



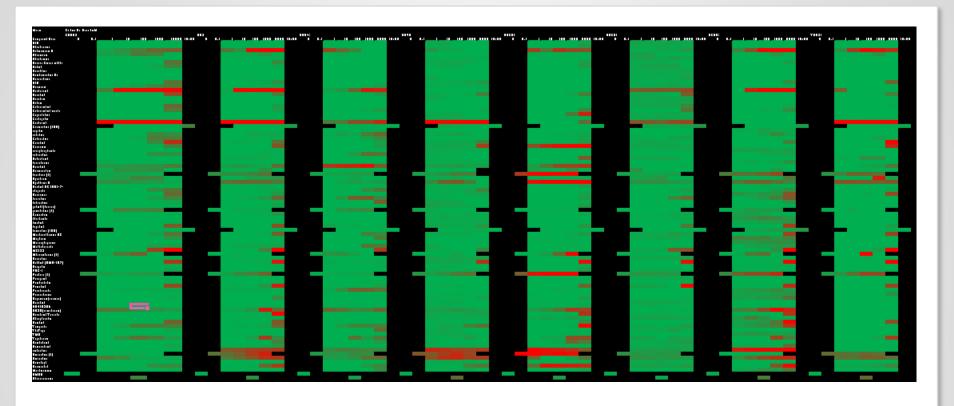


## Typical data produced by Genetic Analysis

Cell line	Genotype 20 genes (alterations in sequence and putative copy number for Akt1/2/3, ARID1A, BRCA1/2, BRAF, C110RF30, CCNE1, CTNNB1, ErbB2, KRAS, MAP2K4, MYC, NF1, Notch3, PIK3CA, PTEN, Rb1, TP53						
KURAMOCH.	Akt2/3 gain, ARID1A gain, BRAF gain, BRCA1 hetloss, BRCA2 mut (ns.), CCNE1 gain, CTNNB1 hetloss, ErbB2 hetloss, KRAS amp, MYC amp, NF1 homdel, Notch3 hetloss, PTEN hetloss, TP53 mut (ms)						
OVSAHO .	Akt/13 gain, BRAF gain, BRCA2 homdel, CCNE1 gain, MAP2K4 hetloss, MYC gain, Notch3 gain, PIEN gain, Rb1 homdel, TP53 mut (nc) and hetloss						
SNU119 .	Akt1 hetloss, Akt2/3 gain, BRAF gain, BRCA2 hetloss, C110RF30 gain, CTNNB1 hetloss, KRAS gain, MAP2K4 hetloss, MYC mut (ms) and amp, NF1 homdel, Notch3 gain, PIK3CA gain, PTEN hetloss, Rb1 amp, TP53 mut (ms) and hetloss						
COV362 .	ARID1A hetloss, BRAF gain, BRCA1 mut (ss and fs) and hetloss, BRCA2 hetloss, C110RF30 gain, FbB2 hetloss, MAP2K4 hetloss, MYC amp, NF1 hetloss, PTEN gain, Rb1 homdel, TP53 mut (ms) and hetloss						
OVCAR4 .	Akt2/3 gain, BRAF gain, BRCA1/2 hetloss, CCNE1 gain, CTNNB1 hetloss, ErbB2 hetloss, MAP2K4 hetloss, MYC gain, NF1 hetloss, Notch3 gain, PTEN gain, BRCA1/2 hetloss, TPS3 mut (ms) and hetloss						
COV318 .	Akt/12/3 gain, ARID1A gain, BRAF gain, C110RF30 gain, CCNE1 amp, CTNNB1 hetloss, KRAS hetloss, PIK3CA gain, TP53 mut (ms) and hetloss						
	Akt2/3 gain, ARID1A hetloss, BRAF gain, BRCA2 gain, C110RF30 gain, CCNE1 gain, MAP2K4 hetloss, MYC mut (ms) and gain, NF1 hetloss, Noteh3 gain, PIK3CA gain, PTEN gain, Rb1 gain, TP53 mut (ms) and hetloss						
	Akt3 quin, BRAF quin, KRAS hetloss, MYC quin, TP53 mut (ms)						
	Akt 2 agin, Akt 3 mp, ARIDIA agin, BRAF agin, CCNEI agin, KRAS agin, MYC amp, NFI agin, PLASAS arin, Akt 3 mp, ARIDIA agin, BRAF agin, CCNEI agin, KRAS agin, MYC amp, NFI agin, PLASAS arin, Akt 3 mp, ARIDIA agin, BRAF agin, CCNEI agin, KRAS agin, MYC amp, NFI agin, PLASAS arin, Akt 3 mp, ARIDIA agin, BRAF agin, CCNEI agin, KRAS agin, MYC amp, NFI agin, PLASAS agin, MYC agin						
	Akt/13 gain, ARID1A hetloss, BRAF gain, BRCA1 hetloss, CHORF30 gain, KRAS amp, MAP2K4 homdel, MYC gain, PIK3CA amp, Rb1 hetloss, TP53 mut (fs) and hetloss						
	Akt2/3 hetloss, BRCA1 mut (ms), C110RF30 gain, CTNNB1 gain, MAP2K4 hetloss, MYC gain, NF1 mut (ms), PIK3CA gain, TP53 mut (ss) and hetloss						
	Akt/12 gain, BRAF gain, BRCA1 hetloss, BRCA2 gain, C1130ORF gain, CTNNB1 hetloss, ErbB2 hetloss, KRAS hetloss, MAP2K4 hetloss, PIK3CA amp, PTEN gain, Rb1 hetloss, TPS3 mut (ns) and hetloss						
	Akt3 hetloss, KRAS gain, Rb1 gain, TP53 mut (fs)						
	Akt2 amp, ARIDIA hetloss, BRCA1/2 hetloss, C110RF30 amp, CCNE1 amp, ErbB2 hetloss, KRAS amp, MYC gain, NF1 gain, Notch3 hetloss, PIK3CA gain, Rb1 hetloss, TP53 mut (ms) and hetloss						
	Akt/12 gain, ARID1A hetloss, BRCA1 gain, CONE1 amp, CTNNE1 hetloss, ErbB2 gain, KFAS gain, KFAS gain, MF muts (ms and ms) and homdel, MAP2K4 hetloss, MYC amp, Notch3 hetloss, PIR3CA gain, RB1 hetloss, TP53 mut (ms)						
	Akt2 amp, ARIDIA hetioss, BRCAY2 hetioss, C110RF30 amp, CONE1 amp, ErbB2 hetioss, KRA3 gain, NPT gain, Notch3 hetioss, PIK3CA gain, Bb1 hetioss, TP3 amt (m2) and hetioss						
	Akt hetoes, BRAF mut (me) and asin, BRCA2 hetoes, CONET hetoes, KRAS hetoes, MAPEX4 asin, MYC asin, Rb1 hetoes, TPS3 mut (me)						
	PARE INVESTIGATION INVESTIGATION OF THE PROPERTY OF THE PROPER						
