC14* up-regulation were evident in mRNA levels of primary tumors (n = 8/20, 40%). This up-regulation also is closely associated with lymph node status (p = 0.019).
Conclusions: These results suggest that *ZDHHC14* expression may be correlated with lymph node metastasis and offer clues to the planning of new treatments such as early detection, prevention, and therapy for TSCC metastasis.

1334 POSTER

Spleen tyrosine kinase as a novel candidate tumour suppressor gene for human oral squamous cell carcinoma

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Background: Spleen tyrosine kinase (Syk) is a non-receptor type of protein-tyrosine kinase that is widely expressed in several epithelial cells. We analyzed the mutational and methylation status of the *spleen tyrosine kinase* (*Syk*) gene and both mRNA and protein levels in primary oral squamous cell carcinoma (OSCC) and OSCC-derived cell lines and examined the function of the *Syk* gene in OSCC-derived cell lines in vitro.
Material and Methods: The seven human OSCCs-derived cell lines used in this study were Ca9−22, Ho-1-N-1, HSC-2, Ho-1-u-1, HSC-4, KON and KOSC-2. Primary cultured normal oral keratinocytes (NOKs) were used as a normal control. Tumors with patient-matched normal oral tissues (when