Molecular basis of chemosensitivity of platinum pre-treated ovarian cancer to chemotherapy

S Glaysher¹, FG Gabriel¹, P Johnson¹, M Polak¹, LA Knight¹, K Parker¹, M Poole², A Narayanan³ and IA Cree⁴,¹ for the NHS Collaborative Research Programme for Predictive Oncology

¹Translational Oncology Research Centre, Queen Alexandra Hospital, Portsmouth PO6 3LY, UK; ²School of Computing, University of Portsmouth, Buckingham Building, Portsmouth PO1 3HE, UK; ³School of Computing and Mathematical Sciences, Auckland University of Technology, Private Bag 92006, Auckland 1142, New Zealand

BACKGROUND: Ovarian cancer shows considerable heterogeneity in its sensitivity to chemotherapy both clinically and in vitro. This study tested the hypothesis that the molecular basis of this difference lies within the known resistance mechanisms inherent to these patients’ tumours.

METHODS: The chemosensitivity of a series of 31 ovarian tumours, all previously treated with platinum-based chemotherapy, was assessed using the ATP-based tumour chemosensitivity assay (ATP-TCA) and correlated with resistance gene expression measured by quantitative reverse-transcriptase polymerase chain reaction (qRT-PCR) in a TaqMan Array following extraction of mRNA from formalin-fixed paraffin-embedded tissue. The results were standardised against a housekeeping gene (PBGD), and assessed by multiple linear regression.

RESULTS: Predictive multiple linear regression models were derived for four single agents (cisplatin, gemcitabine, topotecan, and treosulfan), and for the combinations of cisplatin + gemcitabine and treosulfan + gemcitabine. Particularly strong correlations were obtained for cisplatin, gemcitabine, topotecan, and treosulfan + gemcitabine. No individual gene expression showed direct correlation with activity in the ATP-TCA. Genes involved in DNA repair and apoptosis were strongly represented, with some drug pumps also involved.

CONCLUSION: The chemosensitivity of ovarian cancer to drugs is related to the expression of genes involved in sensitivity and resistance mechanisms.

Keywords: ovarian cancer; chemosensitivity; chemoresistance; gene expression; ATP; RT–PCR

The variable response to chemotherapy in ovarian cancer is well recognised clinically. Patients crossing from one regimen to the alternative in clinical trials often show responses (Piccart et al, 2000; Muggia, 2003). This suggests that it might be possible to optimise therapy if it was also possible to develop a test to determine which regimen would be most effective for an individual patient. We and others have used cellular chemosensitivity tests to show similar heterogeneity in ovarian cancer, and clinical comparisons suggest that these tests correlate relatively well with outcome (Andreotti et al, 1995; Kurbacher et al, 1998; Konecny et al, 2000; Sharma et al, 2003; Cree et al, 2007) despite the rapid development of resistance in many patients (Di Nicolantonio et al, 2005). Clinical use of such tests is more problematic and requires access to specialist laboratory facilities, as well as a large amount of fresh tumour tissue. These assays have therefore failed to be widely accepted into clinical practice.

Molecular assays offer the prospect of developing predictive assays capable of wider use. However, studies of single genes have shown little predictive efficacy, unless they happen to be the targets of the drugs concerned. Multi-gene signatures are likely to be required. There are two feasible approaches to the generation of multi-gene signatures for predictive testing. The first is to screen very large numbers of genes using hybridisation arrays, correlate these with clinical outcome, and apply sophisticated statistical methods to generate predictive gene signatures (Wigle et al, 2002; Potti et al, 2006). The second is to take an hypothesis-driven approach to generate gene sets based on knowledge of the pathways involved in resistance and sensitivity to individual drugs that can then be correlated with in vitro chemosensitivity data or clinical outcome (Kikuchi et al, 2003). We have taken the latter approach and have designed gene sets for chemosensitivity prediction based on published reports and previous studies.