	Dead into (int) and gain, bench into into (int) and into (int) and int) and						
	Akt/2 het/oss, BRAF gain, BRCAT het/oss, CCNET het/oss, CTNRST het/oss, ETB2 gain, MAP2K4 het/oss, PIX2G gain, MF1 amp, Notch3 het/oss, PIX2G gain, TP33 mix (fs) and het/oss						
	ARIZ quin, BRAY gain, CDNS I tectoss, CURL in tectoss, CHANG I tectoss, CH						
	Akt2 gain, ARIDIA hetloss, BRAF hetloss, CONEI gain, CTNNBI hetloss, MAP2K4 hetloss, Notch3 hetloss, TFEN hetloss, TFEN and hetloss						
	Akt 1 gain, BRAF hetloss, C110RF30 amp, CCNE1 met (ms), KRAS gain, MYC gain, Notch3 hetloss, PTEN met (fs), Rb1 met (ms), TPS3 met (ns)						
	Akt/13 gain, BRCA1 gain, CTNNB1 mvt (me), ErbB2 gain, KPAS gain, MAP2K4 gain, MYC gain, NF1 gain, TPS3 mvt (me) and gain						
	Akt3 gain, ARID1A hetloss, C110RF30 gain, CTNNB1 mut (ms), ErbB2 mut (ms), KRAS mut (ms), MYC gain, TP53 mut (ss)						
	Akti homdel, BRAF gain, BRCA2 hetloss, C110RF30 gain, MAP2K4 mut (ms) and hetloss, Notch3 hetloss, PTEN hetloss						
	Akti/3 gain, ARIDIA hetloss, BRAF hetloss, MAP2K4 hetloss, MYC gain, Notch3 hetloss, PIK3CA mut (ms), TPS3 hetloss						
	Akt2 gain, Akt3 homdel, BRAF gain, CCNE1 gain, MYC gain, Notch3 gain, PTEN mut (ns), Rb1 mut (fs)						
	Akt2 gain, ARID1A mut (fs), BRAF hetloss, BRCA1 gain, BRCA2 hetloss, C110RF30 hetloss, CNE1 gain, CTNNB1 hetloss, ErbB2 gain, MAP2K4 hetloss, MYC gain, NF1 gain, PK3CA gain, Rb1 hetloss, TP53 hetloss						
	Akt3 gain, ARID1A mut (fs) and gain, BRCA1 gain, ErbB2 gain, KRAS hetlos, MYC gain, PIK3CA mut (ms) and gain, PTEN hetloss						
	C110RF30 gain						
	Akt2 gain, ARID1A muts (ns and ns), BRCA1 gain, BRCA2 mut (ms), CCNE1 gain, ErbB2 gain, KRAS gain, MAP2K4 hetloss, NF1 gain, PIK3CA mut (ms) and gain, TP53 hetloss						
	Akt/12 gain, Akt3 hetloss, BRCA1 gain, BRCA2 hetloss, CCNE1 homdel, ErbB2 amp, MAP2K4 homdel, Rb1 gain, TP53 homdel						
	BRAF1 mut (ms) and hotloss, C110RF30 gain, KRAS mut (ms) and gain, MYC gain, MYC gain, MYC gain, MYC gain (MYC gain)						
	KRAS mut (ms) and gain, PIKSCA mut (ms), PTEN gain						
COV434	ARIDIA mut (ms)						
OV56 .	ARID1A mut (fs), BRAF hetloss, KRAS mut (ms), MYC gain, PTEN mut (ms)						
SKOV3 .	ARID1A mut (ns), BRAF hetloss, CTNNB1 hetloss, ErbB2 amp, KRAS gain, MAP2K4 hetloss, NF1 mut (ms), PKEN hetloss, TP53 hetloss						
A2780 .	Akt3 gain, ARID1A muts (ne and fs), BRAF mut (ms), Notch3 mut (ms), PIK3CA mut (ms), PTEN mut (del)						
IGROV1 .	ARID1A muts (fs and fs), BRCA1 mut (fs), BRCA2 mut (ms), Notch3 mut (ms), PIK3CA muts (ms and nonstop), PTEN muts (ms and fs), TP53 mut (ms)						
OVK18	Akt3 gain, ARID1A mut (fs), KRAS mut (ms), PTEN muts (ms, ms and fs) and gain, TP53 mut (fs)						
EF027 .	ARID1A muts (fs and ns), ErbB2 mut (ms), MYC mut (ms), NF1 mut (ms), PIK3CA mut (ms), PTEN mut (fs), TP53 muts (ms and ss)						
OC316 .	Akt1 gain, ARID1A muts (ns and ns), BRAF mut (ms) and gain, BRCA2 mut (fs) and hetloss, CTNNB1 gain, PIK3CA mut (ms), Rb1 gain						
TOV21G	ARIDIA mute (fe and fe), CTNNB1 mut (fe), KRAS mut (me), PIK3CA mut (me), PTEN mute (fe and fe) and gain						

- In just these 20 genes the combinations of mutations, copy number changes is vast.
- In order to make use of these complex data one needs to create a statistical model based on a clinical training data set.
- Genotypic signatures cannot be trained to recognise drugs that are never used in the clinic to treat a particular cancer.
- The degrees of freedom in the statistical model make it very prone to over fitting the training set.

