

RETOS DE LA MEDICINA DE PRECISIÓN

XXV ANIVERSARIO

Servicio de Oncología médica

Hospital de Basurto

Francisco Ayala de la Peña
Hospital G. Universitario Morales Meseguer
Universidad de Murcia

DECLARACIÓN DE POTENCIALES CONFLICTOS DE INTERESES

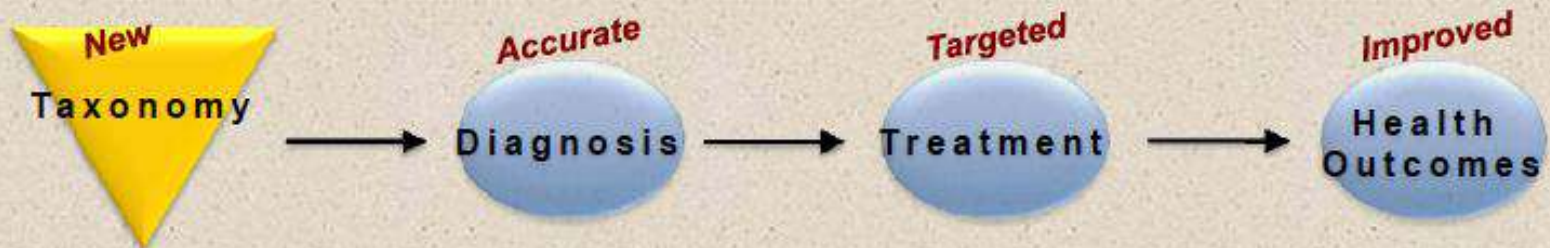
Título de la presentación: Retos de la Medicina de Precisión

Autor: Francisco Ayala de la Peña

- Relativas a esta presentación existen las siguientes relaciones que podrían ser percibidas como potenciales conflictos de interés:
 - Advisory: Pfizer, Roche
 - Fondos para investigación: Celgene, Roche
 - Charlas en reuniones promovidas por industria: AstraZeneca, Celgene, Eisai, Novartis, Pfizer, Pierre Fabre, Roche
 - Congresos/Symposia: Celgene, Eisai, Pfizer, Pierre Fabre, MSD, Roche
 - Programas educativos: MSD, Roche

Toward Precision Medicine: Building a Knowledge Network for Biomedical Research and a New Taxonomy of Disease

A new data network that integrates emerging research on the molecular makeup of diseases with clinical data on individual patients could drive the development of a more accurate classification of disease and ultimately enhance diagnosis and treatment. Recent advances in biomedical research have caused an explosion of data, offering the potential to develop a “New Taxonomy” that defines disease based on underlying molecular and environmental causes, rather than on physical signs and symptoms. This report outlines how research and clinical data can be captured in a “Knowledge Network” that will be broadly accessible to researchers and clinicians. As well as improving health care, the new data network could also improve



Patient 1: Consulting with her medical oncologist following breast cancer surgery

LAS “PROMESAS” DE LA MEDICINA DE PRECISIÓN

Conocimiento molecular de la enfermedad y estratificación pronóstica

Identificación de dianas terapéuticas y disponibilidad de biomarcadores predictivos

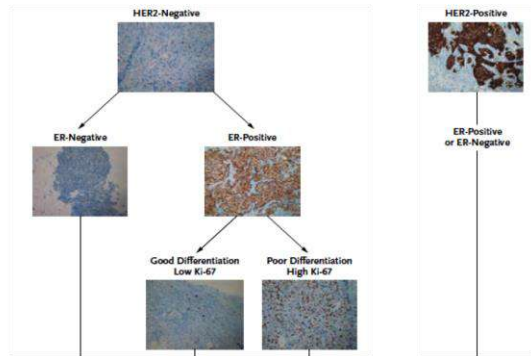
Conocimiento molecular de la evolución de la neoplasia y adaptación del tratamiento

Conocimiento de las características del huésped y personalización del tratamiento de acuerdo a la respuesta o toxicidad esperables

Precisión en el diagnóstico precoz

Mejora de los resultados del tratamiento

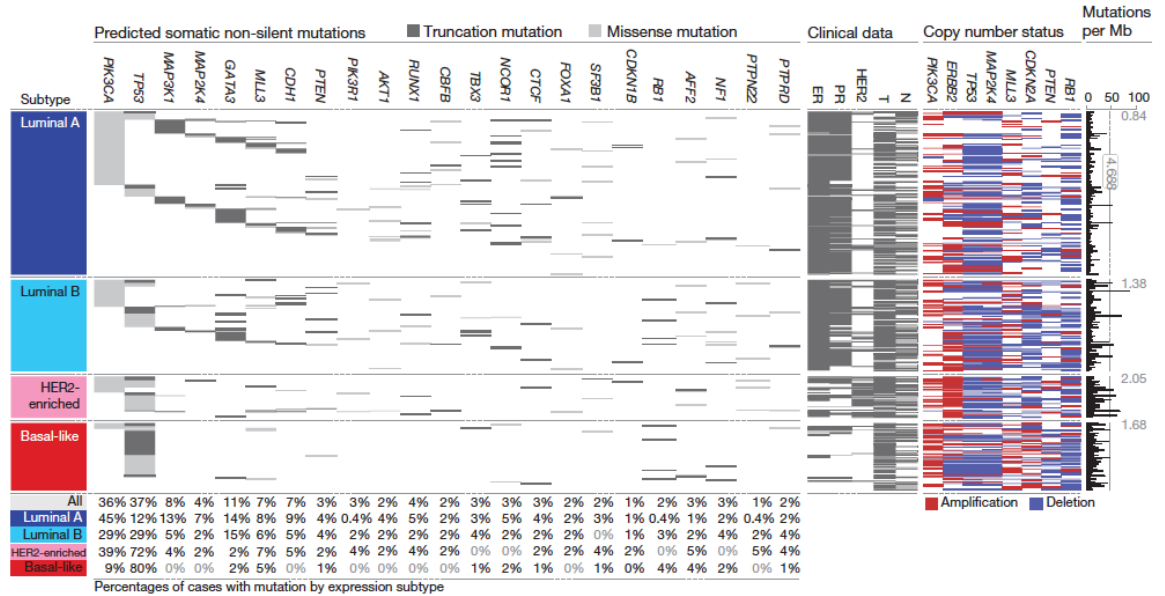
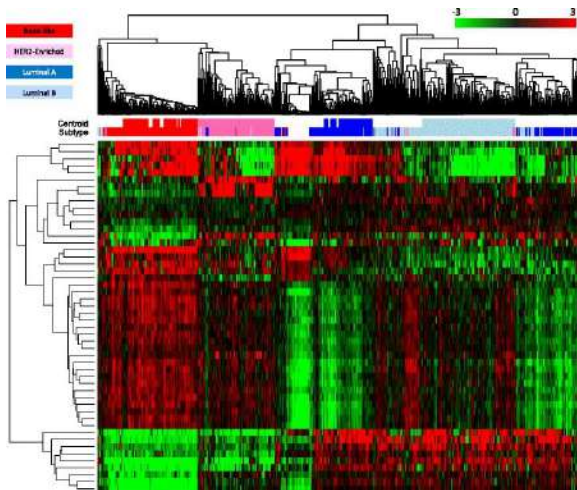
Clasificación molecular del cáncer de mama



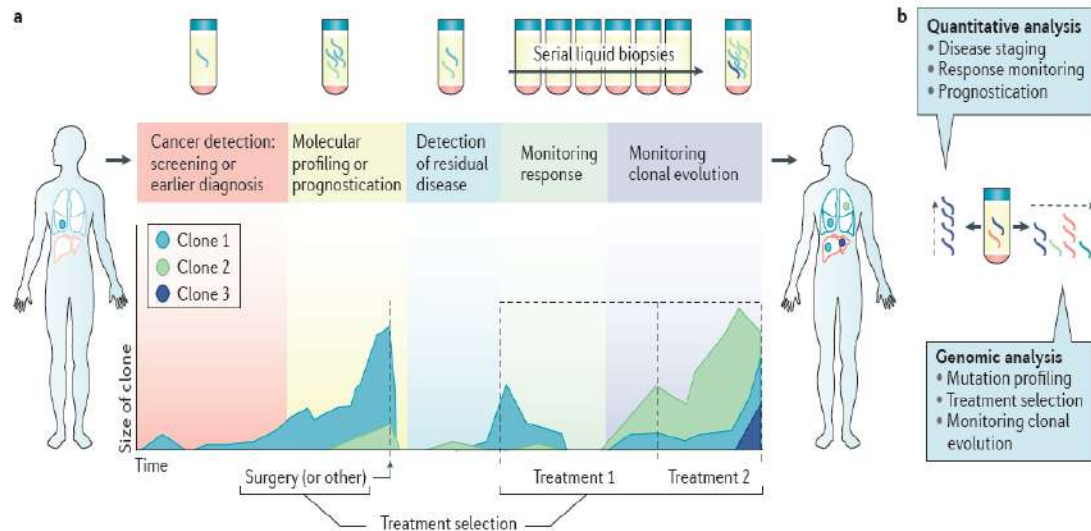
CM triple negative
Her2-, RE-, RP-
(CK5/6, EGFR)

CM luminal u hormonosensible
RE+ o/y RP+
(Ki67: LumA/ LumB)

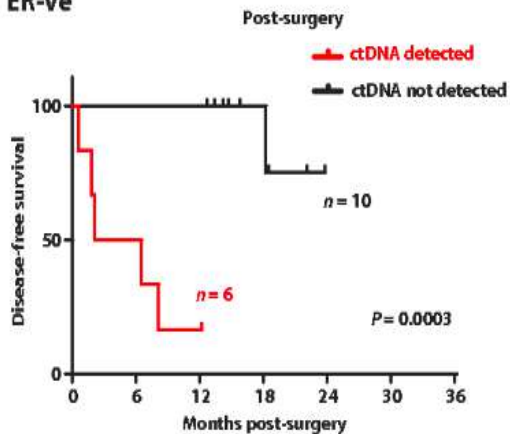
CM Her2+
Her2+++
(RE/RP + o -)



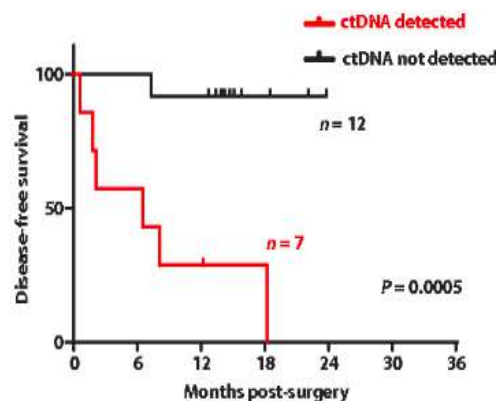
Biomarcadores (ctDNA, CTC) para identificar grupos de mal pronóstico



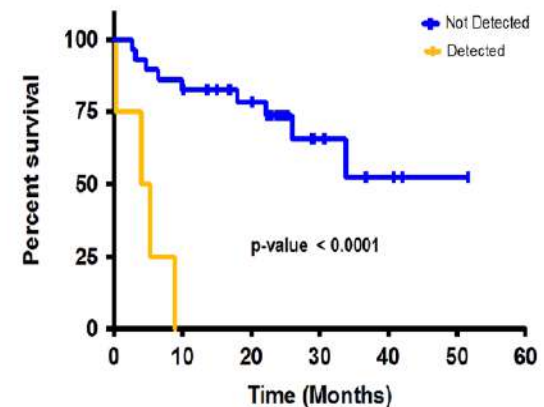
ER-ve



Mutation tracking



BRE09-146 DFS Stratified by Presence of Tumor Mutation in Plasma



Identificación de nuevas dianas

LUNG CANCER IN 2018

A banner year for immunotherapy and targeted therapy

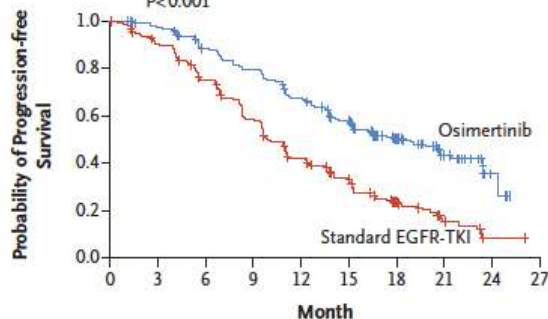
Jennifer W. Carlisle and Suresh S. Ramalingam

Osimertinib in Untreated EGFR-Mutated Advanced Non-Small-Cell Lung Cancer

A Progression-free Survival in Full Analysis Set

	No. of Patients	Median Progression-free Survival (95% CI) mo
Osimertinib	279	18.9 (15.2–21.4)
Standard EGFR-TKI	277	10.2 (9.6–11.1)

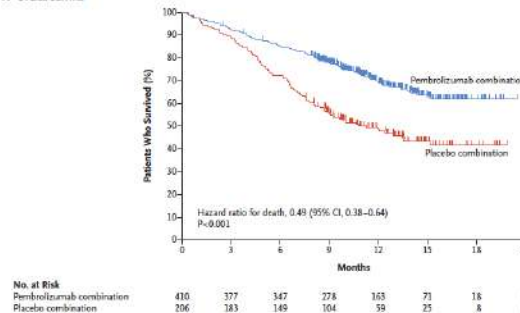
Hazard ratio for disease progression or death, 0.46 (95% CI, 0.37–0.57)
P<0.001



No. at Risk										
Osimertinib	279	262	233	210	178	139	71	26	4	0
Standard EGFR-TKI	277	239	197	152	107	78	37	10	2	0