In ovarian cancer, platinum (usually carboplatin) is the mainstay of treatment in the primary setting, with single-agent response rates around 60% (Lokich and Anderson, 1998). Single agents such as paclitaxel, topotecan, and liposomal doxorubicin are used as second-line treatments with response rates around 20% (Sharma et al, 2003). Other drugs such as alkylating agents (e.g. treosulfan) also have activity and we have shown that the combination of treosulfan + gemcitabine is particularly active (Cree, 2003; Sharma et al, 2003). Combination of gemcitabine with platinum, even following previous treatment is effective due to the ability of gemcitabine to reverse resistance associated with enhanced DNA repair (Cree, 2003).
The mechanisms of resistance to these agents have been studied in some detail. Clinical studies using genome-wide gene expression arrays have been performed and have shown signatures associated with resistance to a number of agents (Richardson and Kaye, 2005; Tsuda et al., 2005; Olivier et al., 2006). It is generally assumed that the same resistance mechanisms used by cells to circumvent single-agent activity will also be used against combinations of these drugs. However, there are few mechanistic studies of resistance to the combinations used in ovarian cancer to confirm or refute this supposition.

This study has tested the hypothesis that the molecular basis of the observed heterogeneity of chemosensitivity of ovarian cancer is determined by the known resistance mechanisms expressed by these patients’ tumours. Resistance to anti-cancer drugs involves many mechanisms (Cree et al., 2002a, b), and an array-based approach to study the genes involved is therefore sensible. The mechanisms of cellular (i.e. non-pharmacokinetic) resistance to chemotherapy include down-regulation of target expression, drug metabolism, membrane-located xenobiotic pumps, altered susceptibility to apoptosis, and altered growth/cell cycle or differentiation. Knowledge of these pathways enabled us to design a TaqMan Array microfluidic quantitative reverse-transcriptase PCR (qRT-PCR) card to include 91 genes known to be involved in drug resistance/sensitivity to anthracyclines, 5-FU, alkylating agents, and taxanes. The card also included five housekeeping genes to allow standardisation of the results for comparison of individual tumour data. The gene set chosen was not intended to be comprehensive, but to establish proof of principle for the use of in vitro sensitivity data with gene expression data to determine the contribution of individual genes to drug sensitivity and resistance in ovarian cancer.

PATIENTS AND METHODS

In this study we have used qRT-PCR to examine the expression of genes previously shown to be involved in resistance to chemotherapy with platinum, anthracyclines, taxanes, and alkylating agents in ovarian cancer. The expression profiles have been compared with quantitative chemosensitivity data obtained for the same tumours using the ATP-based chemosensitivity assay tumour chemosensitivity assay (ATP-TCA).

Patients and samples

A series of 31 ovarian tumour samples were obtained from surgical specimens of platinum-pre-treated patients undergoing surgery or at staging laparoscopy with written consent from 2001 to 2006. Ethics committee approval was obtained and the study conformed to the Declaration of Helsinki Principles. The fresh samples were used to obtain sensitivity data, and patients also had formalin-fixed paraffin-embedded (FFPE) material taken for histology. This provided a source of material for qRT-PCR. The age of patients ranged from 18 to 57 years (average 38 years), and all were FIGO stage 3c or IV. Histologically, 10 tumours were classified as papillary serous, 4 as clear cell, 3 endometrioid, 1 mixed Mullerian, 1 mucinous, and the remaining 12 as poorly differentiated by the reporting pathologist. In 12 cases paclitaxel was given in addition to platinum as first-line treatment, 1 case received cisplatin + paclitaxel, and the remainder received carboplatin alone. Twelve cases presented with early recurrence during or within 6 months of initial treatment consistent with clinical resistance to platinum. Nine patients were relapse cases following second-line treatment, whereas the remainder were first relapse cases.

ATP-TCA

The ATP-TCA was performed as previously reported (Andreotti et al., 1995; Cree, 1998). Samples from solid tumours were transported to the laboratory in 25 ml specimen bottles containing cooled transport medium consisting of DMEM (Sigma, Poole, Dorset, UK) with added antibiotics. Tumour cells were obtained by enzymatic dissociation, washed in a serum-free complete assay medium (CAM; available from DCS, Hamburg, Germany), and purified by density centrifugation to remove debris. The cells were washed, re-suspended in CAM, and plated in 96-well polypropylene plates at 20 000 cells per well with six doubling dilutions of four drugs or combinations, tested in triplicate from a 200% test drug concentration (TDC) to 0.625 TDC. The concentrations of the drugs used are given in Table 1. One row of each plate contained medium only and one row a maximum inhibitor control. The plates were incubated for 6 days at 37°C with 5% CO₂, following which ATP was extracted with tumour cell extraction reagent (DCS). Aliquots of the extract were transferred to a white 96-well polystyrene plate to which an equal amount of luciferin-luciferase was added. The resulting luminescence was read in a luminometer (MPLX; Berthold Diagnostic Systems GmbH, Pforzheim, Germany) and the data were transferred to an Excel (Microsoft) spreadsheet for analysis. The results were expressed as the percentage inhibition at each concentration tested compared with an untreated control, and a summary index was calculated as the sum of the surviving cell fraction at each concentration calculated as 600–Sum(InhibitionindexInhibitionindex) for comparison with qRT-PCR results, where IndexSUM = 0 indicates complete inhibition and IndexSUM > 600 indicates no effect (Hunter et al., 1993).