## Our data set is measuring cell death directly so much easier to interpret.



We only have one parameter in our data set that needs calibrating against clinical response, using a clinical training set, and that is *in vitro* drug dose.

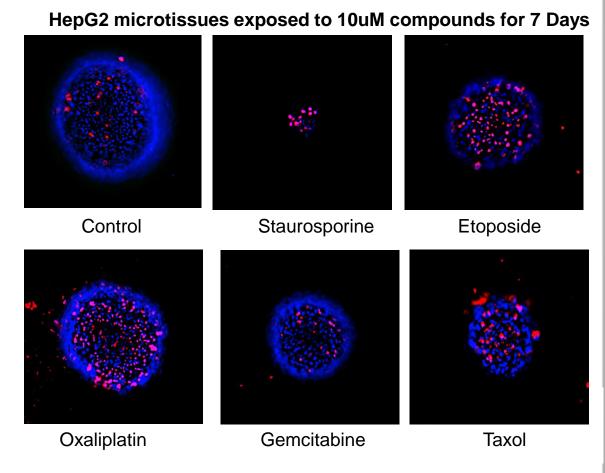


# A 3D Cell Death Assay

Originally developed using InSphero's GravityTRAP™ specifically designed for scaffold-free microtissue culture.

- 3D Liver model for toxicity
- 3D Tumour microtissues for anti-cancer drug testing
- HCA allows measurement of both tissue shrinkage and cell death within the tissue.
- Analysis in 96 well plates increases throughput allowing dose responses to be performed or the number of compounds tested increased.

- Blue- Nuclei staining
- Red- permeability stain



## Summary of Ovarian Screen in Standard DMEM in IB Media

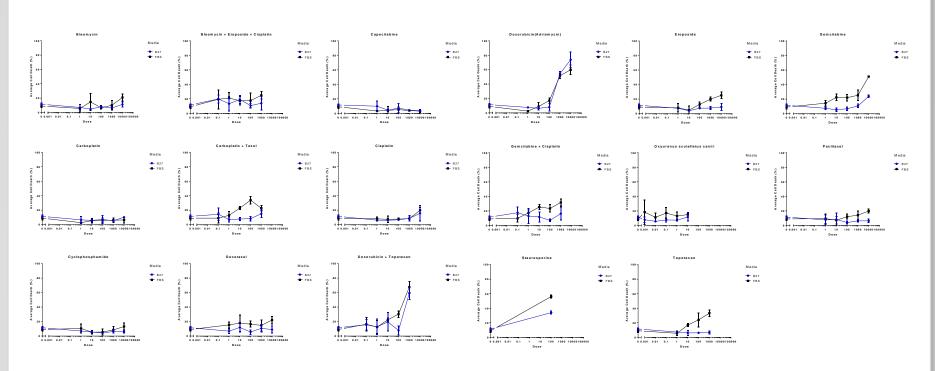




- Response is highly patient-dependent with some patients sensitive to the majority of treatments others highly insensitive to all treatment.
- Background cell death is a critical factor when looking at these particular heatmaps of multiple patients together.
- Background cell death is low in FBS, but in the selective media it can vary suggesting a subpopulation of 'normal' cells are being eliminated.



## Patient 1995T1Fa



- Sensitive to Doxorubicin
- Gemcitabine
- Topotecan (in FBS only)
- First example of how we could improve our growth media to make the assay more predictive.



## Patient response matchup with assay prediction

# Green- Correct prediction Pink - Incorrect

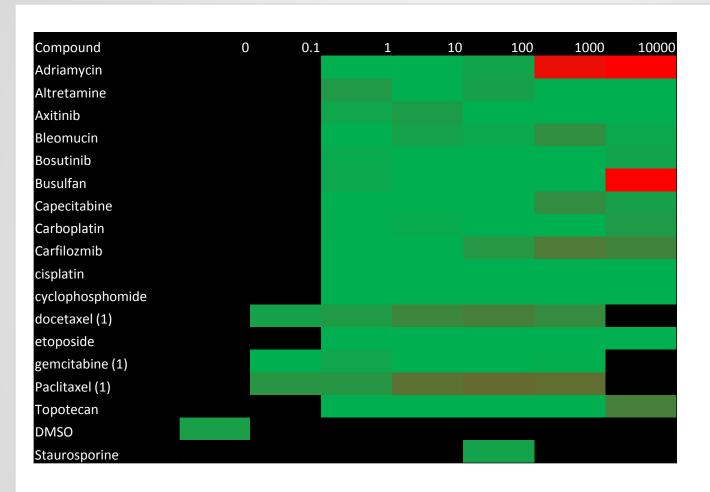
## Blue highlights represent actual clinical responders