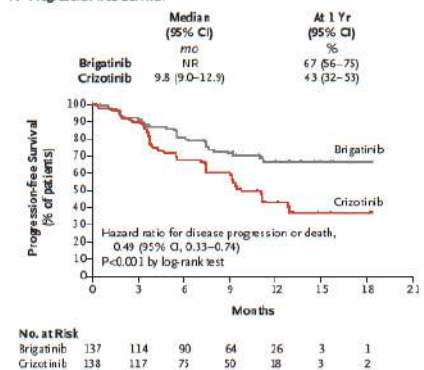
Pembrolizumab plus Chemotherapy in Metastatic Non-Small-Cell Lung Cancer

A Overall Survival

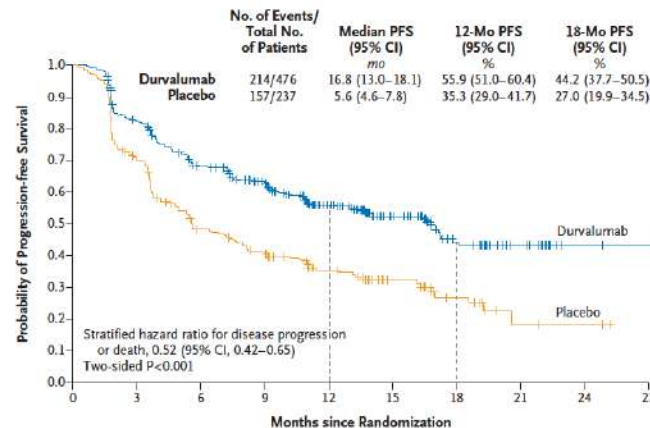


Brigatinib versus Crizotinib in ALK-Positive Non-Small-Cell Lung Cancer

A Progression-free Survival



Durvalumab after Chemoradiotherapy in Stage III Non-Small-Cell Lung Cancer



No. at Risk										
Durvalumab	476	377	301	264	159	86	44	21	4	1
Placebo	237	163	106	87	52	28	15	4	3	0

Identificación de nuevas dianas agnósticas (o casi agnósticas)

ARTICLE

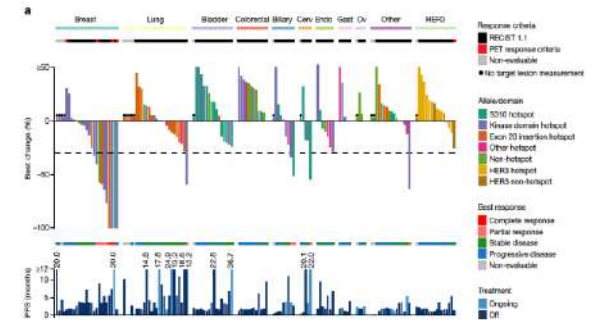
doi:10.1038/nature25475

HER kinase inhibition in patients with HER2- and HER3-mutant cancers

David M. Hyman¹, Sarina A. Piha-Paul², Helen Won³, Jordi Rodon⁴, Cristina Saura⁵, Geoffrey L. Shapiro⁶, Dejan Juric⁷, David I. Quinn⁸, Victor Moreno⁹, Bernard Dugre¹⁰, Ingrid A. Mayer¹¹, Valentina Boni¹², Emiliano Calvo¹³, Sherene Loi¹⁴, Albert C. Lockhart¹⁵, Joseph R. Ertmer¹⁶, Maurizio Scaltriti¹⁷, Gary A. Ulaner¹⁸, Juber Patel¹⁹, Jiajin Tang²⁰, Hannah Beer²¹, S. Durgu Selcuklu²², Aphroditis J. Hamrahian²³, Nancy Bouvier²⁴, Myra Melcer²⁵, Rajmohan Murali²⁶, Alison M. Schram²⁷, Lillian M. Smyth²⁸, Komal Jhaveri²⁹, Bob T. Li³⁰, Alexander Drilon³¹, James J. Harding³², Gopa Iyer³³, Barry S. Taylor³⁴, Michael F. Berger³⁵, Richard E. Cutler Jr³⁶, Feng Xu³⁷, Anna Butturi³⁸, Lisa D. Eli³⁹, Grace Mann⁴⁰, Cynthia Farrell⁴¹, Alshad S. Lalani⁴², Richard P. Bryce⁴³, Carlos L. Arteaga⁴⁴, Funda Meric-Bernstam⁴⁵, José Baselga⁴⁶ & David B. Solit⁴⁷

Mutación HER2-3

Neratinib



HHS Public Access

Author manuscript
Science. Author manuscript; available in PMC 2017 August 30.

Published in final edited form as:
Science. 2017 July 28; 357(6349): 409–413. doi:10.1126/science.aan6733.

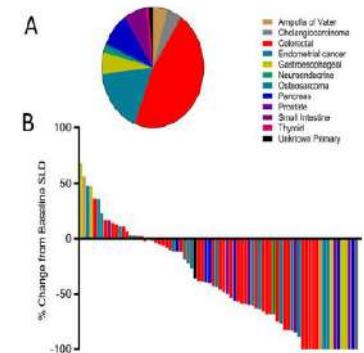
Mismatch-repair deficiency predicts response of solid tumors to
PD-1 blockade

THE NEW ENGLAND JOURNAL of MEDICINE

ORIGINAL ARTICLE

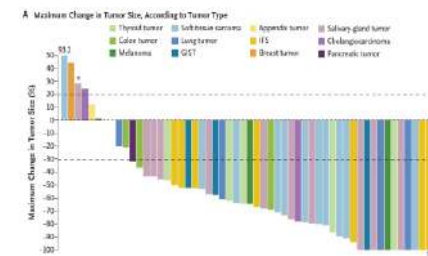
MSI-high

Pembrolizumab



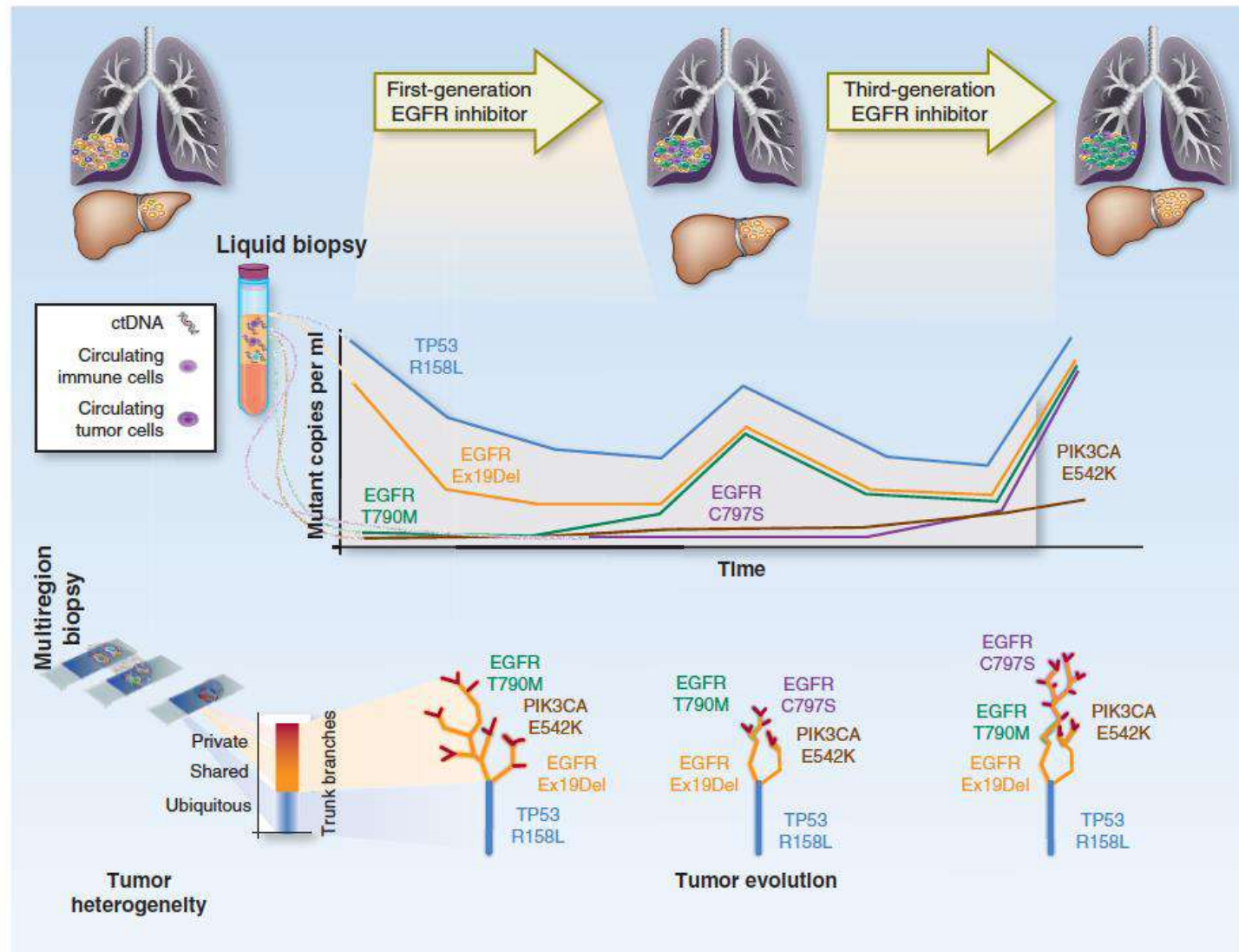
Fusión TRK

Larotrectinib

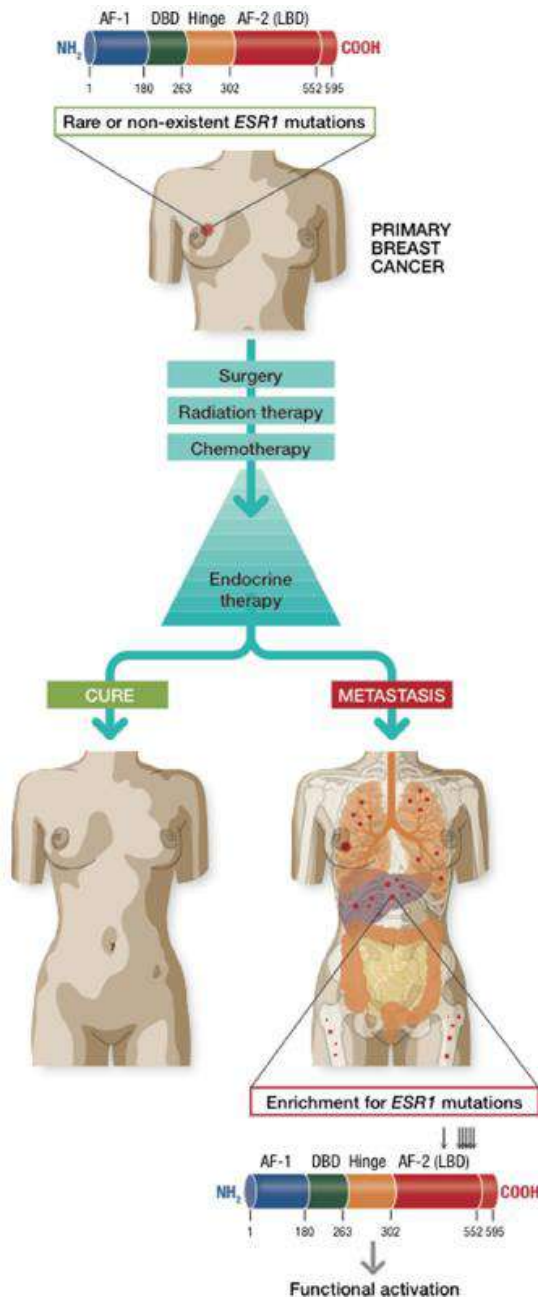


Efficacy of Larotrectinib in TRK Fusion-
Positive Cancers in Adults and Children

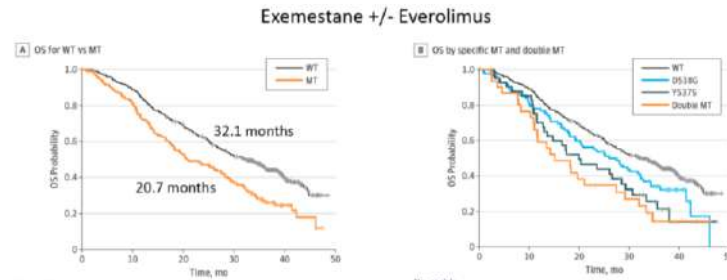
Resistencia al tratamiento: EGFR TKI



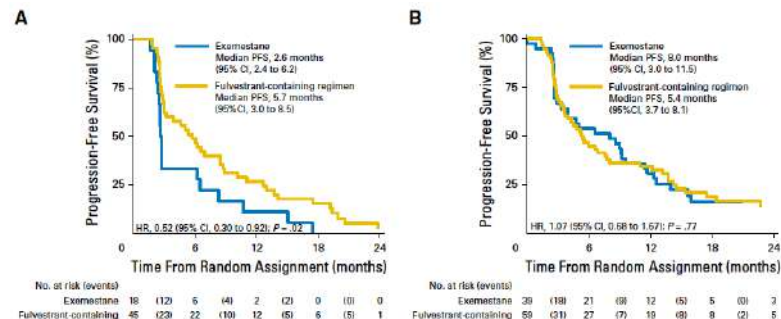
Resistencia a tratamiento: inhibidores de aromatasa



■ Valor pronóstico en CMM luminal (BOLERO-2)