Extraction of mRNA from FFPE tumor tissue

The H&E-stained sections of selected FFPE blocks of ovarian tumor tissue, previously marked with tumour areas of interest (AOI) by a pathologist, were matched and overlaid onto the corresponding FFPE block to give > 80% neoplastic cells, comparable with the ATP-TCA (Andreotti et al., 1995). The manual tissue arrayer (MTA1; Beecher Instruments Inc., Sun Prairie, WI) fitted with the use device for the use of ATO was aligned over the desired AOI, which was punched out from the block. The stylet was decontaminated (Ambion DNA and RNA Zap) and cleaned (70% alcohol) between each FFPE block. A minimum of two 1.0 mm punches were obtained from each block and placed in a sterile labelled 1.5 ml microcentrifuge tube.

The remainder of the extraction process was performed as previously reported (Glaysher et al., 2009). In brief, the tubes were heated at 70°C in a Stuart SBH200D heating block (Bibby Scientific Limited, Stone, Staffordshire, UK) for 20 min. Excess paraffin wax was subsequently removed and xylene was added to the tube for 10 min at 50°C. The microtube was removed from the heating block, centrifuged at 12 000g for 2 min in a Sanyo MSE Micro Centaur centrifuge (MSE (UK) Ltd, Lower Sydenham, London,

---

**Table 1** Drug list for ATP-TCA with manufacturer and 100% TDC used in the assay and the number of tumours tested with each drug

| Drug or combination | Manufacturer | 100% TDC (µM) | Number tested |
|---------------------|--------------|---------------|---------------|
| Cisplatin           | Bristol-Myers-Squibb* | 10.00 | 27 |
| Doxorubicin         | Eli Lilly    | 0.92 | 19 |
| Gemcitabine         | Eli Lilly    | 40.04 | 26 |
| Paclitaxel          | Bristol-Myers-Squibb | 15.90 | 26 |
| Topotecan           | GlaxoSmithKline† | 1.78 | 23 |
| Treosulfan          | Medac‡       | 71.86 | 23 |
| Cisplatin+Gemcitabine | As single agents | As single agents | 27 |
| Treosulfan+Gemcitabine | As single agents | As single agents | 26 |

Abbreviation: TDC = test drug concentration. Some samples had too few cells for all single agents and combinations to be tested. *Bristol-Myers Squibb Pharmaceuticals Limited, Uxbridge, Middlesex, UK. †Eli Lilly and Company Limited, Basingstoke, Hampshire, UK. ‡GlaxoSmithKline plc, Brentford, Middlesex, UK. ¶Medac GmbH, Hamburg, Germany.
Translational Therapeutics

et al. (2009) described (Glasyer & Ambion RecoverAll kit (catalogue no. AM1975; Applied Biosystems). Evaporation of any residual ethanol at 50°C once more. The microfuge tube lids were opened to allow the ethanol to be removed by pipette, and the process was repeated once more. The microfuge tubes were then placed in a 0°C freezer for 10 min, before protease digestion.

Protease digestion and RNA extraction were performed using an Ambion RecoverAll kit (catalogue no. AM1975; Applied Biosystems) according to the manufacturer’s instructions as previously described (Glasyer et al., 2009). The lysates resulting from protease digestion were stored at −20°C before RNA extraction.

Two-step RT–PCR

Reverse transcription (RT) was performed using an High-Capacity cDNA Archive Kit (catalogue no. 4322171; Applied Biosystems) according to the manufacturer’s instructions and as previously reported (Glasyer et al., 2009) in a 0.2 ml PCR tube. The final RNA concentration in the RT mix was 1 – 20 ng µl⁻¹. Cycling conditions were as follows: step 1, 25°C for 10 min, step 2, 37°C for 120 min. After removal from the thermal cycler, the samples were pulse spun in a microfuge at 12,000 g for 30 s and stored overnight at 4°C. The following day cDNA content was measured using a NanoDrop spectrophotometer before use in the TaqMan Array.