Responder?	Identifier	Туре	When Sample was taken	Response?	Prediction correct?
	1901	Stage Illa high grade endometrioid adenocarcinoma of ovarian type	post treatment	N	Υ
	1987	stage 3c high grade serous	Pre treatment	N	Υ
	2170	poorly differentiated carcinoma of ovarian origin with omental mets	Pre treatment	N	Υ
	2175	Stage 4, mixed endometrioid and	Pre treatment	N	Υ
	2218	Colon,Metastatic sigmoid cancer	Post treatment	N	Y
	1980T1(B27)	Ovarian	Pre treatment	N	Υ
	215T1	Stage 3c/4 high grade serous adenocarcinoma of ovarian or primary peritoneal origin	Post treatment	N	Υ
	C001952	Stage 3c primary peritoneal/ovarian	Post treatment	N	Υ
	C001962T2AFa	Psammocarcinoma of ovarian	Post treatment	N	Υ
	C002075 T1A Fa	Stage 3c/4 adenocarcinoma of primary ovarian	Post treatment	N	Υ
•	- <b>∞</b> 002138 T1AFa	Unknown origin	Pre treatment	N	Υ
	C002220 TAFa	Stage 4 ovarian/peritoneal cancer	Pre treatment	N	Y
	C002254 T2AFa	Stage 3c High grade serious ovarian/ fallopian tubes/ primary peritoneal carcinoma	Pre treatment	N	Υ
	C002272	Stage 3/4 Low grade serous carcinoma	Pre treatment	N	Υ
	C002284T1	Stage 3c ovarian high grade serous carcinoma	Post treatment	N	Υ
	C002287T1AFa	High grade serous ovarian adeno carcino ma	Pre treatment	N	Υ
	C002346T1AFa	Primary tumour stage 4 ovarian cancer,	post treatment	N	Υ
	C002375T1AFa	Stage 3c low grade serous ovarian carcinoma	M id treatment	N	Υ
	C002393T1AFb	Relapsed stage 3C high	M id treatment	N	Y
	C002406T1	Recurrent high serous carcinoma	Post treatment	N	Υ
Υ	2122	High Grade serous adenocarcinoma,	Pre treatment	Υ	Υ
Y	C001874T1AFa	Stage IIIc ovarian cancer	Pre treatment	Υ	Υ
Y	C001926	Carcinosarcoma of the ovary, at least stage 3c Primary Peritoneal Cancer/Ovarian Stage 3c, poorly differentiated high grade	M id treatment	Υ	Υ
Y	C002222T1AFa	adenocarcinoma	Pre treatment	Y	Y
Y	C002307	poorly differenciated carcinoma	Pre treatment	Y	N
Y	C002307 C002350T¼Fa	poorly differentiated carcinoma  Poorly differentiated carcinoma of the ovary	Pre treatment		N Y
Y Y Y				Υ	

Cancer of unknown primary



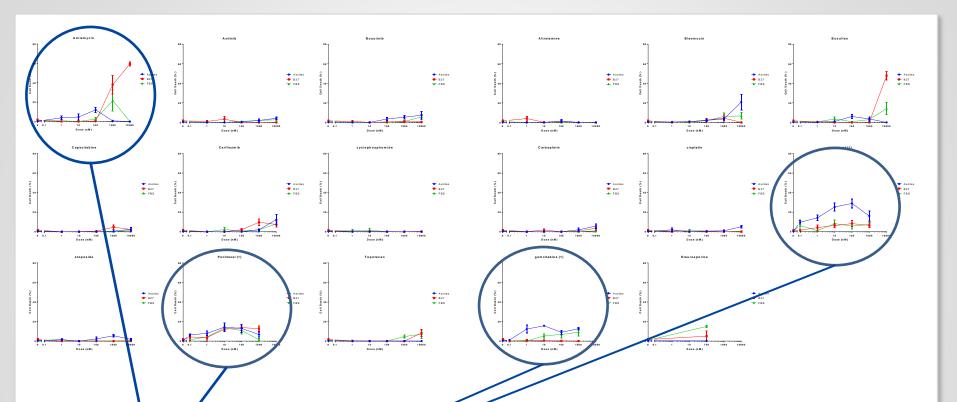
## Patient 2138 Cancer of Unknown Primary



Cancer very resistant to standard chemotherapies



## Patient 2138 Cancer of Unknown Primary

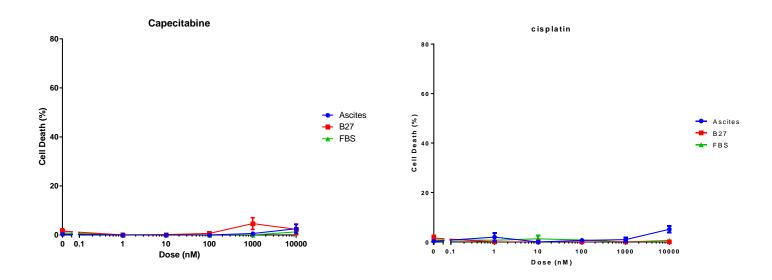


- This patient was analysed early in our development when we were comparing different culture media.
- Red line response is our own proprietary media. Cancer appears to respond to Adriamycin but only at high doses.
- Cancer may also be sensitive to docetaxel, gemcitabine and paclitaxel.



## Patient 2138 Received

## (Epirubicin, Oxaliplatin & Capecitabine) 16/06/2014 - 03/10/2014



Patient passed away 22/10/2014



## Summary of Assay Predictive Rate

- 28 samples 27 correct predictions (overall prediction 96%)
- All predictions indicating positive response were correct (7/7 100% specificity)
- Only 1 prediction indicating no response was incorrect
- The rest were correct (7/8 88% sensitivity)

Why do we out perform earlier in vitro cell death assay studies?

**Growth medium:** Our data demonstrates cells grown in FBS have a lower prediction rate of *in vivo* tumour response.

**Timing:** The assay needs to be performed immediately.

Sample C002287: Our assay showed correctly there would be no response. Stable cell line derived after several months in FBS showed incorrectly it would respond. This satisfies the strongly held position that cells change when you grow them on plastic long term.

