

April 28 (Thu) - 30 (Sat), 2016 The Shilla Jeju Hotel, Jeju Island, Korea

> Better Thinking for Better Life: Exploring Advancing and Transforming Cancer Care



Physician Scientist's View

Innovative Clinical Trial in the Era of Genomics

Yeon Hee Park, M.D., Ph.D. Breast Cancer Center Medical Oncology Samsung Medical Center Seoul, Korea



Contents

- Overview of precision medicine
- Genomics-driven clinical trials
- Oncoseq in patients with refractory MBC in SMC
- Incorporation of immune-oncology into precision medicine





Genetic Heterogeneity in Human Disease

Jon McClellan^{1,*} and Mary-Claire King^{2,*} ¹Department of Psychiatry ²Departments of Medicine and Genome Sciences University of Washington, Seattle, WA 98195-7720, USA *Correspondence: drjack@uw.edu (J.M.), mcking@uw.edu (M.-C.K.) DOI 10.1016/j.cell.2010.03.032

Strong evidence suggests that rare mutations of severe effect are responsible for a substantial portion of complex human disease. Evolutionary forces generate vast genetic heterogeneity in human illness by introducing many new variants in each generation. Current sequencing technologies offer the possibility of finding rare disease-causing mutations and the genes that harbor them.

"Happy families are all alike; each unhappy family is unhappy in its own way."

Leo Tolstoy, Anna Karenina

Enabling Components for Genomicsdriven Cancer Medicine



Levi A, Garraway. J Clin Oncol 31:1806-1814, 2013.

"Tonight, I'm launching a new **Precision Medicine** Initiative to bring us closer to curing diseases like cancer and diabetes — and to give all of us access to the personalized information we need to keep ourselves and our families healthier."—









Declaring War Against Cancer

The signing of the National Cancer Act of <u>1971</u> by then U.S. President Richard Nixon is viewed as the beginning of the war on cancer.



President Richard Nixon signs the National Cancer Act, Dec. 23, 1971, Iaunching a \$1.6 billion federal crusade to conquer cancer. (AP)





The workflow of integrating omics data in cancer research and clinical application



Shyr and Liu Biological Procedures Online 2013, 15:4

'Genomic Tsunami'



Nature 2009, 458; 719-724

November 2015 / Vol 527 / Issue No 7576

Breast Cancer Treatment in 10 years

Predictions



- The era of HER2 is almost over.
- BRCA testing will become ubiquitous.
- We will continue to target proliferation and survival pathways.
- Cancer genomics will become ubiquitous, but we won't like what we find.
- We will need to do something different.

Norman Sharpless of the University of North Carolina works with IBM Watson Health to analyse DNA data.



Reshaping the cancer clinic

CancerLinQ Completes Agreements with Over Thirty-Five "Vanguard" Practices; Benefits for Practices Who Sign Up by June 1, 2016

CANCER-LINQ

CancerLinQ LLC is working with "vanguard" practices to begin implementing CancerLinQTM. In addition, ASCO is encouraging more of its members to have their practices become early adopters of CancerLinQ. Practices who sign up before June 1, 2016, will receive benefits.

CONQUER



LEARN MORE ABOUT BECOMING AN EARLY ADOPTER

Big data's war on cancer is still in the early stages, but the front line is advancing.

ASCO CANCER+LINO^T

In late 2015, the ASCO is expecting to launch CancerLinQ, <u>a</u> platform designed to deliver clinical benefits by analyzing aggregated electronic health records from thousands of oncology practices.

"Much of what we know about treating cancer comes from clinical trials that enroll just 3% of the patients diagnosed with cancer every year,"

"With CancerLinQ, we're trying to learn from the remaining 97% who don't participate in these studies."

ASCO CancerLinQ Newsletter

Amazing Science: Top 10 Medical Innovations for 2016

October 28, 2015 / By News Wire Team

Take a look at the top 10 medical innovations from Cleveland Clinic's 2016 Medical Innovation Summit.