TaqMan Arrays (Applied Biosystems) were run according to the manufacturer’s instructions (Glasyer et al., 2009). Samples were made up with TaqMan × 2 Universal Master Mix with UNG Amperase (catalogue no. 4364338; Applied Biosystems) and mixed with an equal volume of cDNA to give a final concentration of 300 ng µl⁻¹ DNA. All four samples were then each pipetted into two ports (100 µl per port) of the 384-well card, for the 96 genes arrayed in a Chemosensitivity Gene Expression Array (CGEA-1; CanTech Ltd., Portsmouth, UK). The genes on each card are given in Table 2. The loaded card was then placed, port upwards, into a balanced centrifuge (type, address) and spun for 60 s at 380 g to fill the card. This was checked and the card was spun again for 60 s at 380 g to remove any air bubbles. The card was then placed in a TaqMan Array slide sealer for sealing, and the loading ports were cut from the card before it was read in an 7900HT thermal cycler, Applied Biosystems. PCR was performed for 90 min with the following conditions: AmpErase UNG Activation for 2 min at 50°C; AmpliTaq Gold DNA Polymerase Activation for 10 min at 94.5°C, followed by 40 cycles each of Melt Anneal/Extend for 30 s at 97°C and 1 min at 59.7°C. The ‘Auto Threshold Cycle’ function was performed at the end of the run and C values were transferred to a Microsoft Excel spreadsheet, controls were checked, and the data were transferred to a Microsoft Access database for further analysis.

C values were standardised against HMBS (PBGD), the least variable housekeeping gene, to avoid errors due to differences in efficiency between the housekeeping and test genes, which were present from cycle 27 to 35 in most cases. A logarithmic gene expression ratio was calculated as Ln(2 ^ (Ct(test) - Ct(PBGD))) and used for comparison with ATP-TCA data by multiple linear regression using SPSS version 14.0 (SPSS Inc., Chicago, IL, USA) and Analyse-It software (Analyse-it Software Ltd, Leeds, UK) applications.

Data analysis

The ATP-TCA and qRT-PCR data were collected into an Access database (Microsoft), from which descriptive statistics were generated. Comparison of ATP-TCA results for individual drugs or combinations with gene expression data was performed by multiple linear regression with forward selection of variables using SPSS version 15.0. For each variable, inclusion was dependent upon a probability of F > 0.1, that is, the threshold for inclusion of a gene into the model within SPSS, based on initial assessment of the most appropriate model size using Akaike Information Criterion, a function of model error and size that penalises large models (data not shown). The prediction residual sum of squares method was used as this is an adjusted regression method helpful in preventing overfitting of the data as it uses a ‘leave one out’ method of analysis. Genes were added by forward regression according to their univariate correlations following entry of each gene into the model, and no intercept term was included.

RESULTS

ATP-TCA

In keeping with previous results from a number of articles (Andreotti et al., 1995; Sharma et al., 2003), the results from the ATP-TCA show considerable heterogeneity for each of the drugs and combinations tested. The frequency histograms show the greatest activity (i.e. lowest Indx50% for treosulfan + gemcitabine, whereas the single agent showed weaker but more variable activity (Figure 1).

qRT-PCR

Although these qRT-PCR studies were performed using RNA extracted from FFPE tissue, all samples were regarded as evaluable on the basis of the housekeeping gene C values (i.e. HMBS/PBGD, C > 37 cycles). Variation in housekeeping gene levels was limited, with a normal distribution of C values (HMBS/PBGD, mean = 31.61, 95% CI = 30.43 – 32.78). C values within the detectable range were present for most of the genes present on the TLDA, though
DISCUSSION

In this study we have examined single-agent and combination effects for the same tumours using the ATP-TCA, and compared this experimental in vitro chemosensitivity data with the expression of a large number of potential resistance mechanisms using qRT-PCR to study FFPE biopsy material. The TaqMan Array assay can be performed with a few nanograms of RNA extracted from FFPE blocks stored in pathology, and this gives it a considerable advantage over the ATP-TCA that requires large amounts of fresh tissue. Most of the samples used in this study were from surgical material, but in each case we have used just two 1.0 mm punches from the FFPE blocks. The ability to use small punches of tumour identified by the pathologist in paraffin blocks makes this a potentially very valuable technique, as it is also be possible to measure gene amplification or mutation by PCR of DNA markers.