**Assay:** We measure cell death directly not a surrogate marker of cell count.

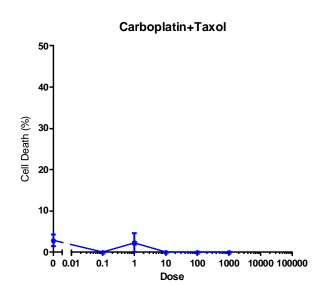
Overall the 1990s data did show prediction of response but not improvement in survival (PM is only as good as the best drug you have available to treat the patient)

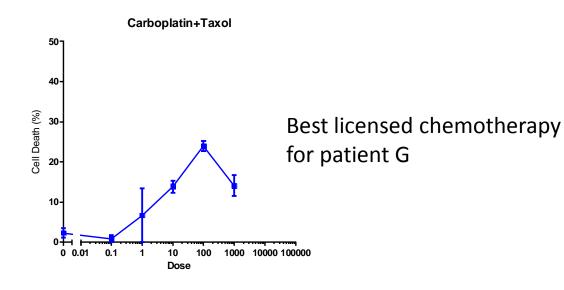
## **Our Contention**

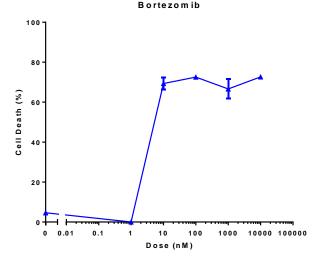
If you used our assay with standard licensed therapies then you will not have the statistical power to see significant shift on overall survival curves and this is the mistake that was made in the 1990s.