- 1. Vaccines to prevent public health epidemics
- 2. Genomic directed clinical trials
- 3. Gene editing using CRISPR
- 4. Water purification system for prevention of infectious diseases
- 5. Cell-free fetal DNA testing
- 6. Cancer screening via protein biomarker analysis
- 7. Naturally controlled artificial limbs
- 8. First-ever treatment for HSDD
- 9. Frictionless remote monitoring
- 10. Neurovascular stent retriever

Randomized trial designs with integral biomarkers

- Basket design
- Umbrella design
- Enrichment design with biomarker
- Stratified design according to with or without biomarker
- Hybrid design



Clinical trial designs utilizing molecular profiling





Nature 2015, 526; 361-370; JNCI J Natl Cancer Inst, (2015) 107(4): djv003

Precision-medicine clinical trials

| Study | Tumour | Phase/design | Location | Arms | Patients ⁺ | Clinical trial ID | References |
|-----------------|----------------------|-------------------------------------|----------------|---------|-----------------------|---------------------------------|------------|
| Bisgrove | All | Phase II, non-randomized | United States | N/A | 84 | NCT00530192 | 19 |
| IMPACT | All | Phase I | United States | N/A | 1,144 | NCT00851032 | 20 |
| MOSCATO 01 | All | Phase I | France | N/A | 420 | NCT01566019 | 21 |
| Lung-MAP | Squamous lung | Phase II/III, randomized | United States | 5 | 10,000 | NCT02154490 | 49 |
| BATTLE | NSCLC | Umbrella, route to four phase II | United States | 4 | 300 | NCT00409968 (umbrella) | 31, 66, 67 |
| | | "Master protoc | col" or "F | Platfor | m pr | otocol" | |
| | | | | | | NCT00410189 | |
| BATTLE-2 | NSCLC | Phase II randomized | United States | 4 | 450 | NCT01248247 | N/A |
| BATTLE-FL | NSCLC | Phase II randomized | United States | 4 | 225 | NCT01263782 | N/A |
| I-SPY 2 | Breast cancer | Phase II randomized | United States | 8 | 800 | NCT01042379 | 68, 69 |
| NCI-MPACT | All | Phase II stratified, non-randomized | United States | 6 | 700 | NCT01827384 | 70 |
| NCI-MATCH | Solid | Phase II stratified, non-randomized | United States | 20 | 3,000 | Umbrella, route to phase II‡ | 48 |
| V-BASKET | All | Phase II stratified, non-randomized | Global | 2 | 160 | NCT01524978 | 71 |
| CREATE | Selected | Phase II stratified, non-randomized | European Union | 6 | 582 | NCT01524926 | N/A |
| WINTHER | All | Stratified, non-randomized | European Union | 2 | 200 | NCT01856296 | 72 |
| SHIVA | All | Phase II stratified, controlled | France | 10 | 1,000 | NCT01771458 | 38 |
| MOST | All | Phase II stratified, randomized | France | 5 | 560 | NCT02029001 | N/A |
| SAFIR 02 Lung | NSCLC | Phase II stratified, randomized | France | 8 | 650 | NCT02117167 | 73 |
| SAFIR 02 Breast | Breast cancer | Phase II stratified, randomized | France | 18 | 460 | NCT02299999 | N/A |
| Lung MATRIX | NSCLC | Phase II stratified, non-randomized | United Kingdom | 21§ | 2,000 | EudraCT 2014-000814-73 | 65 |
| FOCUS 4 | Colorectal cancer | Phase II/III randomized | United Kingdom | 4 | 643 | EudraCT 2012-005111-12 | 74 |
| IMPaCT | Pancreatic cancer | Phase II stratified, randomized | Australia | 4 | 90 | ACTRN 12612000777897 | 47 |

Nature 2015, 526; 361-370

Screening programmes that feed into precision-medicine trials

| I-SPY | Breast cancer | Phase II, diagnostic study | United States | Genomic, imaging | 221 | NCT00043017 |
|-------------|-------------------|------------------------------------|----------------|--|--------|-------------|
| NCI-MATCH | Solid | Screening, route to phase II | United States | NGS¶ | 3,000 | N/A |
| VIKTORY | Gastric cancer | Screening, route to phase II | Asia | NGS, other# | 600 | NCT02299648 |
| LC-SCRUM | NSCLC | Screening, route to phase II/III | Asia | As needed** | Open†† | N/A |
| AURORA | Breast cancer | Screening, route to phase I/II/III | European Union | NGS, other‡‡ | 1,300 | NCT02102165 |
| SPECTAColor | Colorectal cancer | Screening, route to phase I/II/III | European Union | NGS | 2,600 | NCT01723969 |
| SPECTALung | Lung | Screening, route to phase I/II/III | European Union | NGS | 500§§ | NCT02214134 |
| MOSCATO | All | Screening, route to phase I/II | France | CGH array, sequencing | 1,050 | NCT01566019 |
| SAFIR 01 | Breast cancer | Screening, route to phase I/II | France | CGH, sequencing, gene expression array | 423 | NCT01414933 |
| CRUK SMP1 | Selected | Screening, feasibility | United Kingdom | Bespoke panel | 9,000 | N/A |