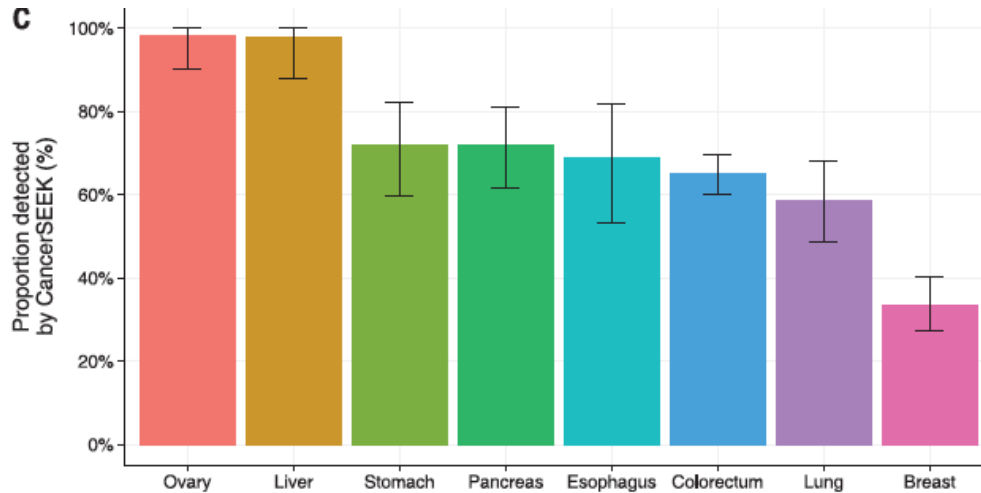
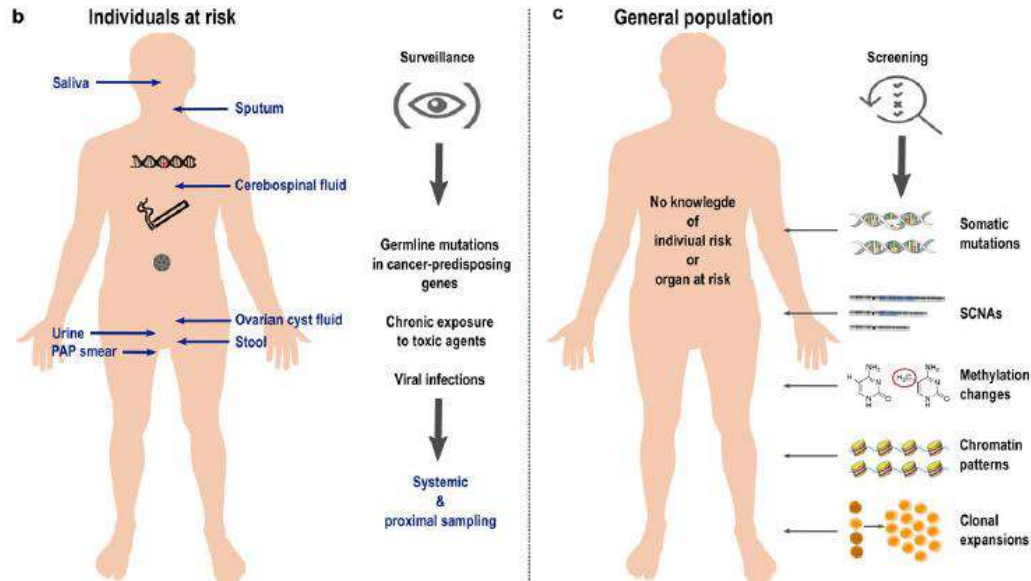
■ Valor predictivo de beneficio de fulvestrant (SG) superior a IA (SOFEA)



■ Relación con beneficio de everolimus (BOLERO-2) en mut Y537S

Toy, Nat Gen 2013; Yamamoto-Isubiki, BMC Med 2015; Ma, Nat Rev Cancer 2015; Prat, IMPAKT 2017; Jeselsohn, Clin Cancer Res 2014; Chandarlapaty, JAMA Oncol 2016; Fribbens, J Clin Oncol 2016

Precisión en el diagnóstico precoz: ctDNA

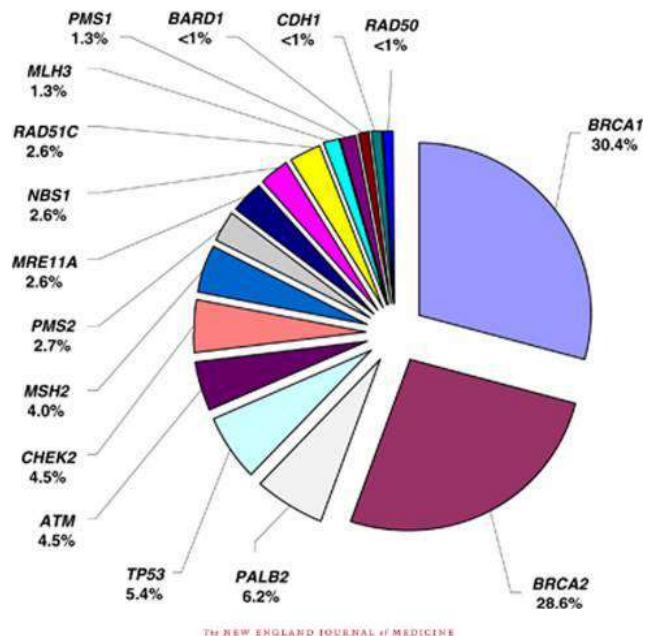


CANCER

Detection and localization of surgically resectable cancers with a multi-analyte blood test

Joshua D. Cohen,^{1,2,3,4,5} Lu Li,⁶ Yuxuan Wang,^{1,2,3,4} Christopher Thoburn,³ Bahman Afsari,⁷ Ludmila Danilova,⁷ Christopher Douville,^{1,2,3,4} Ammar A. Javed,⁸ Fay Wong,^{1,3,4} Austin Mattox,^{1,2,3,4} Ralph H. Hruban,^{3,4,9} Christopher L. Wolfgang,⁸ Michael G. Goggins,^{3,4,9,10,11} Marco Dal Molin,⁴ Tian-Li Wang,^{3,9} Richard Roden,^{3,9} Alison P. Klein,^{3,4,9,12} Janine Plak,^{1,2,3,4} Lisa Dobbyn,^{1,3,4} Joy Schaefer,^{1,3,4} Natalie Silliman,^{1,2,3,5} Maria Popoli,^{1,3,4} Joshua T. Vogelstein,¹³ James D. Browne,¹⁴ Robert E. Schoen,^{15,16} Randall E. Brand,¹⁵ Jeanne Tie,^{17,18,19,20} Peter Gibbs,^{17,18,19,20} Hui-Li Wong,¹⁷ Aaron S. Mansfield,²¹ Jin Jen,²² Samir M. Hanash,²³ Massimo Falconi,²⁴ Peter J. Allen,²⁵ Shihui Zhou,^{1,3,4} Chetan Bettegowda,^{1,3,4} Luis A. Diaz Jr.,^{1,3,4,6} Cristian Tomasetti,^{3,6,7} Kenneth W. Kinzler,^{1,3,4} Bert Vogelstein,^{1,2,3,4} Anne Marie Lennon,^{3,4,6,10,11} Nickolas Papadopoulos^{1,3,4}

Medicina de precisión: pacientes



THE NEW ENGLAND JOURNAL of MEDICINE

ORIGINAL ARTICLE

Olaparib for Metastatic Breast Cancer in Patients with a Germline BRCA Mutation

Mark Robson, M.D., Seock-Ah Im, M.D., Ph.D., Elzbieta Senkus, M.D., Ph.D., Bingjie Xu, M.D., Ph.D., Susan M. Domchek, M.D., Norikazu Masuda, M.D., Ph.D., Suzette Delalogi, M.D., Wei Li, M.D., Nadine Tung, M.D., Anne Armstrong, M.D., Ph.D., Wenting Wu, Ph.D., Carsten Goessl, M.D., Sarah Rumsick, Ph.D., and Pierfranco Conte, M.D.

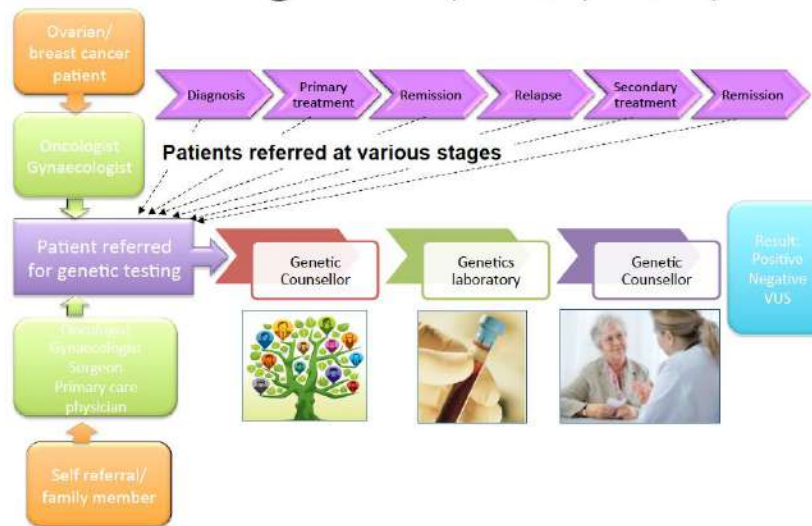
THE NEW ENGLAND JOURNAL of MEDICINE

ORIGINAL ARTICLE

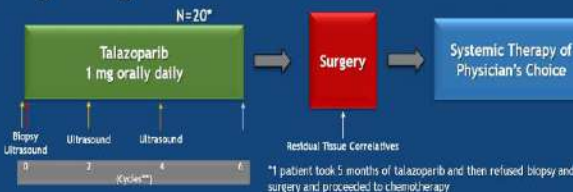
Talazoparib in Patients with Advanced Breast Cancer and a Germline BRCA Mutation

Jennifer K. Litton, M.D., Hope S. Rugo, M.D., Johannes Ettl, M.D., Sara A. Hurvitz, M.D., Anthony Gonçalves, M.D., Ph.D., Kyung-Hun Lee, M.D., Ph.D., Louis Fehrenbacher, M.D., Rinat Yarushtalmi, M.D., Lida A. Mina, M.D., Miguel Martin, M.D., Ph.D., Henri Roché, M.D., Ph.D., Young-Hyuk Im, M.D., Ph.D., Ruben G.W. Quirk, Ph.D., Denka Markova, Ph.D., Julia C. Tudor, Ph.D., Alison L. Hannish, M.D., Wolfgang Eiermann, M.D., and Joanne L. Blum, M.D., Ph.D.

BRCA testing: Current patient pathway



Study Design



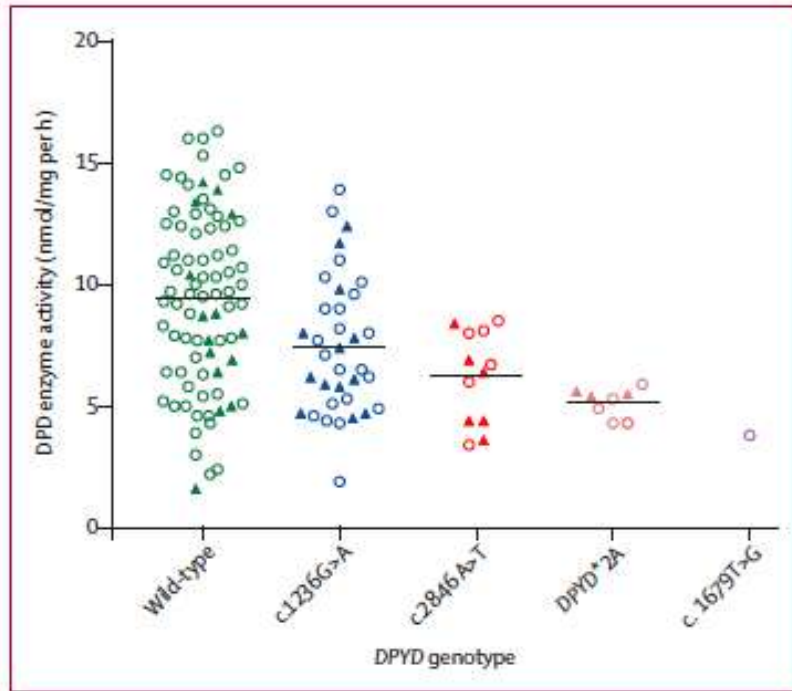
• Pathologic responses to single agent talazoparib

• pCR: 10/19 = 53%, 95% CI = 32%, 73%

• RCB-O+I: 12/19 = 63%, 95% CI = 41%, 81%

• First study of a single targeted therapy to achieve pCR in BRCA+ patients, including TNBC

Medicina de precisión: pacientes



Toxicidad grado ≥ 3

	DPYD variant carriers treated with reduced dose (current study)*	DPYD variant carriers treated with full dose† (previous meta-analysis)
c.1236G>A	1.69 (1.18–2.42)	1.72 (1.22–2.42)
c.2846A>T	2.00 (1.19–3.34)	3.11 (2.25–4.28)
DPYD*2A	1.31 (0.63–2.73)	2.87 (2.14–3.86)
c.1679T>G	NA‡	4.30 (2.10–8.80)

DPYD genotype-guided dose individualisation of fluoropyrimidine therapy in patients with cancer: a prospective safety analysis