## Responder versus non responder



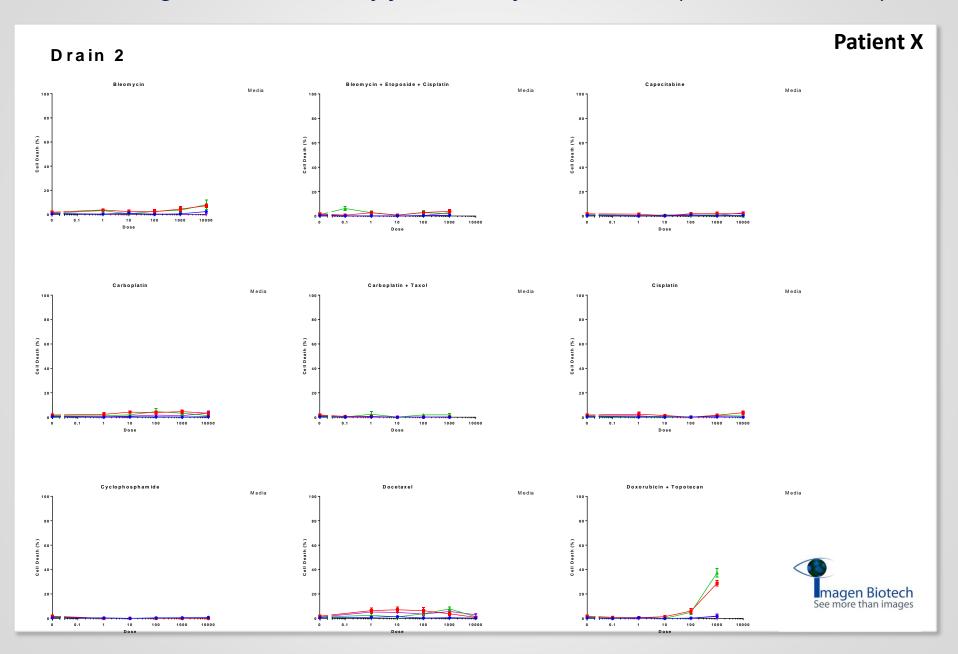




Best response in larger 56 chemotherapy screen for patient Y

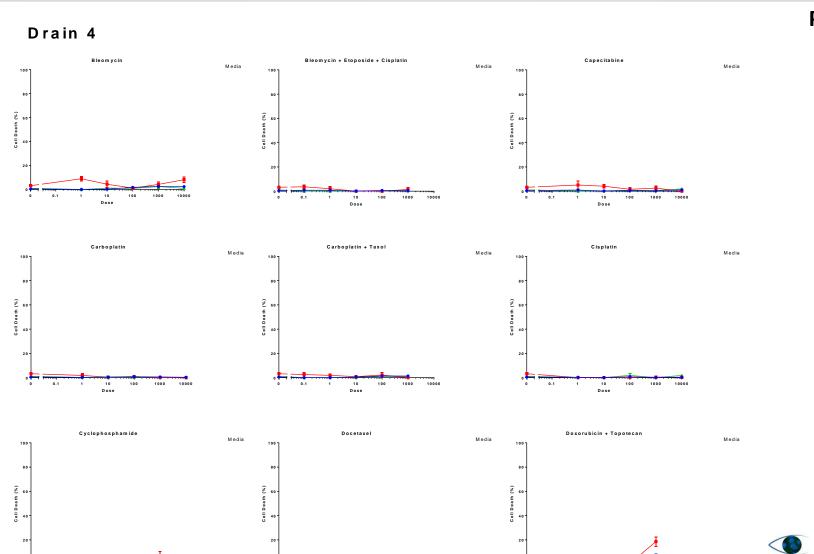


# The Drugs Don't Work they just make you worse ... (The Verve, 1997)



## The Drugs Don't Work they just make you worse ... (The Verve, 1997)

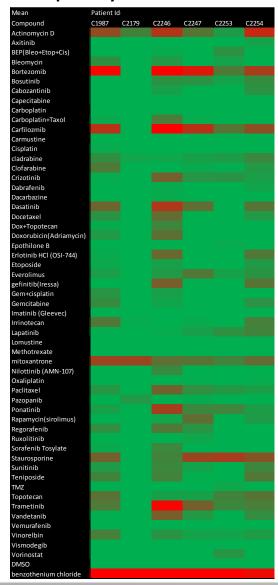
#### **Patient X**





## Larger Screen with 54 chemotherapies

#### **Proprietary Culture Media A**

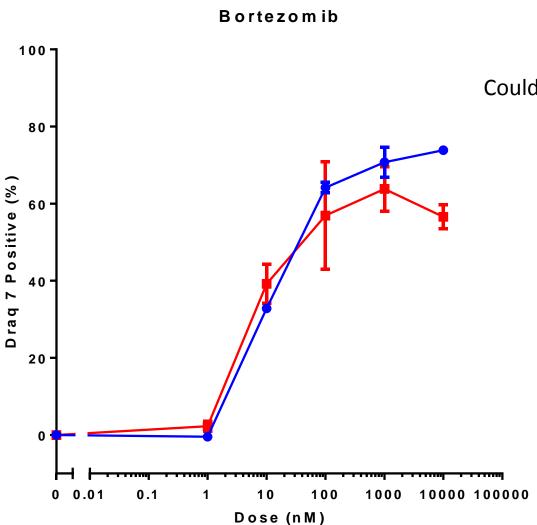


- 2D measure is % cell death.
- Each block represents the mean response across a log scale dose response curve.
- Heat map code:
  - 1. Green = all data where death is below the 50 percentile.
  - 2. Red = all data where death is above the 97 percentile.
  - 3. 51-97 percentile coded in green/red colour mixtures proportional to the percentile value.



## Patient X Response to Bortezomib

#### Patient X

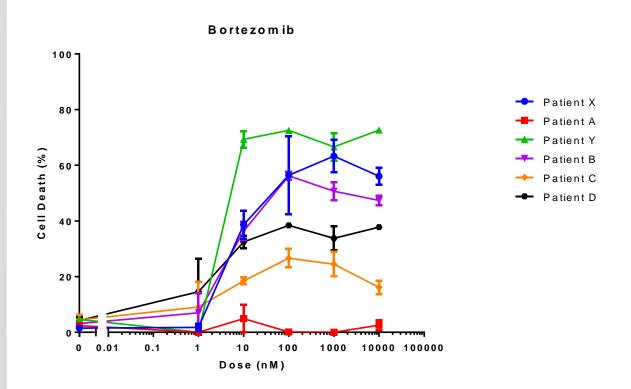


Could this be an assay false positive?



## Background Dose Response Curves for 6 patients

- Can use the data set a group of patients to address the question of in vitro assay false positives. If
  heterogeneous responses are observed for a particular drug in different patients then this suggests
  the assay is picking up true patient differences in chemosensitivity profiles for the particular drug
  under study (as shown below).
- Disturbingly these data predict that Bortezomib will work in only a subset of ovarian patients so how this will translate in a clinical trial is uncertain.





## Phase I Clinical Trial – Bortezomib with Carboplatin

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JOURNAL OF CLINICAL ONCOLOGY

ORIGINAL REPORT

#### Phase I Trial of Bortezomib and Carboplatin in Recurrent Ovarian or Primary Peritoneal Cancer

C. Aghajanian, D.S. Dizon, P. Sabbatini, J.J. Raizer, J. Dupont, and D.R. Spriggs

ABSTRACT

#### Purpose

To determine the maximum-tolerated dose, pharmacodynamics, and safety of the combination of bortezomib and carboplatin in recurrent ovarian cancer.

#### Patients and Methods

Fifteen patients were treated with a fixed dose of carboplatin (area under the curve [AUC] 5) and increasing doses of bortezomib (0.75, 1, 1.3, and 1.5 mg/m²/dose). Patients must have received upfront chemotherapy and up to two prior chemotherapy regimens for recurrent disease. Neurologic evaluation was performed at baseline and after every two cycles by the Functional Assessment of Cancer Therapy/Gynecologic Oncology Group neurotoxicity questionnaire and examination by an attending neurologist. All patients received carboplatin alone in cycle 1 to establish baseline pharmacodynamics for nuclear factor-kappa B (NF-kB). Starting with cycle 2, patients were treated with carboplatin on day 1 and bortezomib on days 1, 4, 8, and 11.

#### Results

Diarrhea, rash, neuropathy, and constipation (with colonic wall thickening on computed tomography) were dose-limiting toxicities, occurring in the two patients treated at the 1.5 mg/m²/dose level. The Functional Assessment of Cancer Therapy/Gynecologic Oncology Group neurotoxicity questionnaire was helpful in guiding the need for dose reductions. Neurotoxicity was manageable through six cycles, with appropriate dose reductions. Carboplatin had no effect on bortezomib pharmacodynamics as measured by percent inhibition of the 20S proteasome. Bortezomib decreased carboplatin-induced NF-kB. The overall response rate to this combination was 47%, with two complete responses (CR) and five partial responses, including one CR in a patient with platinum-resistant disease.

- 47% response rate
- 2 out of 15 complete responders
- 1 in platinum sensitive 1 in platinum resistant group

# Conclusion of study is very positive and recommends progression to phase 2 trial

"The preclinical activity of bortezomib makes it a promising agent for combination therapy in overcoming chemotherapy resistance. The CR seen in this study in a platinum-resistant patient is also encouraging."

apy Service, Merrorial Sloen-Kettering Cancer Certer, New York, NY: The Program in Werman's Oncology. Wormen & Infenta' Heapinel, Brown Medical School, Providence, RI; and Department of Neurology, Northwestern University, Feinberg School of Medicine, Chicago, IL. Submitted February 14, 2005, expected

From the Developmental Chemother

Submitted February 14, 2005; accepted May 9, 2005.