The NCI National Clinical Trials Network (NCTN) structure



Adaptive Bayesian Clinical Trial Design



Clinical trials testing large panel of genes for treatment decision

| Trial | Technology | n screened | Matched therapy | Outcome | | |
|-----------------------|---|---------------|---------------------|--|--|--|
| SAFIR01 ¹ | CGH / | 423 | 55 (13%) | 30% OR and/or | | |
| (brea MOSC/ seq | No evidence from large clinical trial that ths sequencing large panel of genes improves outcome!! | | | | | |
| MDACC ³ | 11-50 genes | 2 000 | 83 (4%) (P1 trials) | Not available | | |
| Princess Margaret⁴ | 48 genes | 1595 | 64 (4%) | 22% OR | | |
| T-Gen⁵ | Gene expression | 86 | 66* | 27% PFS ratio of ≥ 1.3 | | |
| SHIVA ⁶ | NGS | 741 | 195 ^{\$} | hazard ratio 0.88, 95% Cl 0.65–1.19, p=0.41 | | |

Is it a new generation of garbage-in/garbage-out???

1. Andre, Lancet Oncol, 2014, 2. Ferte, AACR, 2014, 3. Meric-Bernstam, JCO, 2015, 4. Bedard, ENA, 2015, 5. Von Hoff, JCO, 2010, 6. Letourneau, Lancet Oncol, 2015 This presentation is the intellectual property of the author/presenter. Contact them at fandre@igr.fr for permission to reprint and/or distribute

Lessons from Genome Profiling Clinical Trials

- Why these trials failed ?
 - Drugs are not bioactive and/or not well matched to alterations.
 - Method for driver identification is not optimal: validated and robust tools to interpret biology at the individual level were not available

• Rare mutations are....rare.

- Uncommon and rare mutations make it very hard to do studies to get drugs approved.
- RCT(randomized clinical trials) vs. SOC (standard of care) can be very difficult: Unappealing to pts and their doctors

Oncoseq Project for Patients with Refractory MBC in SMC

Screening program for 'N of 1 trial' experience in SMC for patients with MBC

- Genomic platform for the treatment of the patients with refractory malignancies in SMC based on multiomics
- 2012-
- WES, WTS, CancerSCAN (targeted sequencing)

Work flow for NGS

BC Lab

Oncoseq Breast [Pathology QC Chart] 1. Tissue Information Oncoseq Breast No. CB_ 15-0109 BR No. 환자번호 환자이름 검 체 명 조직채취방법 OP 과제명 임상교수님 HEART CCD 접수일자 CCD 담당자 비고 Surgery

0 1 2

Core biopsy

1 2 3

2. Pathology QC (검사)



Informed Consent

Tissue delivery



판특열 BC Lab Oncoseg Breast (BC Lab OB)

Necrosis QC Result (F/I/A)

DNA

ANDIANA

Surgery

Core biopsy

2015 eft.10

2. \$2401E 2022(b)

연락치

BR No.