Linda M Henricks*, Corn A T C Lunenburg*, Femke M de Man*, Didier Meulendijks, Geert W J Frederix, Emma Kleinbuis, Geert-Jan Creemers, Arnold Boers, Vincent O Dezentjé, Alexander L T Timholz, Frank J F Janssen, Johanna E A Portielje, Rob L H Jansen, Paul Hamberg, Albert J ten Tije, Helga J Droogendijk, Miriam Koopman, Peter Nisboer, Marlene H W van de Poel, Caroline M P W Mandigers, Hilde Rosling, Jos H Beijnen, Erik van Werkhoven, André B P van Kullenburg, Ron H N van Schaik, Ron H J Mathijssen, Jesse J Swen, Hans Gelderblom, Annetiekke Cats, Henk-Jan Guchelaar, Jan H M Schellens

Summary

Background Fluoropyrimidine treatment can result in severe toxicity in up to 30% of patients and is often the result

European Journal of Cancer 107 (2019) 60–67



Available online at www.sciencedirect.com

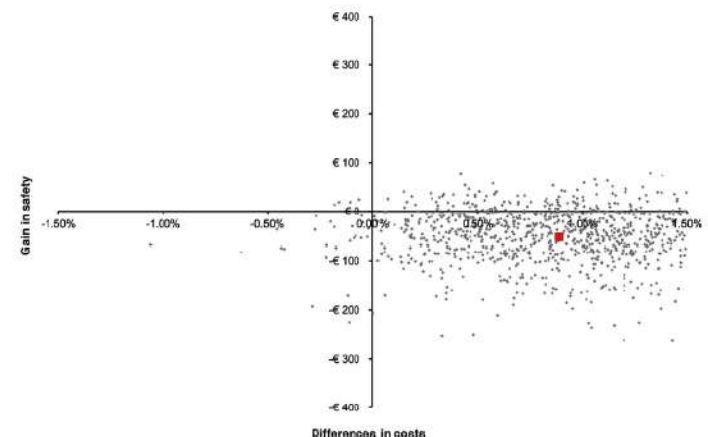
ScienceDirect

Journal homepage: www.ejancer.com

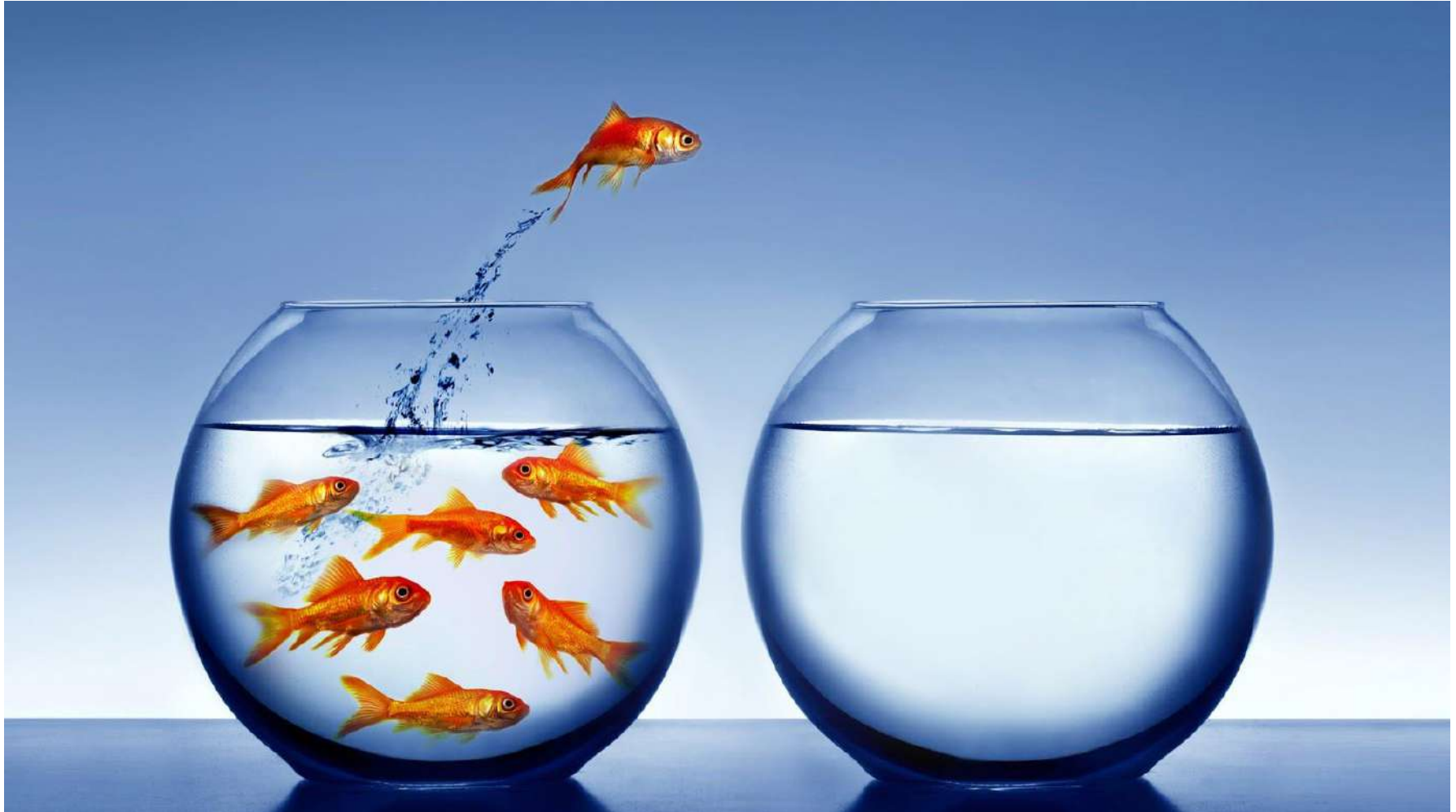


Original Research

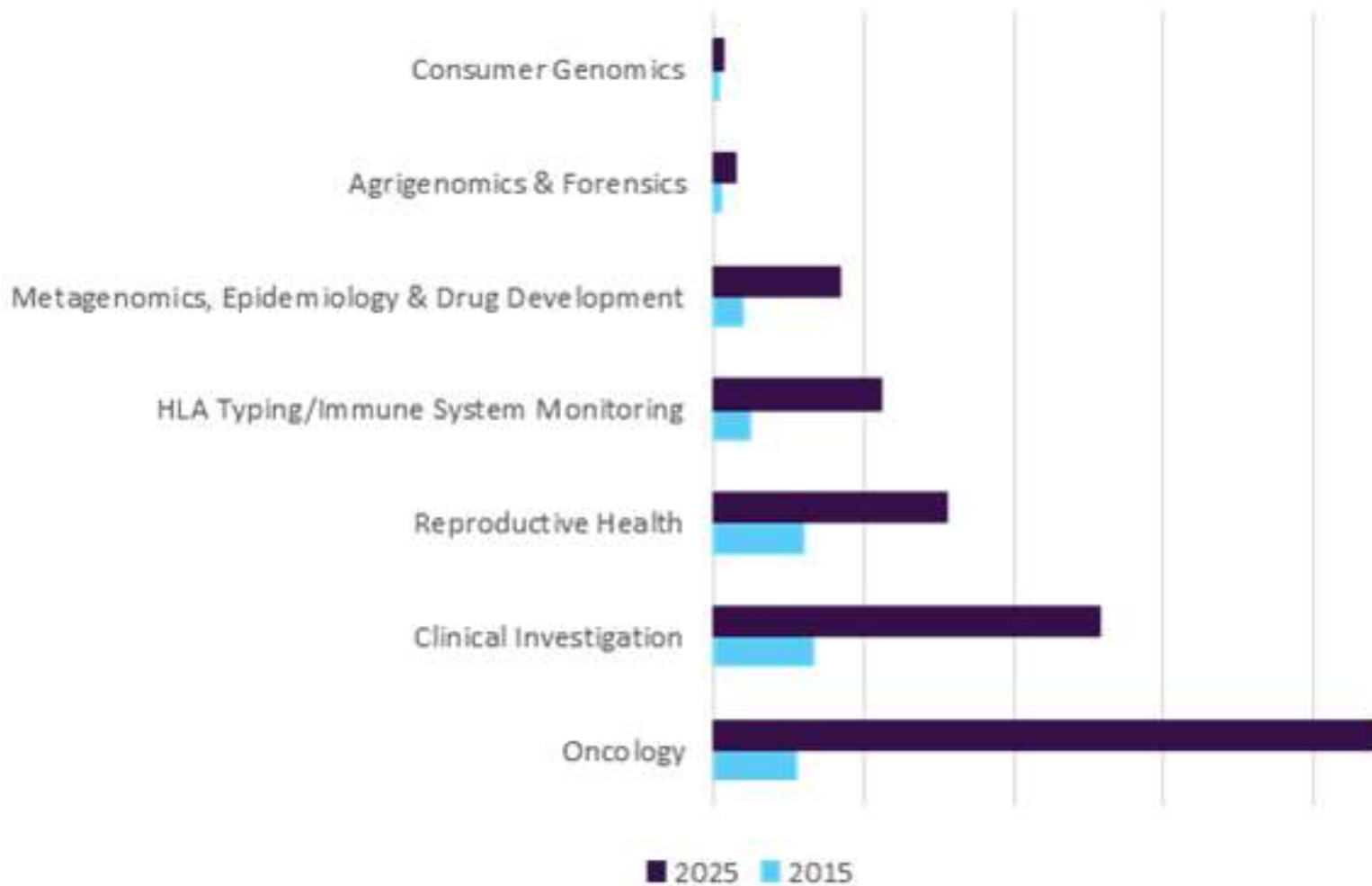
A cost analysis of upfront *DPYD* genotype-guided dose individualisation in fluoropyrimidine-based anticancer therapy



ENTORNO RÁPIDAMENTE CAMBIANTE



NGS / BIOMARCADORES



MEDICINA DE PRECISIÓN: ¿HASTA DONDE?

Tratamientos dirigidos $\neq$ Tratamientos precisos

**Biomarcadores predictivos imperfectos +
heterogeneidad: combinaciones vs secuencia de
tratamientos dirigida por resistencia**

¿Mejora real de los resultados del tratamiento?

**Rentabilidad diagnóstica frente a pérdidas de
oportunidad: ¿NGS para todos los pacientes o
selección por criterios clínicos? ¿En todos los
tumores?**

¿Predicción en los escenarios más comunes?

Dirigidos pero imprecisos

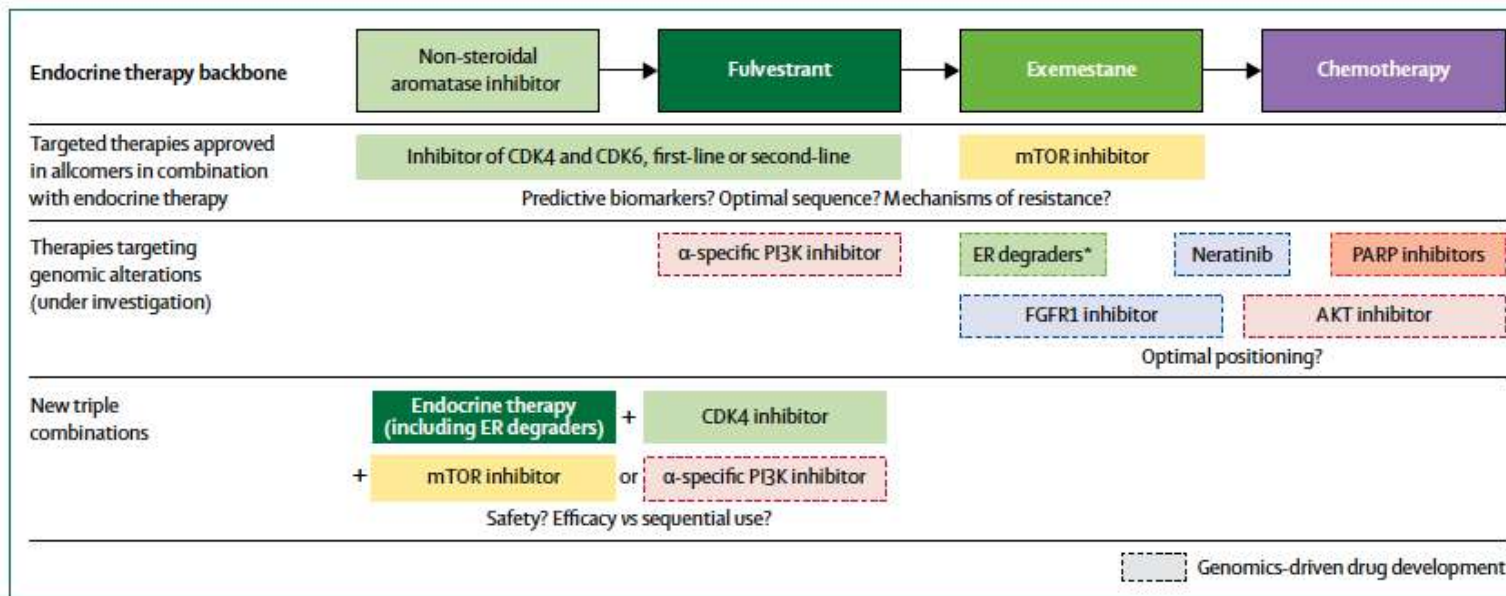
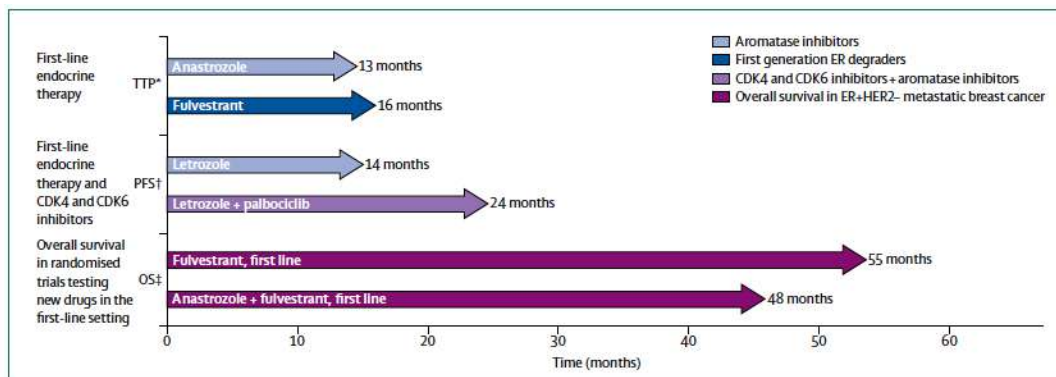
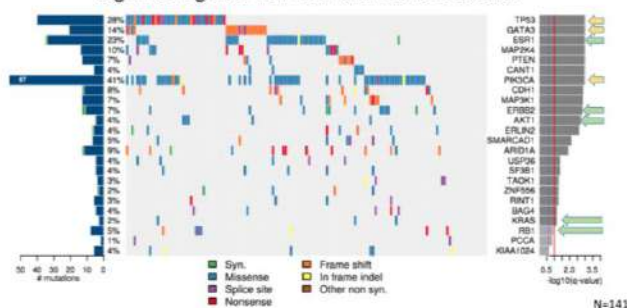