Unlike direct correlation of gene expression with clinical data, the comparison of quantitative gene expression data (CoV 2%) with in vitro chemosensitivity data from the ATP-TCA (CoV 15%) means that relatively small numbers of tumours are required to obtain data on the genes relevant to resistance and sensitivity to drugs tested in the assay. This may prove to be particularly useful to investigate the mechanisms of sensitivity and resistance for drugs that are rarely used as single agents, and to develop predictive molecular assays for new drugs about to enter the clinical use. It is undoubtedly true that our array does not include all the genes of relevance to the drugs tested – the lack of good correlation with genes linked to these mechanisms (Figure 2), consistent with the known resistance mechanisms for DNA-damaging agents. The topotecan model includes a drug pump, including MRP4, and several of the genes identified are involved in several known mechanisms of chemoresistance, including drug metabolism, membrane drug pumps, and DNA repair. These are relatively specific to particular drugs, but in nearly all of the models generated, expression of drug resistance mechanisms was significantly correlated with chemosensitivity data.

Correlation of mechanisms with ATP-TCA data

Some were more rarely expressed than others. NTC remained undetectable throughout the study indicating that the reagents and cards in use had not been contaminated. Control data showed an intra-assay coefficient of variation (CoV) for one sample of 0.69% for PBGD/HMBS. The inter-assay variation for PBGD/HMBS with six samples varied between 1 and 3%.

Figure 1  Box and whisker plot showing the sensitivity of tumours to each drug tested. IndexSUM is higher in resistance, lower in sensitive tumours.
Figure 2  Multiple linear regression analysis by unsupervised forward selection for (A) cisplatin — Adj $R^2 = 0.836$, $P < 0.001$; (B) doxorubicin — Adj $R^2 = 0.524$, $P < 0.007$; (C) gemcitabine — Adj $R^2 = 0.524$, $P < 0.001$; (D) paclitaxel — Adj $R^2 = 0.646$, $P < 0.001$; (E) topotecan — Adj $R^2 = 0.751$, $P < 0.001$; (F) treosulfan — Adj $R^2 = 0.977$, $P < 0.001$; (G) cisplatin + gemcitabine — Adj $R^2 = 0.743$, $P < 0.001$; (H) treosulfan + gemcitabine — Adj $R^2 = 0.753$, $P < 0.001$. 

Translational Therapeutics
Table 3 Genes found to correlate in multivariate linear regression analysis

| Model                      | Unstandardized errors | Collinearity statistics |
|----------------------------|-----------------------|-------------------------|
| (A)                        |                       |                         |
| Capcitabine                | 0.949                 | 0.901                   | 0.836                   | 35.226 | P < 0.001 |
| Dovorubicin                | 0.797                 | 0.636                   | 0.524                   | 98.669 | P < 0.007 |
| Gemcitabine                | 0.766                 | 0.586                   | 0.524                   | 88.312 | P < 0.001 |
| Paclitaxel                 | 0.848                 | 0.720                   | 0.646                   | 78.669 | P < 0.001 |
| Topotecan                  | 0.900                 | 0.811                   | 0.751                   | 60.457 | P < 0.001 |
| Treosulfan                 | 0.994                 | 0.997                   | 0.977                   | 10.679 | P < 0.001 |
| Capcitabine+Gemcitabine   | 0.899                 | 0.807                   | 0.743                   | 63.769 | P < 0.001 |
| Treosulfan+Gemcitabine    | 0.904                 | 0.817                   | 0.753                   | 33.823 | P < 0.001 |

genes involved in apoptosis proved to be important, suggesting that the general susceptibility of the cell to undergo apoptosis may outweigh other determinants of tumour chemosensitivity (Cree et al., 2002a; Glaysher et al., 2009). In general, the genes we have found to be important match well with those thought to be important from previous studies. There are some discrepancies, for instance in which membrane pumps are involved in doxorubicin or topotecan resistance. Such instances may be explained by covariance, as several such pumps tend to be up-regulated together following exposure of ovarian cancer cells to pumped drugs (Di Nicolantonio et al., 2005). The number of tumours in this study is relatively small, and it is important not to draw too much from these data – the likelihood of the signatures described here being optimal for prediction of chemosensitivity is remote, and much larger studies using clinical samples will be required to validate signatures for clinical use. It is however conceivable that gene signatures may be similar for patients with resistance to particular agents. Sub-clustering of groups with distinct mechanisms of resistance is conceivable in bigger studies, and could allow stratification of patients in clinical trials.