환자이름

조직채취방법

영상교수님

CCD 담당자

Cells

| 2월 21월 48 1872년 1971년 18 28년 8 28년 8 | | 13 | | | | | | 6/08/24 | 274.0 |
|--|----------------------|-----------------------|--------------------|----------|---------------|--------------------------|---------------------------|------------|-------|
| -18 118 48 (목가철 (무역문자명 (목연호 | 493.0 | 7.21 | | | | | | | |
| 1年가중 2 2 개인자(B 2 유민호 | 442.0 | 7.21 | And the local | | | | | | |
| 20112178 20112 | and an inclusion | | 04 1-9 | | 2004-0834 | | 1.7.0 | | |
| 7352 | | FM . | 24 94 | Frages (| Cellisian. | | -144 | | |
| | | | 21.84 | C Timat | 🗆 Cell pellet | 7(6) | 08-88 | 2016-8 | |
| 시력할 주수 | | | 24.18 | | 3.64 | | Report 1277 | 2016 1 | |
| 149 7 | | | \$19.70 (\$6E) | | 6N3 | | 8.2.9 (955) | 24 | |
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| Country on Party | in the second second | | | | No. 0 1 | 4-100000 | | DisAndvier | _ |
| U.R. | Sample ID | Sample ID (option) | 554 80 | 256/289 | 265/250 | Conc. | Total Amount | RIN | Grade |
| 1 | OR 35,0054,05 | | 8.95.0099.87.975 | 20 | 2.0 | 479.0 | 10445 | 310 | 710 |
| 2 | OR MORE IN | | R. M. MIRC 27, WTS | 2.0 | | 47)4 | 10434 | 800 | 719 |
| 3 | 08.00.000.01 | | 8,36,0091,07,NTS | 21 | 1.9 | 248.3 | 1.02 | 6.9 | 712 |
| 4 | OR 21,0238,05 | | R 34,00082 RT INTS | 21 | | 186.9 | 6.54 | 98 | 712 |
| 3 | OR \$5,0008.00 | | R. M. MIRE RT. WTS | 20 | 0.0 | 1345 | 40 | 73 | 719 |
| | | 2000 1000 200 | | _ | - | | | | |
| <mark>QC 29에도</mark> 35 개매 | | 25 | | Tetal | 2014 | _ | | | |
| | | | | | | *7* | N Grade 13 위험(는)월2/부위험 | | |

NGS

SGI

| 1. Tissue Inform | nation | attiology QC | chur tj |
|-------------------|------------|------------------|-----------|
| ncoseq Breast No. | 00-15-0119 | BR No. | BR03N-030 |
| 환자번호 | | 환자이름 | 765-21 |
| 검 채 명 | | 조직채취방법 | Bx |
| 과제명 | | 임상교수님 | 767102 |
| CCD 접수일지 | | | |
| 비고 | | community of the | |

0112345



MBC WES (WTS paired 34 samples)

- Final mutation data : SNV 3,069 + indel 209 = 3,278
- Most frequent variant : TP53 (n=22 / SNV=14, indel=8)
- 2nd : PIK3CA (n=10, SNV=10)



SNV + INDEL





- TN samples have more SNVs than other groups, especially HER2+.
- ER+/HER2+ samples have fewer indels than other groups.



Case 1. Medical history (F/36)

Rt breast ca(pT2(3cm)N(3/8))(ER-/PR-/HER2-)(2007.8)

s/p Rt PM with ALND

```
s/p AC #4 + paclitaxel #4 + Radiotherapy (2007.10.1-2008.4.28)
```

```
- progression on lung (multiple hematogeneous lung metastses) (NED :2Y7M)
```

s/p palliative PG #20 (2010.03.04-2011.04.18) with CR -> PD

```
s/p capecitabine #3 (2011.10.24-2012.02.06) -> PD (Pleura)
```

```
s/p GP #6 (2012.03.12-2012.07.03) -> SD -> PD
```

```
s/p DC #14 (2013.12.16-2014.10.2) -> PR -> PD (Pleura, lung)
```

```
s/p eribulin #7 (2015.1.8-2015.6.4) -> SD -> PD
```

```
s/p vinorelbine #2 (2015.6.25-2015.7.23)
```

s/p VATS pleural biopsy and talc pleurodesis, Lt. (2015.8.19)

: metastatic carcinoma, ER/PR/HER2 (+(3)/-/-)ki-67(2+),EGFR(-), AR (-) DDK4/FGFR1 fusion, FGFR1 amplification (+)

s/p CMF #1 (2015.9.7)

```
- progression on CNS
```

s/p WBRT 30Gy/10Fx's (2015.9.16-2015.9.30)

s/p pazopanib (2015.11.20-2016.01.03) with SD

CNV 6 rows

| Class 🔺 | Gene 🔶 | Drug \$ | Position \$ | CNV \$ | Log2Ratio \$ | Copy No. 💠 Known 💠 |
|---------|---------|---|----------------|--------|--------------|--------------------|
| C1 | FGFR1 | Fibroblast growth factor receptor 1 (DB08577) | 8p11.23-p11.22 | Amp. | 1.28 | 4.9 Known |
| C1 | FGFR1 | Fibroblast growth factor receptor 1 (DB08577) | 8p11.23-p11.22 | Amp. | 1.28 | 4.9 Keown |
| C2 | MYC | | 8q24.21 | Amp. | 1.07 | 4.2 Known |
| C3 | GPR124 | | 8p11.23 | Amp. | 1.29 | 4.9 Unknown |
| C3 | WHSC1L1 | | 8p11.2 | Amp. | 1.31 | 5.0 Unknown |
| NA | ZNF703 | | 8p11.23 | Amp. | 1.25 | 4.8 NA |