Tackling endocrine resistance in ER-positive HER2-negative advanced breast cancer: A tale of imprecision medicine
Alexios Matikas*, Theodoros Fotakis, Jonas Bergh



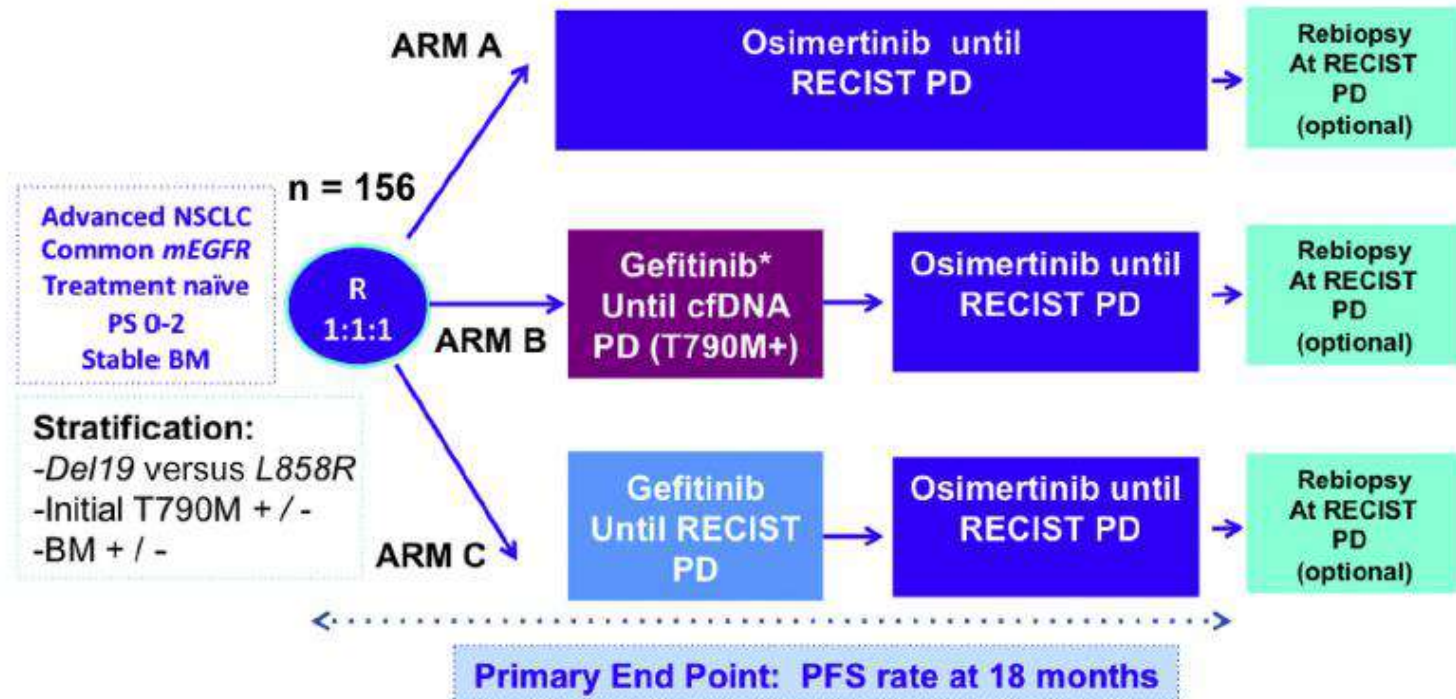
September 1, 2017

Mutational landscape of ER+ MBC - Significant genes with SNV and indel alterations



Biomarcadores imperfectos + heterogeneidad tumoral: “condenados” a la combinación

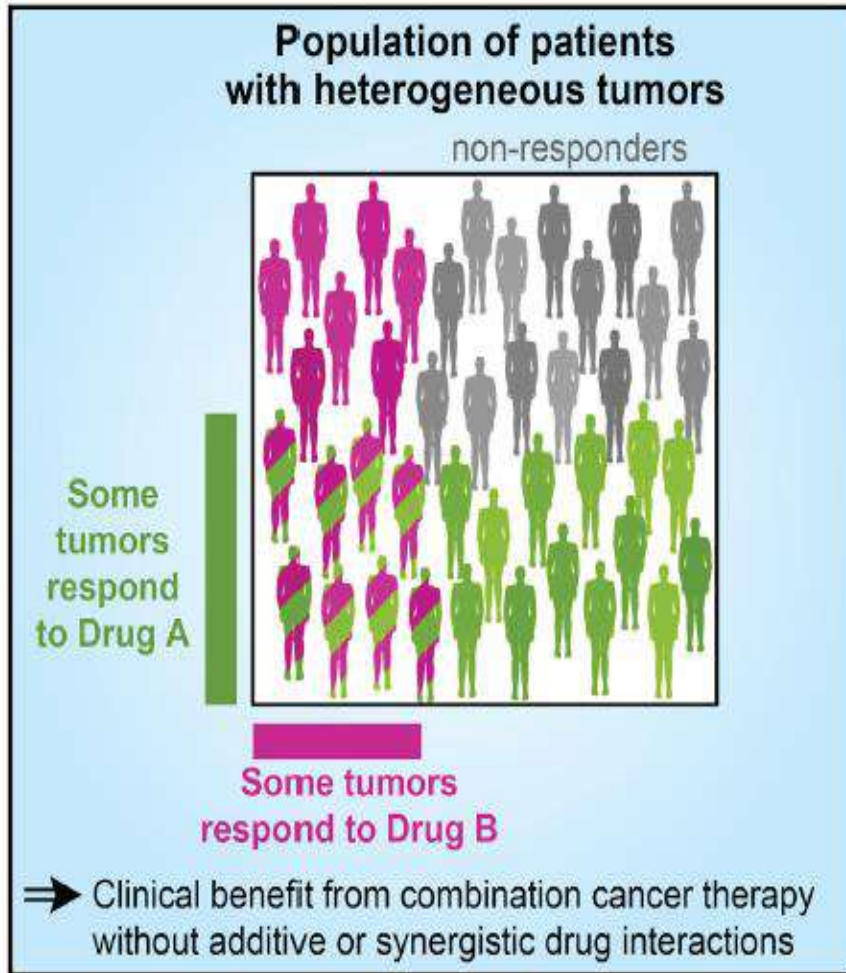
EORTC APPLE



(cfDNA using cobas every 4 weeks and CT scan of the brain-thorax-abdomen every 8 weeks all arms)

*In case of RECIST progression without T790M+, patients will be switched

Biomarcadores imperfectos + heterogeneidad tumoral: “condenados” a la combinación



Neoplasias menos agresivas en las que la secuencia no suponga pérdida considerable de pacientes entre líneas

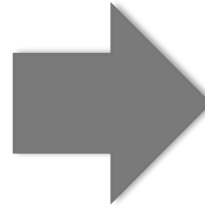
Neoplasias menos agresivas en las que seamos capaces de identificar claramente el desarrollo de resistencias con biomarcadores claros

Neoplasias en las que la presión menos nuevas vulnerabilidades (¡identificables!)

¿ A DONDE VAMOS?

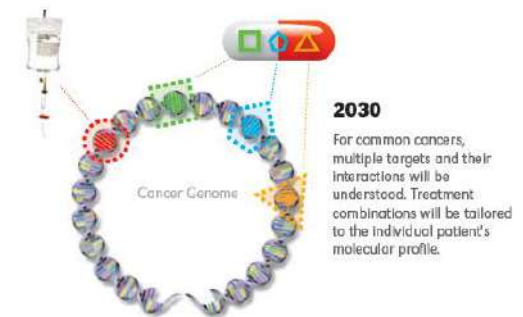
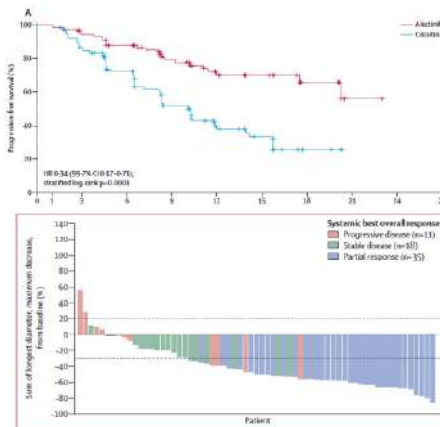
1ª generación

- ❑ Secuenciación regiones codificantes
- ❑ Estadios avanzados
- ❑ Éxitos en enfermedades con alteración clonal única



2ª generación

- ❑ Valoraciones moleculares completas y nuevos enfoques bioinformáticos
- ❑ Estadios más precoces
- ❑ Tratamientos de combinación frente a múltiples dianas



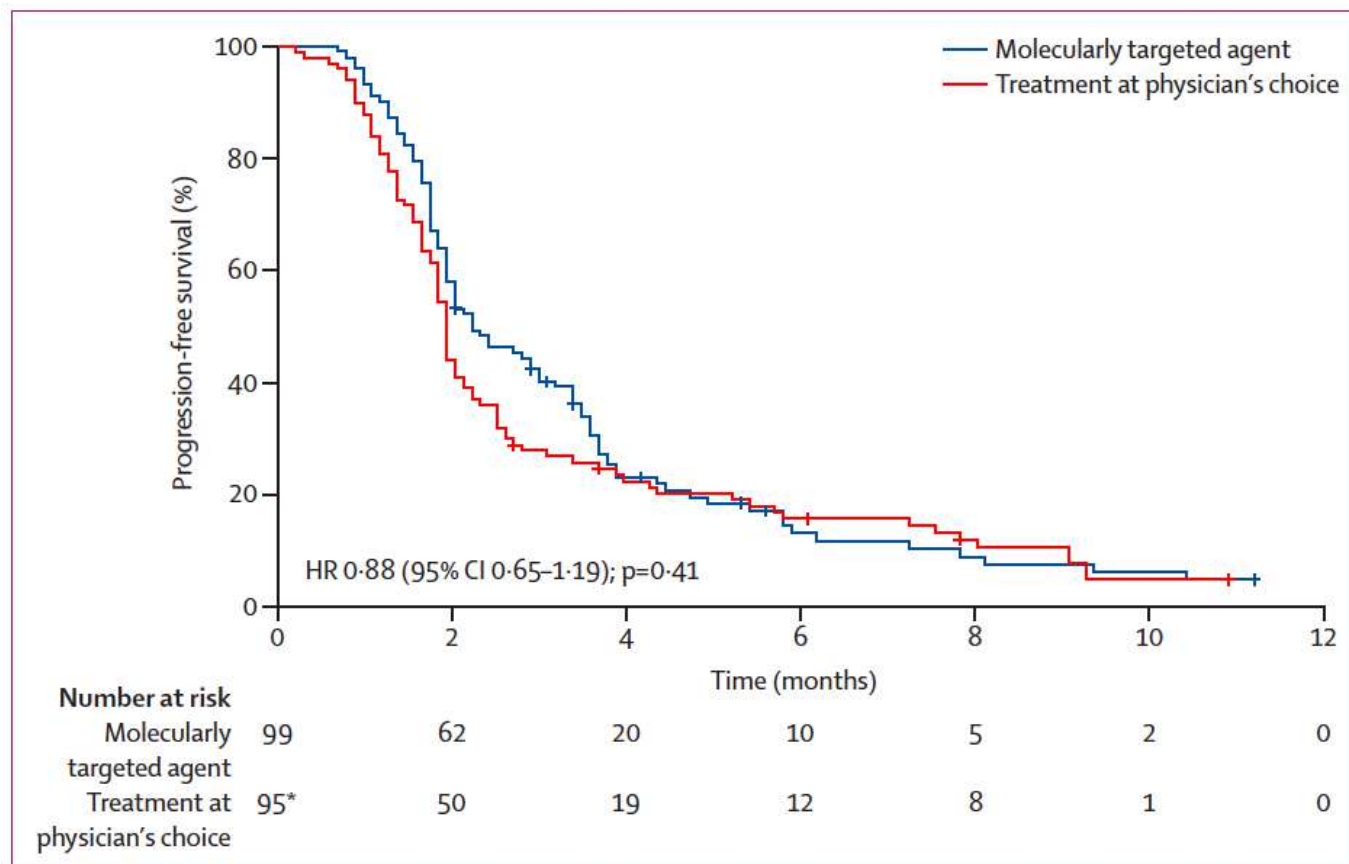
2030
For common cancers, multiple targets and their interactions will be understood. Treatment combinations will be tailored to the individual patient's molecular profile.