CONCLUSION

This study supports the hypothesis that the molecular basis of the observed difference in sensitivity between ovarian tumours lies within the known resistance mechanisms inherent to these patients’ tumours, as we have described in lung cancer (Glaysher et al., 2009). The TaqMan Array is well suited to investigate the presence of these mechanisms in ovarian cancers alongside cellular chemosensitivity testing and clinical results, and its ability to use small fragments of tumour tissue makes it suitable to developed for future clinical use.
ACKNOWLEDGEMENTS

The tissue collection and ATP-TCA were funded by CanTech Ltd; the molecular analysis was funded by Applied Biosystems; and the analysis was funded by CanTech Ltd. We thank Tim Johns and Judy Pellatt for their assistance in obtaining consent from patients included in this study. We also thank Chirag Patel (Applied Biosystems) for assistance with the estimates of model size. This study was supported by Applied Biosystems and CanTech Ltd.

REFERENCES

Andreotti PE, Cree IA, Kurbacher CM, Hartmann DM, Linder D, Harel G, Gleiberman J, Caruso PA, Ricks SH, Untch M, Sartori C, Bruickner HW (1995) Chemosensitivity testing of human tumors using a microplate adenosine triphosphate luminescence assay: clinical correlation for cisplatin resistance of ovarian carcinoma. Cancer Res 55: 5276–5282

Cree IA (1998) Luminescence-based cell viability testing. Methods Mol Biol 198: 169–177

Cree IA (2003) Chemosensitivity testing as an aid to anti-cancer drug and regimen development. Recent Results Cancer Res 161: 119–125

Cree IA, Knight L, Di Nicolantonio F, Sharma S, Gulliford T (2002a) Chemosensitization of solid tumor cells by alteration of their susceptibility to apoptosis. Curr Opin Investig Drugs 3: 641–647

Cree IA, Knight L, Di Nicolantonio F, Sharma S, Gulliford T (2002b) Chemosensitization of solid tumors by modulation of resistance mechanisms. Curr Opin Investig Drugs 3: 634–640

Cree IA, Kurbacher CM, Lamont A, Hindley AC, Love S (2007) A prospective randomized controlled trial of tumour chemosensitivity assay directed chemotherapy vs physician’s choice in patients with recurrent platinum-resistant ovarian cancer. Anticancer Drugs 18: 1093–1101

Di Nicolantonio F, Mercer SJ, Knight LA, Gabriel FG, Whitehouse PA, Sharma S, Fernandez A, Glaysher S, Di Palma S, Johnson P, Sommers SS, Toh S, Higgins B, Lamont A, Gulliford T, Hurren J, Yangou C, Cree IA (2005) Cancer cell adaptation to chemotherapy. BMC Cancer 5: 78

Fernando A, Glaysher S, Conroy M, Pekalski M, Smith J, Knight LA, Di Nicolantonio F, Cree IA (2006) Effect of culture conditions on the chemosensitivity of ovarian cancer cell lines. Anticancer Drugs 17: 913–919

Fiebig HH, Maier A, Burger AM (2004) Clonogenic assay with established human tumour xenografts: correlation of in vitro to in vivo activity as a basis for anticancer drug discovery. Eur J Cancer 40: 802–820

Glaysher S, Taniakalis D, Gabriel FG, Johnson P, Polak ME, Knight LA, Goldthorpe Z, Pereglin K, Gyi M, Modi P, Rahamim J, Smith ME, Amer K, Addis B, Poole M, Narayan A, Gulliford TJ, Andreotti PE, Cree IA (2009) Resistance gene expression determines the in vitro chemosensitivity of non-small cell lung cancer (NSCLC). BMC Cancer 9: 300

Hunter EM, Sutherland LA, Cree IA, Dewar JA, Preece PE, Wood RA, Linder D, Andreotti PE (1993) Heterogeneity of chemosensitivity in human breast carcinoma: use of an adenosine triphosphate (ATP) chemiluminescence assay. Eur J Surg Oncol 19: 242–249

Kituchi T, Daigo Y, Katagiri T, Tsuchida T, Okada K, Kikuchi S, Zembutsu H, Furukawa Y, Kawamura M, Kobayashi K, Imai K, Nakamura Y (2003) Expression profiles of non-small cell lung cancers on cDNA microarrays: identification of genes for prediction of lymph-node metastasis and sensitivity to anti-cancer drugs. Oncogene 22: 2192–2205