Translocation 2 rows

| Class 🔺 | ChrA 🔶 | GeneA 🔶 | DrugA 🜲 | BreakpointA 🗢 | Direction | ¢ ChrB ¢ | GeneB ♦ | DrugB | BreakpointB ♦ | Total reads ♦ |
|---------|--------|---------|---------|-----------------------|-----------|----------|---------|---|----------------------|------------------|
| Т3 | 8 | DKK4 | | 42233274 [E2(4)] | A->B | (| B FGFR1 | Fibroblast growth factor receptor 1 (DB08577) | 38303524 [12(18)] | 118 |
| Т3 | 6 | GPSM3 | | Not_estimated [11(8)] | B->A | (| NOTCH4 | | 32163541 [I-121(30)] | 10 |

FGFR1

- Fibroblast growth factor receptor 1
- Chr8:38,411,139-38,468,834
- FGFR1 amplification
 - SCLC, SqCC of lung, Breast cancer
- TACC1-FGFR1 (FGFR1-TACC1)
 - Glioblastoma, Prostate cancer, bladder cancer

DKK4

- Dickkopf WNT Signaling Pathway Inhibitor 4
- Chr8:42,229,586-42,236,674

IGV bam file



| Class | ChrA | GeneA | DrugA | BreakpointA | Direction | ChrB | GeneB | DrugB | BreakpointB |
|-------|------|-------|-------|------------------|-----------|------|-------|--|-------------------|
| Т3 | 8 | DKK4 | - | 42233274 [E2(4)] | A->B | 8 | FGFR1 | Fibroblast growth factor receptor1 (DB08577) | 38303524 [I2(18)] |

1. RT-PCR

2. Q-PCR

0.1

0

S03013

OB_15_0177_1



OB_15_0177_1 : DKK4-FGFR1 fusion

3. Sequencing



Identification of **Targetable FGFR Gene Fusions in Diverse Cancers**

Yi-Mi Wu^{1,2}, Fengyun Su^{1,2}, Shanker Kalyana-Sundaram^{1,2}, Nickolay Khazanov¹⁰, Bushra Ateeq^{1,2}, Xuhong Cao^{1,7}, Robert J. Lonigro^{1,8}, Pankaj Vats^{1,2}, Rui Wang^{1,2}, Su-Fang Lin¹¹, Ann-Joy Cheng¹², Lakshmi P. Kunju^{1,2}, Javed Siddiqui^{1,2}, Scott A. Tomlins ^{1,2}, Peter Wyngaard ¹⁰, Seth Sadis¹⁰, Sameek Roychowdhury^{1,4}, Maha H. Hussain³ Felix Y. Feng^{1,4,8} Mark M. Zalunski³



Case 1: MO 1036

4,000 (8) -2

| Patient | 34-year-old female |
|--------------|-----------------------------|
| Cancer type | Cholangiocarcinoma |
| SNVs | 8 mutations (ARID1A, PBRM1) |
| Gene fusions | 8 fusions (FGFR2-BICC1) |



aPCR: FGFR2-BICC1

H2O MO- C1 C2 C3 C4 C5 C6 1036

1.29



Aberrant FGFR signalling occurs by diverse mechanisms in many cancer types

Amplification

| FGFR1 | ER+ breast cancer (9-23% SqNSCLC (10-20%) |
|----------|--|
| FGFR2 | Gastroesophageal (9%) |
| Fusion | |
| FGFR2 | Cholangiocarcinoma (15%) |
| FGFR3 | Bladder (6%) Glioblastoma (3-7%) |
| Mutation | |
| FGFR1 | Endometrial (12%) |
| FGFR3 | Bladder (10%-60%) |



ASCO

PRESENTED AT

Selected overview of clinical trials evaluating **FGFR signaling**—targeted therapies currently under development







Case 2 Medical history (F/47)

breast ca with M/stomach, peritoneum, bone & ovary at 2008
(ER+/PR+/HER2-)

s/p palliative ECX #1 (mis-diagnosed as AGC)

s/p palliative AC #7 (2008.10.08-2009.02.20)

s/p docetaxel #10 (2009.03.17-2009.09.28)

s/p AI + goserelin (2009.12.16-2013.12.30) -> PD (Peritoneal carcinomatosis)

s/p PG #12 (2013.1217-2014.08.18)

s/p tamoxifen (2014.11.10-2015.05.03)

s/p eribulin #11 (2015.5.4-2015.12.28) -> SD -> PD

s/p US guided peritoneum biopsy

: metastatic carcinoma, ER/PR/HER2 (+(5)/-/-)