¿Utilidad clínica?



Molecularly targeted therapy based on tumour molecular profiling versus conventional therapy for advanced cancer (SHIVA): a multicentre, open-label, proof-of-concept, randomised, controlled phase 2 trial

Christophe Le Tourneau, Jean-Pierre Delord, Anthony Gonçalves, Céline Givolle, Coraline Dubot, Nicolas Isambert, Mario Carbone, Olivier Trédan, Marie-Ange Massiani, Cécile Mauborgne, Sébastien Armanet, Nicolas Servant, Ivan Bieche, Virginie Bernard, David Gensier, Pascal Jazquel, Valéry Arsignon, Sandrine Boyault, Anne Vincent-Salomon, Vincent Serres, Marie-Paule Sablin, Maud Kama, Xavier Paoletti for the SHIVA investigators

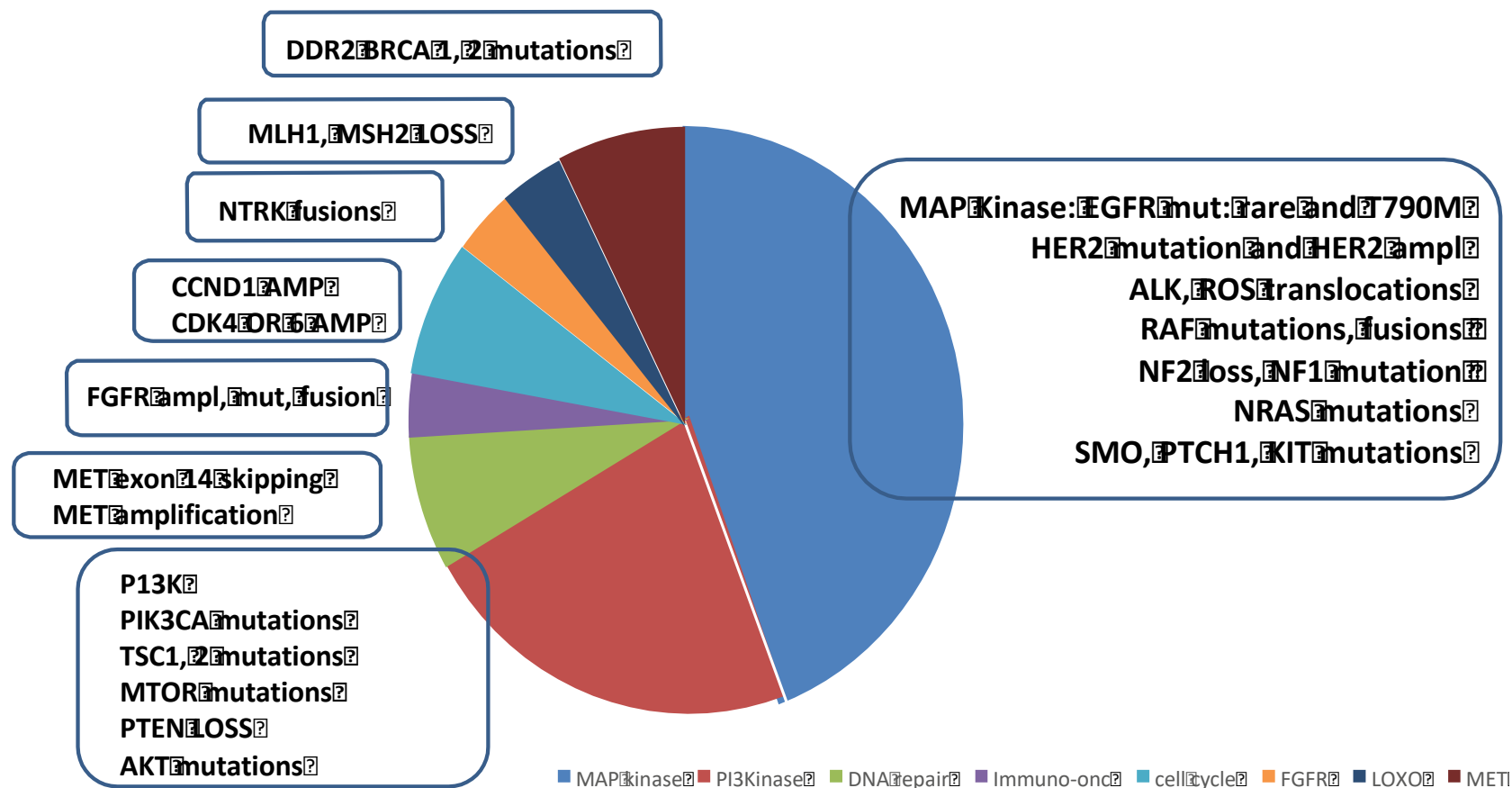


¿Utilidad clínica?

NCI-Molecular Analysis for Therapy Choice
(NCI-MATCH / EAY131)

- Prevalencia alteraciones genéticas: 0-3.5%
- 35 brazos de tratamiento

Treatment Arms in NCI-MATCH by Molecular Pathway



¿Utilidad clínica?

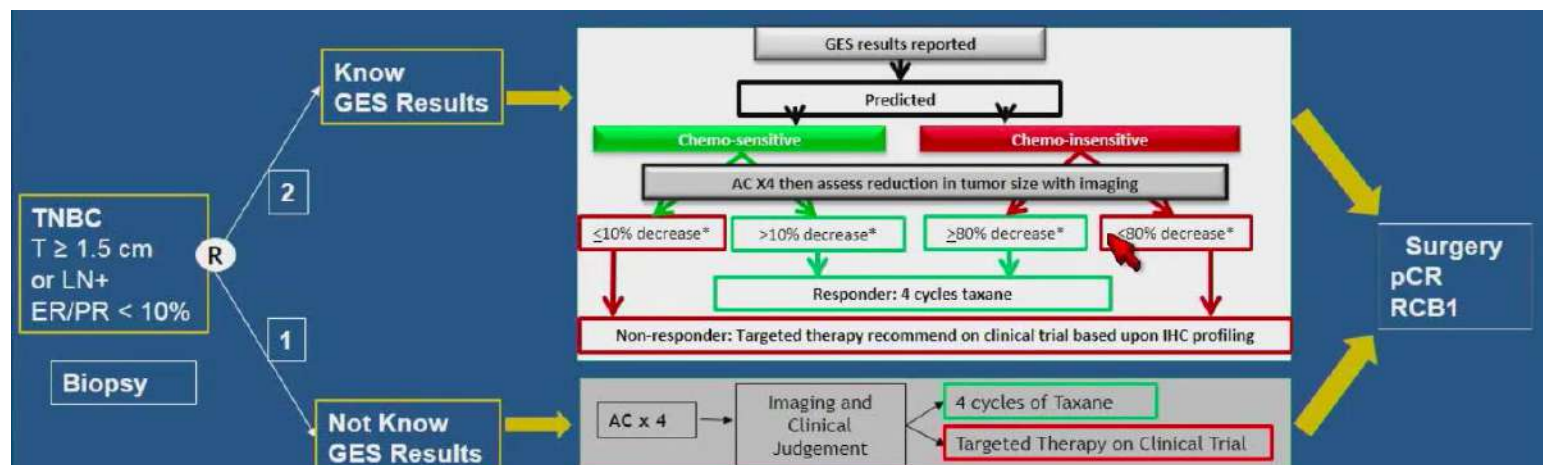
NCI-Molecular Analysis for Therapy Choice (NCI-MATCH / EAY131)

Drug	Drug/Variant	Arm	Primary Result (ORR Confirmed)	Publication/Presentation
Ado-trastuzumab + emtansine	HER2 amplification	Q	8%	Jhaveri KL, ASCO 2018 (oral)
AZD4547	FGFR pathway aberrations	W	8%	Chae YK, ASCO 2018 (oral)
Taselisib	PIK3CA mutations	I	0%	Kropf E, ASCO 2018 (oral)
GSK2636771	PTEN expression loss by IHC	N & P	5% arm N (mut/del) 0% arm P	Janku T, ESMO 2018 (poster discussion)
Capivasertib	AKT mutations	Y	23%	Kalinsky KM, EORTC-NCI-AACR 2018 (oral plenary)
Nivolumab	dMMR status	Z1D	Coming Soon!	
Afatinib	HER2 activating mutations	B		
Palbociclib	CCND1, 2, 3 amplifications and Rb protein expression by IHC	Z1B		
ACD1775	BRCA1 or BRCA2 mutations	Z1I		

¿Utilidad clínica?

Precision neoadjuvant therapy (P-NAT): a planned interim analysis of A Randomized, TNBC Enrolling trial to confirm Molecular profiling Improves Survival (ARTEMIS)

S Moulder, MD, MSCI; K Hess, PhD; R Candelaria, MD; GM Rauch, MD, PhD; L Santiago, MD; B Adrada, MD; WT Yang, MD; M Gilcrease, MD, PhD; L Huo, MD, PhD; MC Stauder, MD; B Arun, MD; R Layman, MD; RK Murthy, MD; S Damodaran, MD; NT Ueno, MD, PhD; AM Thompson, MD; B Lim, MD; E Mittendorf, MD, PhD; J Litton, MD; WF Symmans, MD



Aim: to determine if P-NAT impacts rates of excellent pathologic response [RCB 0-I] in TNBC

- Planned to randomize 360 pts 2:1 to 'know' vs. 'not know' the GES predictor results
- First interim analysis: 133 patients

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Artemis: Results

Interim Analysis Cohort (N=133)			
	"Not Know" GES results (n=42)	"Know" GES results (n=91)	p value
pCR			
Yes – n (%)	21 (50%)	39 (43%)	0.44
RCB Index			
pCR/RCB-I – n (%)	26 (62%)	51 (56%)	0.52
RCB-II/III – n (%)	16 (38%)	40 (44%)	

US Resistant Cohort (n=43)			
	Targeted Treatment (N=31)	SOC (N=12)	p value
pCR			
Yes – n (%)	5 (16%)	0 (0%)	0.3
RCB Index			
pCR/RCB I – n(%)	9 (29%)	2 (17%)	0.7
RCB-II/III – n (%)	22 (71%)	10 (83%)	

❑ Tratamiento basado en GES (VPP 65%, VPN 26%) no mejor que basado en radiología (RMN)/clínica

❑ Interrupción de la aleatorización y continuación como brazo único con IHQ para identificar dianas en tumores sin respuesta

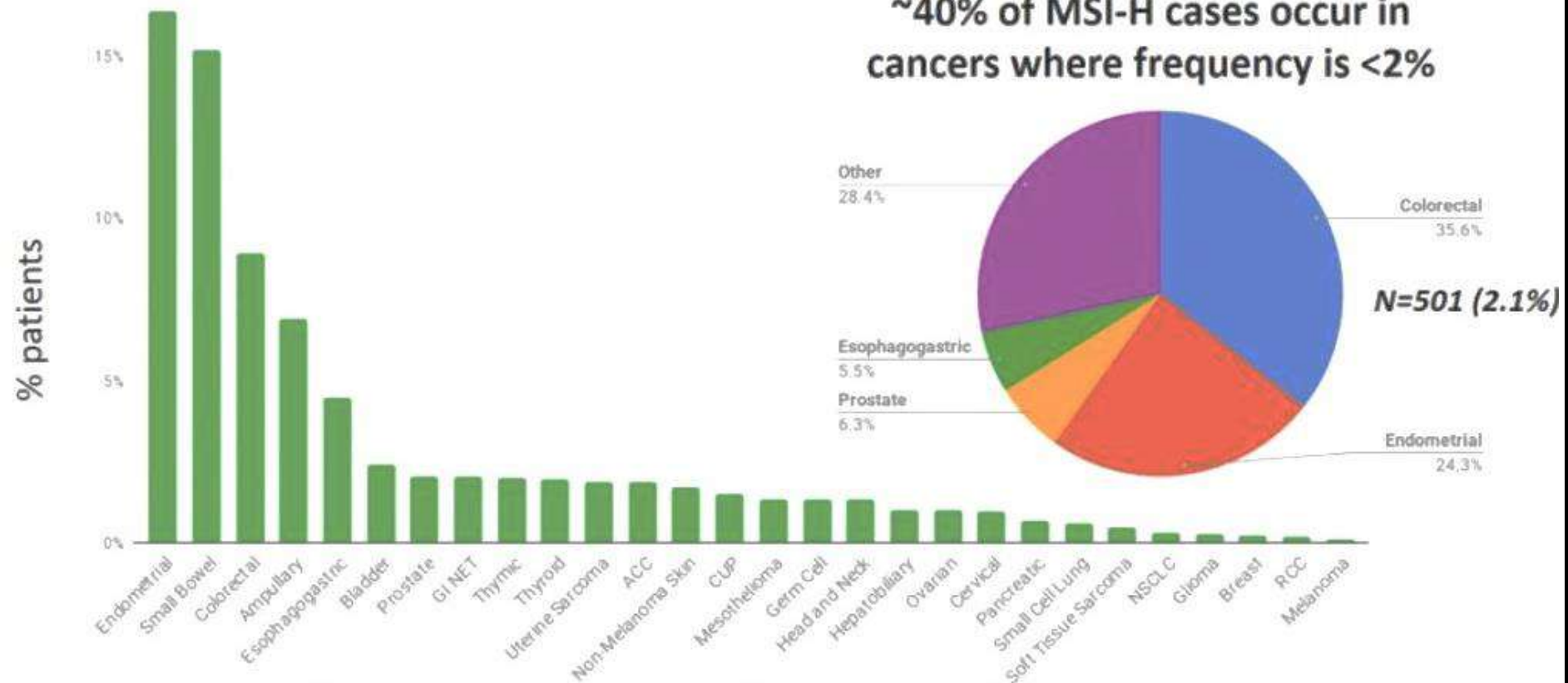
❑ Dificultades para demostrar utilidad clínica

Moulder, ASCO 2018

¿NGS sistemática ?