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Authors' disclasures of potential conflicts of interest are found at the end of this article.

Address reprint requests to Cerol Aghajanian, MD, Memorial Sloen-Kettering Cencer Center, 1275 York Ave, New York, NY 10021; e-mail: aghajano@makcc.org.

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0732-163X/05/2325-5943/\$20.00

DOI: 10.1200/JCO.2006.16.006



## Phase 2 Clinical Trial – Bortezomib with Doxirubicin

#### ORIGINAL STUDY

### An Open-Label Phase 2 Study of Twice-Weekly Bortezomib and Intermittent Pegylated Liposomal Doxorubicin in Patients With Ovarian Cancer Failing Platinum-Containing Regimens

Gabriella Parma, MD,\* Rosanna Mancari, MD,\* Gianluca Del Conte, MD,† Giovanni Scambia, MD,‡
Angiolo Gadducci, MD,§ Dagmar Hess, MD,|| Dionyssios Katsaros, MD,¶ Cristiana Sessa, MD,#
Andrea Rinaldi, PhD,# Francesco Bertoni, MD,# Andrea Vitali, ScD,\*\*
Carlo Vittorio Catapano, MD, PhD,# Silvia Marsoni, MD,\*\* Helgi van de Velde, MD, PhD,††
and Nicoletta Colombo, MD\*‡‡

Background: Pegylated liposomal doxorubicin (PLD) is an established treatment for relapsed ovarian cancer. Preclinical and clinical evidences in other tumor types suggest that the proteasome inhibitor bortezomib can act synergistically with PLD.

Methods: Patients with relapsed ovarian cancer (N = 58), previously treated with platinum (100%) and taxane (95%), received bortezomib, 1.3 mg/m<sup>2</sup> intravenous (days 1, 4, 8, and 11), and PLD, 30 mg/m<sup>2</sup> intravenous (day 1), every 3 weeks. Tumor responses were assessed using Response Evaluation Criteria In Solid Tumors and Gynecologic Cancer Intergroup criteria. An optimal 2-stage design was implemented. Gene expression profiling in peripheral blood was characterized before and during treatment in 10 platinum-sensitive patients enrolled in stage 2 of the study.

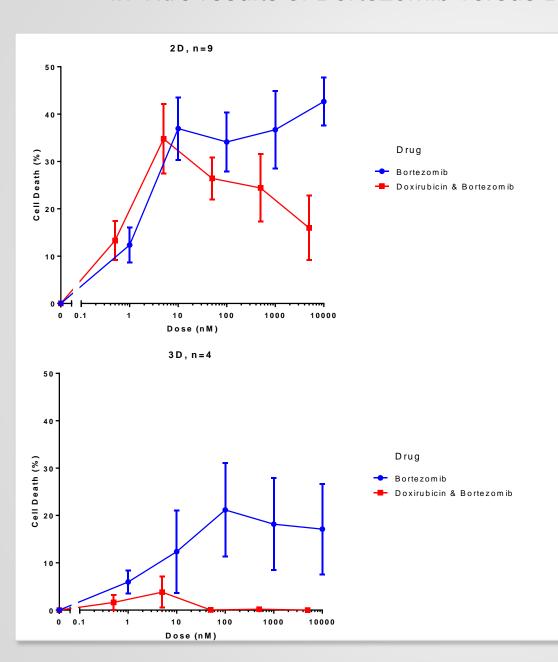
Results: Median number of borte zomib-PLD cycles was 3.5. Of 38 patients in the platinumsensitive group, 9 responses were observed (median duration, 4.8 months). The platinumresistant group was closed at stage 1 owing to lack of response. Toxicity was moderate and Overall conclusion response rate no different from doxirubicin on its own so did not recommend further use.

"Conclusions: The combination of bortezomib and PLD was well tolerated, but the antitumor activity is insufficient to warrant further investigation in ovarian cancer."

Our data suggests that bortezomib does not work as well when combined with doxorubicin.



## In Vitro results of Bortezomib versus Bortezomib & Doxirubicin

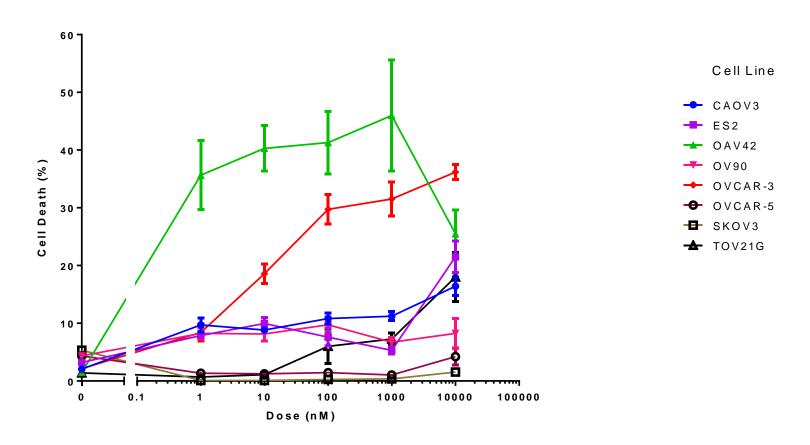


- Large error bars in 2D and 3D bortezomib because of the heterogeneous response of different patients to bortezomib (see slide 14 for example)
- In all 3D samples bortezomib and doxrubicin never worked better than bortezomib on its own.
- Both 2D and 3D data suggests that it is naïve to assume that drug combinations will never interfere with each other.