Konecny G, Cshotn C, Pegram M, Felber M, Lude S, Kurbacher C, Cree IA, Hepp H, Untch M (2000) Correlation of drug response with the ATP tumor chemosensitivity assay in primary FIGO stage III ovarian cancer. Gynecol Oncol 77: 258–263

Kurbacher CM, Cree IA, Bruckner HW, Brenne U, Kurbacher JA, Muller K, Ackermann T, Gilbert TJ, Wilhelm L, Engel H, Mallmann PK, Andreotti PE (1998) Use of an ex vivo ATP luminescence assay to direct chemotherapy for recurrent ovarian cancer. Anticancer Drugs 9: 51–57

Lokich J, Anderson N (1998) Carboplatin vs cisplatin in solid tumors: an analysis of the literature. Ann Oncol 9: 13–21

Matsunuma N, Huang Z, Baba T, Lee PS, Barnett JC, Mori S, Chang JT, Kuo WL, Gubser AH, Whittaker RS, Gray JW, Fujii S, Berchuck A, Murphy SK (2009) Yin yang 1 modulates taxane response in epithelial ovarian cancer. Mol Cancer 7: 210–220

Muggia FM (2003) Sequential single agents as first-line chemotherapy for ovarian cancer: a strategy derived from the results of GOG-132. Int J Gynecol Cancer 13(Suppl 2): 156–162

Olivier RJ, van Beurden M, van’t Veer LJ (2006) The role of gene expression profiling in the clinical management of ovarian cancer. Eur J Cancer 42: 2930–2938

Piccart MJ, Bertelsen J, James K, Cassidy J, Mangioni C, Simonens E, Stuart G, Kaye S, Vargote I, Blom R, Grimshaw R, Atkinson RJ, Swenerton KD, Trope C, Nardi M, Kaem J, Tumolo S, Timmers P, Roy JA, Lhoas F, Lindvall B, Bacon M, Birt A, Andersen JE, Zee B, Paul J, Baron B, Pecorelli S (2000) Randomized intergroup trial of cisplatin-paclitaxel vs cisplatin-cyclophosphamide in women with advanced epithelial ovarian cancer: three-year results. J Natl Cancer Inst 92: 699–708

Potti A, Dressman HK, Bild A, Riedel RF, Chan G, Sayer R, Cragun J, Cottrill H, Kelley MJ, Petersen R, Harpole D, Marks J, Berchuck A, Ginsburg GS, Pebbo P, Lancaster J, Nevin S (2006) Genomic signatures to guide the use of chemotherapeutics. Nat Med 12: 1294–1300

Richardson A, Kaye SB (2005) Drug resistance in ovarian cancer: the emerging importance of gene transcription and spatio-temporal regulation of resistance. Drug Resist Updat 8: 311–321

Sharma S, Neale MH, Di Nicolantonio F, Knight LA, Whitehouse PA, Mercer SJ, Higgins BB, Lamont A, Osborne R, Hindley AC, Kurbacher CM, Cree IA (2003) Outcome of ATP-based tumor chemosensitivity assay directed chemotherapy in heavily pre-treated recurrent ovarian carcinoma. BMC Cancer 3: 19

Smit K, Bergman AM, Eijik PP, Veerman G, van Haperen VW, van den Ijssel P, Ylstra B, Peters GJ (2006) Micro-array analysis of resistance for gemcitabine results in increased expression of ribonucleotide reductase subunits. Nucleosides Nucleotides Nucleic Acids 25: 1001–1007

Tsuda H, Ito YM, Ohashi Y, Wong KK, Hashiguchi Y, Welch WR, Berkowitz RS, Birrer MJ, Mok SC (2005) Identification of overexpression and amplification of ABCF2 in clear cell ovarian adenosarcomas by cDNA microarray analyses. Clin Cancer Res 11: 6880–6888

Wigle DA, Jurisica I, Radulovich N, Pintilie M, Rossant J, Liu N, Lu C, Woodgett J, Seiden I, Johnston M, Keshavjee S, Darling G, Winton T, Breitkreutz BJ, Jorgenson P, Tyers M, Shepherd FA, Tsoa MS (2002) Molecular profiling of non-small cell lung cancer and correlation with disease-free survival. Cancer Res 62: 3005–3008