Distribution of MSI-H Cancers

~40% of MSI-H cases occur in cancers where frequency is <2%



Screening in colorectal and endometrial cancers would miss ~40% of patients

¿Paneles NGS de cáncer hereditario para todos los pacientes?

editorial
Advances in Genetic Testing in Patients with
Breast Cancer, High-Quality Data, and Responsiveness

Kara L. Miller

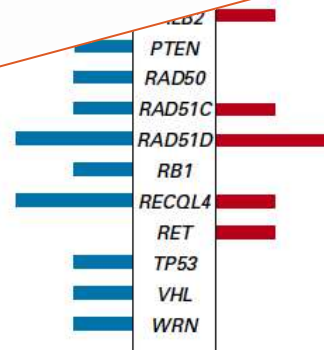
THE AMERICAN SOCIETY OF Breast Surgeons

Consensus Guideline on Genetic Testing for Hereditary Breast Cancer

2. **Genetic testing should be made available to all patients with a personal history of breast cancer.** Recent data support that genetic testing should be offered to each patient with breast cancer (newly diagnosed or with a personal history). If genetic testing is performed, such testing should include BRCA1/BRCA2 and PALB2, with other genes as appropriate for the clinical scenario and family history. For patients with newly diagnosed breast cancer, identification of a mutation may impact local treatment recommendations (surgery and potentially radiation) and systemic therapy. Additionally, family members may subsequently be offered testing and tailored risk reduction strategies.

TABLE 2. Patient

Group	Small Panel (11 genes)	Large Cancer Panel (80 genes)
In guideline	2.51	9.39
Out of guideline	0.63	7.92



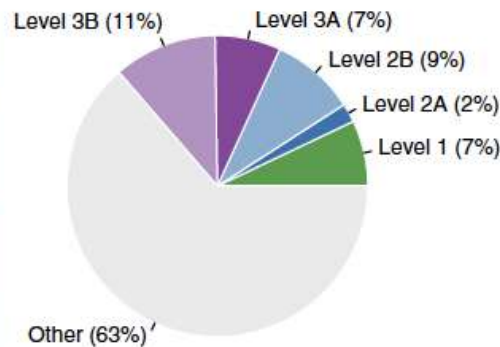
Not Meet NCCN Criteria

6 7 8 9 10

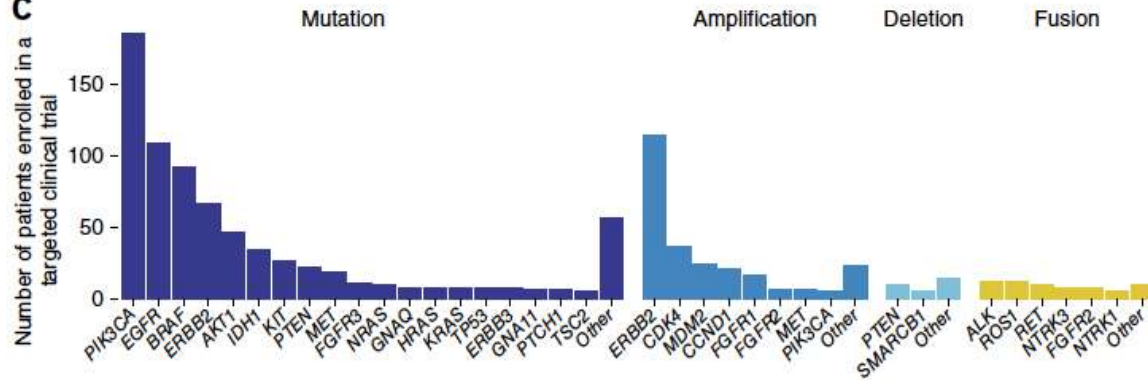
¿NGS sistemática?

a

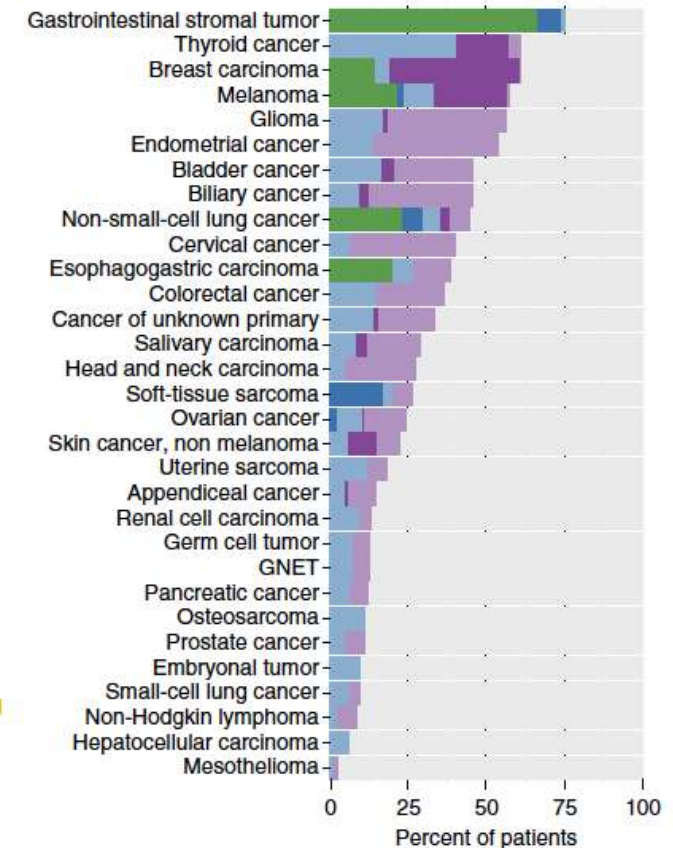
Level 1	FDA-recognized biomarker for an FDA-approved drug in the same indication
Level 2A	Standard of care biomarker for an FDA-approved drug in the same indication
Level 2B	Standard of care biomarker for an FDA-approved drug in another indication
Level 3A	Compelling clinical evidence supporting the biomarker as being predictive of drug response in the same indication
Level 3B	Compelling clinical evidence supporting the biomarker as being predictive of drug response in another indication



c



b



UTILIDAD CLÍNICA: PONIENDO ORDEN

A framework to rank genomic alterations as targets for cancer precision medicine: the ESMO Scale for Clinical Actionability of molecular Targets (ESCAT)

J. Mateo¹, D. Chakravarty², R. Dienstmann¹, S. Jeejee³, A. Gonzalez-Periz⁴, N. Lopez-Bigas^{5,6}, C. K. Y. Ng⁶, P. L. Bedard⁷, G. Tortora^{8,9}, J. -Y. Douillard¹⁰, E. M. Van Allen¹¹, N. Schultz¹², C. Swanton¹³, F. Andre^{13,14} & L. Puozzo¹⁵

Amplificación de HER2

Mutaciones activadoras AKT1

Mutaciones pérdida de función PALB2

Mutaciones activadoras de PI3KCA

Mutaciones activadoras de EGFR

Table 2. The ESCAT

	ESCAT evidence tier	Required level of evidence	Clinical value class	Clinical implication
Ready for routine use	I: Alteration-drug match is associated with improved outcome in clinical trials	I-A: prospective, randomised clinical trials show the alteration-drug match in a specific tumour type results in a clinically meaningful improvement of a survival end point I-B: prospective, non-randomised clinical trials show that the alteration-drug match in a specific tumour type, results in clinically meaningful benefit as defined by ESMO MCBS 1.1 I-C: clinical trials across tumour types or basket clinical trials show clinical benefit associated with the alteration-drug match, with similar benefit observed across tumour types	Drug administered to patients with the specific molecular alteration has led to improved clinical outcome in prospective clinical trial(s)	Access to the treatment should be considered standard of care
Investigational	II: alteration-drug match is associated with antitumour activity, but magnitude of benefit is unknown	II-A: retrospective studies show patients with the specific alteration in a specific tumour type experience clinically meaningful benefit with matched drug compared with alteration-negative patients II-B: prospective clinical trial(s) show the alteration-drug match in a specific tumour type results in increased responsiveness when treated with a matched drug, however, no data currently available on survival end points	Drug administered to a molecularly defined patient population is likely to result in clinical benefit in a given tumour type, but additional data are needed	Treatment to be considered 'preferable' in the context of evidence collection either as a prospective registry or as a prospective clinical trial
Hypothetical target	III: alteration-drug match suspected to improve outcome based on clinical trial data in other tumour type(s) or with similar molecular alteration	III-A: clinical benefit demonstrated in patients with the specific alteration (as tiers I and II above) but in a different tumour type. Limited/absence of clinical evidence available for the patient-specific cancer type or broadly across cancer types III-B: an alteration that has a similar predicted functional impact as an already studied tier I abnormality in the same gene or pathway, but does not have associated supportive clinical data	Drug previously shown to benefit the molecularly defined subset in another tumour type (or with a different mutation in the same gene), efficacy therefore is anticipated for but not proved	Clinical trials to be discussed with patients
	IV: pre-clinical evidence of actionability	IV-A: evidence that the alteration or a functionally similar alteration influences drug sensitivity in preclinical <i>in vitro</i> or <i>in vivo</i> models IV-B: actionability predicted <i>in silico</i>	Actionability is predicted based on preclinical studies, no conclusive clinical data available	Treatment should 'only be considered' in the context of early clinical trials. Lack of clinical data should be stressed to patients
Combination development	V: alteration-drug match is associated with objective response, but without clinically meaningful benefit X: lack of evidence for actionability	Prospective studies show that targeted therapy is associated with objective responses, but this does not lead to improved outcome No evidence that the genomic alteration is therapeutically actionable	Drug is active but does not prolong PFS or OS, probably in part due to mechanisms of adaptation There is no evidence, clinical or preclinical, that a genomic alteration is a potential therapeutic target	Clinical trials assessing drug combination strategies could be considered The finding should not be taken into account for clinical decision

¿NGS sistemática en enfermedad avanzada?

The first FDA-approved broad companion diagnostic for solid tumors with Medicare coverage

FoundationOne CDx provides comprehensive results with a FFPE tissue block or 10 slides (and 1 H&E slide) to save tissue and time compared to sequential single-marker tests.⁴

[Download Specimen Instructions](#)



Clinically Relevant Results
Published Incidences at Diagnosis of CDx Findings



Breast Cancer



Ovarian Cancer

TABLE 2. Selected Genomic Alterations and Relevance for Clinical Trials With Novel Drug Therapies

Molecular Alteration	Subtype Considerations	Drug Class
<i>ERBB2</i> Mutation	2%–4% HER2–negative	HER2 TKI
<i>PIK3CA</i> Mutation	30%–40% ER+/HER2–, 20%–25% HER2+, 10%–15% TNBC	PI3-kinase inhibitor (α -isoform–specific/selective)
<i>AKT1</i> Mutation	2%–5% breast cancer	AKT inhibitor mTOR inhibitor
<i>ESR1</i> Mutation	30%–40% ER+/HER2– after AI	Oral selective estrogen receptor degrader
<i>NTRK</i> Fusion	Enriched in secretory (TNBC)	TRK inhibitor
High Tumor Mutation Burden	1%–5% breast cancers	Immune checkpoint inhibitor
Mismatch Repair Deficiency Signature	< 5% breast cancers	Immune checkpoint inhibitor

PERSPECTIVE



The precision–oncology illusion

Precision oncology has not been shown to work, and perhaps it never will, says **Vinay Prasad**.

New OnlineViews **7,264** | Citations **0** | Altmetric **189****Original Investigation****ONLINE FIRST**

April 17, 2018

Estimation of The Percentage of US Patients With Cancer Who Benefit From Genome-Driven Oncology

John Marquart, BA¹; Emerson Y. Chen, MD²; Vinay Prasad, MD, MPH^{2,3,4}[» Author Affiliations](#)*JAMA Oncol.* Published online April 17, 2018. doi:10.1001/jamaoncol.2018.1660

Prasad, Nature 2016; Marquart, JAMA Oncol 2018; Le Tourneau, Lancet Oncol 2015; Oliveira, SABCS 2017; Kruse, SABCS 2017

PERSONALLY I WON'T BE CONVINCED
ABOUT CLIMATE CHANGE UNTIL I SEE
THE EVIDENCE!



IN THE PIPELINE

Derek Lowe's commentary on drug discovery and the pharma industry. An editorially independent blog from the publishers of *Science Translational Medicine*. All content is Derek's own, and he does not in any way speak for his employer.