HER2 mutation (TKD L755S)

On poziotinib (2016.02.22)





Current Limitations of Genomics-driven Clinical Trials Using Multi-Omics

- Real target? : oncogenic driver mutation << passenger mutations</p>
- Druggable target??
- Clinical application of **Bioinformatics**
- Need functional genomics
- Challenging adaptive clinical trial design
- Intra- and/or inter-tumoral Heterogeneity
- Evolving by-pass tracks → Resistance to target
- Cancer pathway Complexity: <u>multiple targets</u>, <u>cross-talk between pathways</u>

Hope for the Future

Treatments to date improve outcomes

- in both curative and metastatic settings

Clinical trials continue to push the frontier

- to better treatments and outcomes

Genetic testing of tumor tissue (and now blood!)

- helps us understand the driving forces in a cancer
- Clinical trials testing targeted therapies are ongoing
- Immunotherapy holds great promise
 - to better clinical outcomes
 - Clinical trials assessing how to best do this are ongoing



ASCO Plenary 2015

Insights into immune checkpoint blockade
CheckMate trial of immunotherapy in melanoma
Childhood Cancer Survivor Report
Case for preventive neck lymph node surgery
Risks of whole-brain radiation therapy

nature collections

Cancer immunotherapy



natureoutlook

Produced with expect of a standard educative guer have listed Myory Equities with expected of guers from 7. Methodore Coll. and Mines & Du., No. Enhancing natural defences

Panacea for Progress or Pandora's Box?



Room 354, Morial Convention Center Clinical Trials Design: Part 2

Chairperson: Elizabeth M. Jaffee, Baltimore, MD

10:15 a.m. Successes and challenges in designing combination immunotherapy clinical trials for breast cancer. Leisha A. Emens, Baltimore, MD
10:45 a.m. Issues faced by industry in developing safe and effective combination immunotherapies. Ira Mellman, South San Francisco, CA
11:15 a.m. Statistical challenges in designing combination immunotherapy clinical trials. Katy Simonsen, Princeton, NJ
11:45 a.m. FDA's point of view on trial designs for accelerating combination immunotherapies across multiple tumor types. Tatiana Prowell, Silver Spring, MD



Cancers 2015, 7(3), 1815-1846; doi:10.3390/cancers7030864

Incorporation of immune-oncology into precision medicine

New Orleans Theater B, Morial Convention Center Genomics-guided Immunotherapy

Chairperson: Catherine J. Wu, Boston, MA

1:00 p.m. Introduction

1:10 p.m. Tumor-host coevolution: Therapeutic implications. Catherine J. Wu, Boston, MA

1:40 p.m. Immunogenomics and precision cancer medicine. Eliezer Van Allen, Brookline, MA [SY18-02]*

2:10 p.m. RNA based individualized cancer immunotherapy. Ugur Sahin, Mainz, Germany (not eligible for CME credit)

Immunogenomics to search *Neo-antigen, 'inflammed' types, and proper combination therapeutic strategies*



Cocktails for cancer with a measure of immunotherapy

THE **PERFECT BLEND**

The next frontier in cancer immunotherapy lies in <u>combining it with other treatments</u>. Scientists are trying to get the mix just right.

BY HEIDI LEDFORD

COMBINATORIAL EXPLOSION

Ipilimumab, the first approved checkpoint inhibitor, has been tested in dozens of clinical trials since 2001. And like many other drugs in its class, it is increasingly being tested in combination with other therapies.



DESPERATELY SEEKING SURVIVAL

Patients generally respond well to targeted therapies (top), which are directed at specific mutations in a cancer, but only for a short time. Checkpoint immunotherapies (bottom) do not help as many people, but those they do help tend to live longer. Oncologists are trying to get the best out of both strategies by combining the drugs.



Acknowledgements

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- Our lab
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 - Jee Eun Lim
 - Ji-Yeon Kim
- SGI
 - Woong-Yang Park
 - Kyung Hee Park
 - Woosung Jung
- Pl
 - Young-Hyuck Im



SAMSUNG MEDICAL CENTER

GBCC2016 Global Breast Cancer Conference 2016

April 28 (Thu) - 30 (Sat), 2016 The Shilla Jeju Hotel, Jeju Island, Korea

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Thank You!