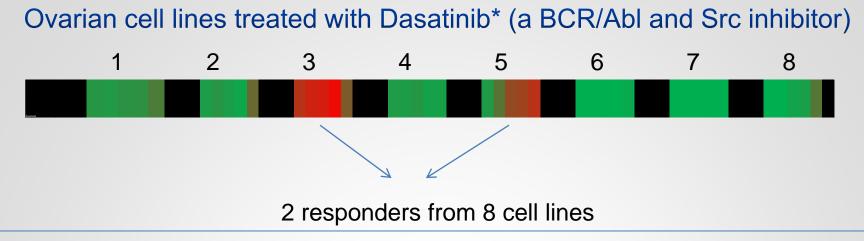
## Targeted Therapeutics- Another example of a personalised response

## **Dasatanib** tested in an 8 Ovarian cell line panel

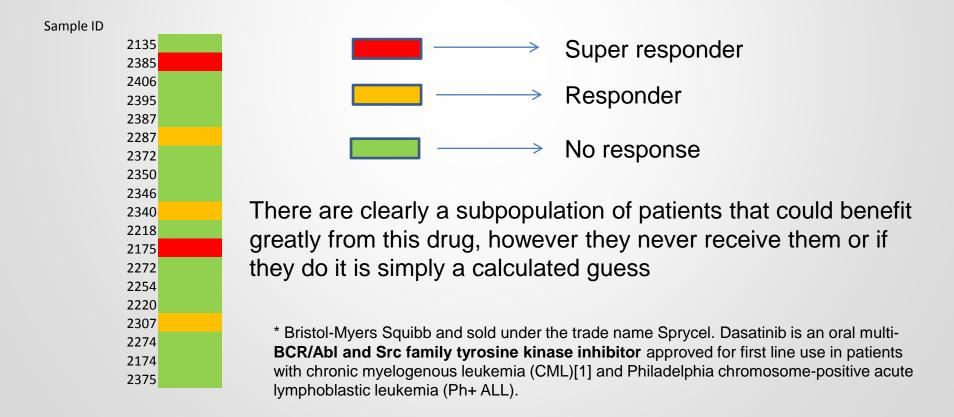


- 6 non-responders, 1 medium responder and 1 super responder.
- Would this pattern repeat in ovarian patients?





We therefore hypothesized that we would get some responders in our Ovarian Panel from patients

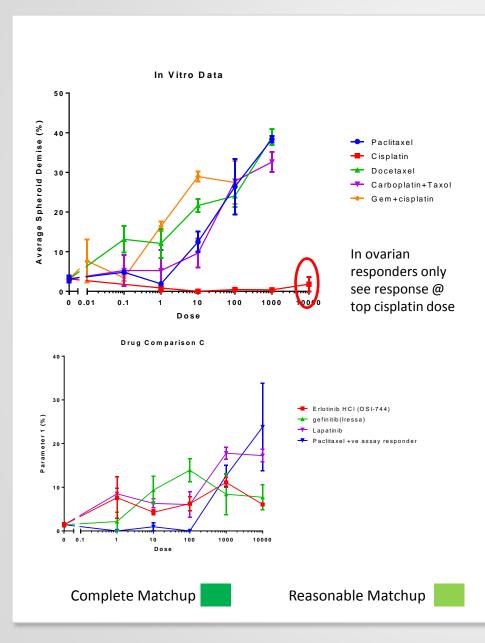


## Initial PDX Match Work

- Have received two frozen samples from a large company that specialised in PDX models.
- The first did not work, from the second we produced a good data set of 56 different chemotherapies.
- The second sample had been frozen for 8 years.
- Our match up with the PDX response was good.
- We will continue to work with this company hopefully moving towards a prospective treatment study where our data is used to directly influence the chemotherapy treatment of the mice.



## **Initial PDX Match Work**



	Drug	Dose (mg/kg)	Route	Schedule	% TGI	
	Paclitaxel	20 mg/kg	iv	q4dx3	33	
	Cisplatin	1.5 mg/kg	ip	qdx5	20	
	Docetaxel	20 mg/kg	iv	q7dx3	78	
	Docetaxel	5 mg/kg	iv	q7dx3	59	
	Paclitaxel	25 mg/kg	iv	q7dx3	44	
	Carboplatin	30 mg/kg	ip	q7dx3		
	Cisplatin	1.5 mg/kg	ip	qdx5	79	
	Gemcitabine	40 mg/kg	ip	q3dx4		
	Carboplatin	30 mg/kg	ip	q7dx3	79	
NT	Paclitaxel	25 mg/kg	iv	q7dx3		
	Bevacizumab	5 mg/kg	ip	q3dx8		
NT	Pemetrexed	200 mg/kg	ip	qdx5x2	0	
	Erlotinib	50 mg/kg	ро	qdx28	66	
	Paclitaxel	10 mg/kg	iv	q4dx6	13	
	Cisplatin	7.5 mg/kg	ip	q7dx4	58	
	Erlotinib	35 mg/kg	ро	qdx23	61	



Possible Mismatch

## **Next Steps**

- We want to publish the data with our clinical colleagues as co-authors as soon as
  possible. Part this process will involve working closely with them to audit our
  matchup data and try to, as best we can mimic Recist categories even though these
  patients were not part of a formal clinical trial.
- We now want to expand quickly into other cancers especially finalising an upstream workflow for the collection of solid tissue from theatre.
- Work with a few surgeons in the MRI to tweak upstream workflow of tissue collection from theatre to Imagen Biotech.
- The next cancers we want to look at in order of preference are:
  - 1. Solid ovarian cancer (so we can compare data with ascites source).
  - 2. Malignant melanoma (because of the BRAF hyper-responder mutation).
  - 3. Cancer of Unknown Primary (CUP) because it does not have a clear chemotherapy protocol for treatment.
  - 4. Breast Cancer
- A prospective PDX animal study to validate our assay's off-license predictive power.



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