By Derek Lowe



CANCER

Cancer Sequencing Hype And Reality

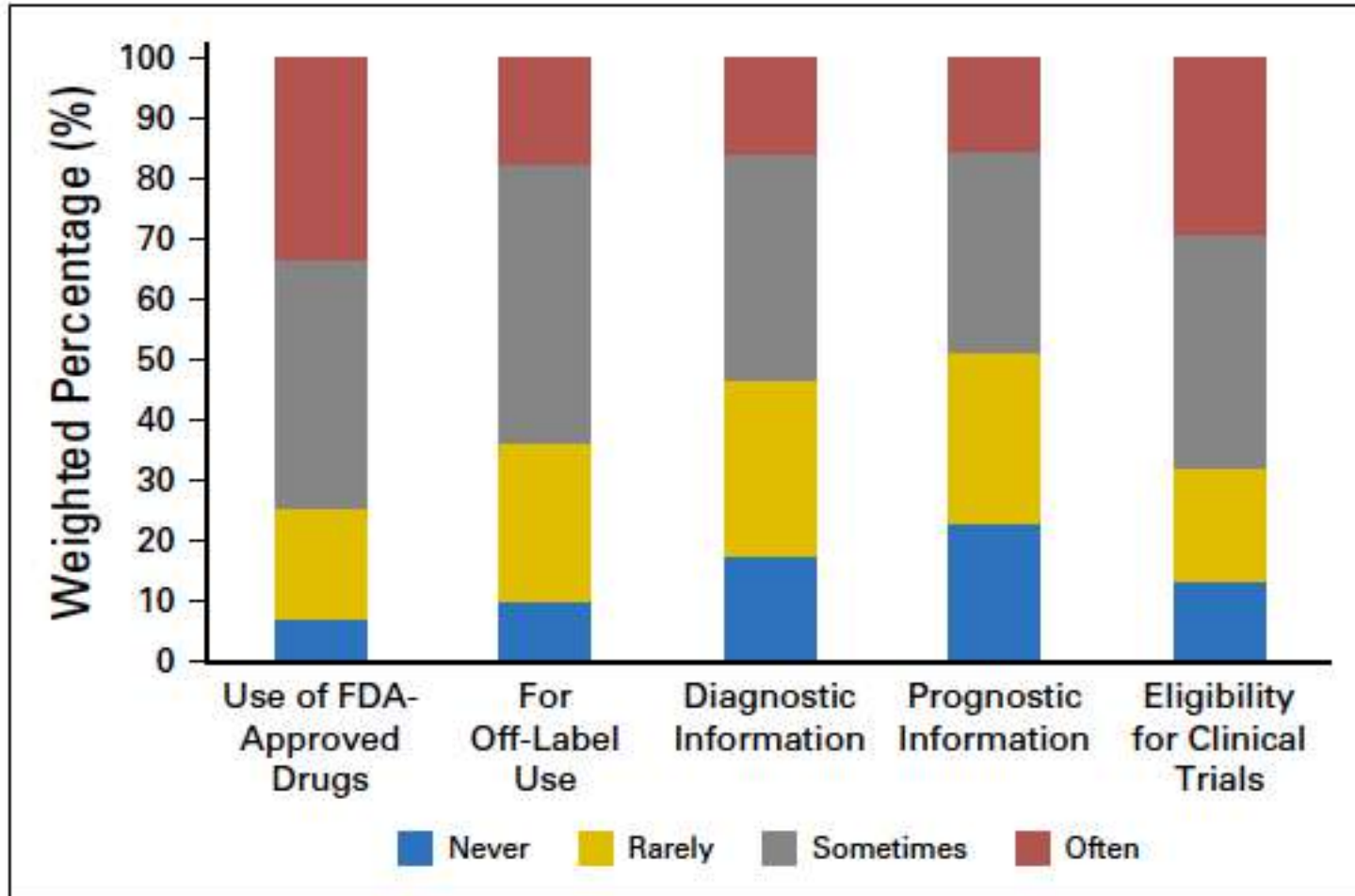
By Derek Lowe | 2 May, 2018

Apocalípticos e integrados

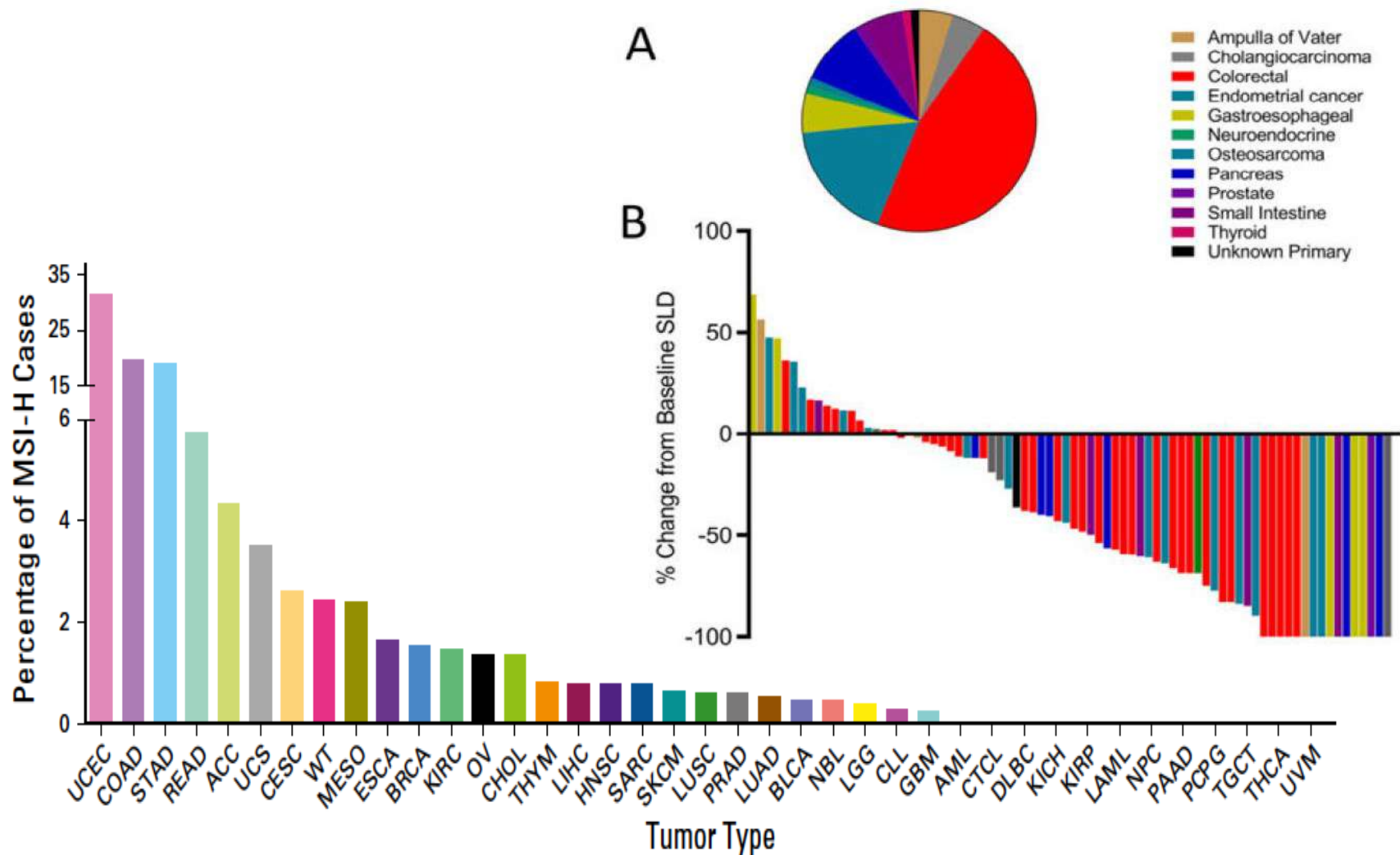


La realidad: uso creciente de NGS

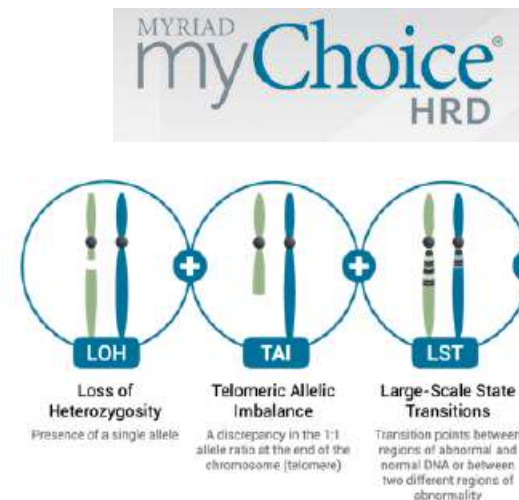
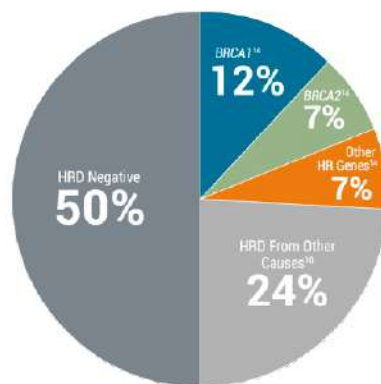
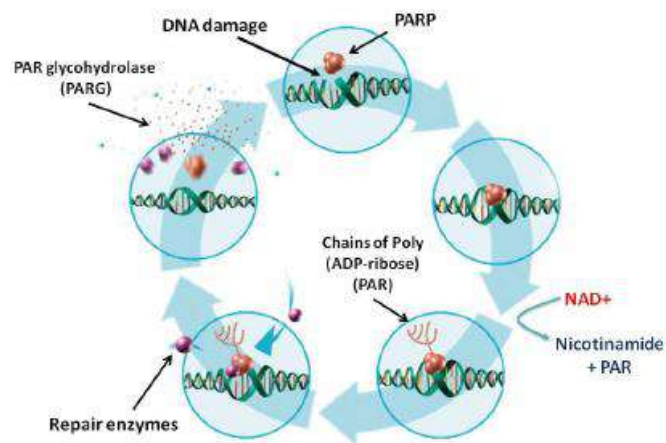
75%



Oportunidades para la eficiencia / ineficiencia: MSI / Pembrolizumab



Oportunidades para la eficiencia/ineficiencia: HRD / iPARP



	OLAPARIB			NIRAPARIB			RUCAPARIB		
	2 ^a -3 ^a L P-Sen BRCA mut	2 ^a -3 ^a L P-s BRCA wt	1 ^a L P-s BRCA mut	2 ^a -3 ^a L P-s BRCA mut	2 ^a -3 ^a L P-s BRCA wt HRD +	2 ^a -3 ^a L P-s BRCA wt HRD -	2 ^a -3 ^a L P-s BRCA mut	2 ^a -3 ^a L P-s BRCA wt HRD +	2 ^a -3 ^a L P-s BRCA wt HRD -
SLP (HR)	0.18 (0.10-0.31)	0.54 (0.34-0.85)	0.30 (0.23-0.41)	0.27 (0.17-0.41)	0.38 (0.23-0.63)	0.58 (0.30-0.92)	0.23 (0.16-0.34)	0.44 (0.26-0.66)	0.58 (0.40-0.85)
Δ SLP	7 meses	2 meses	>36 meses	15 meses	5.6 meses	3.1 meses	11.2 meses	4.3 meses	1.3 meses
SLP control	4.3 meses	5.5 meses	13.8 meses	5.5 meses	3.7 meses	3.8 meses	5.4 meses	5.4 meses	5.4 meses
SG (HR)	0.62 (0.41-0.94)	0.83 (0.55-1.24)	-						
Δ SG	4.7 meses (signific.)	2 meses (NS)	-						
SG control	32 meses	26 meses	-						
Valor clínico ESMO	4	3	3 (vs 4)	3	3	3	3	3	2
Referencia	Ledermann, Lancet Oncol 2014 y Lancet Oncol 2016			Mirza, N Engl J Med 2016			Coleman, Lancet 2017		
Método HRD	--			Myriad My Choice (LOH, LST, TAI)			Foundation Medicine, T5 NGS (cut-off 16% LOH high)		

Toss, J Cancer Sci Ther 2013; Ledermann, Lancet Oncol 2014; Ledermann, Lancet Oncol 2016; Mirza, N Engl J Med 2016; Coleman, Lancet 2017

RETOS PARA EL FUTURO (INMEDIATO)

Prevención

Precisión también para el paciente

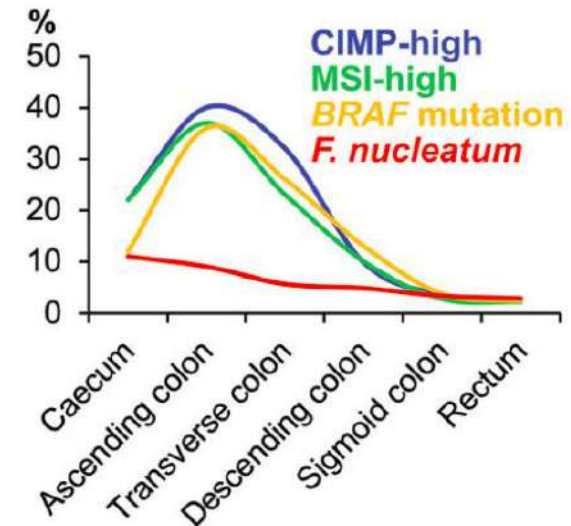
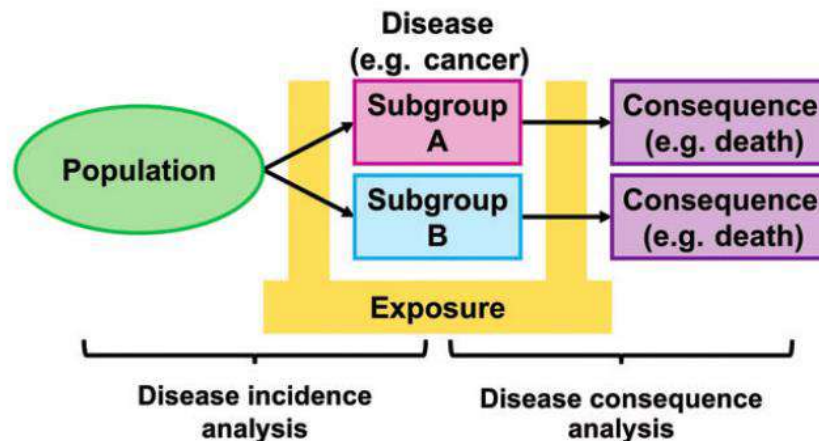
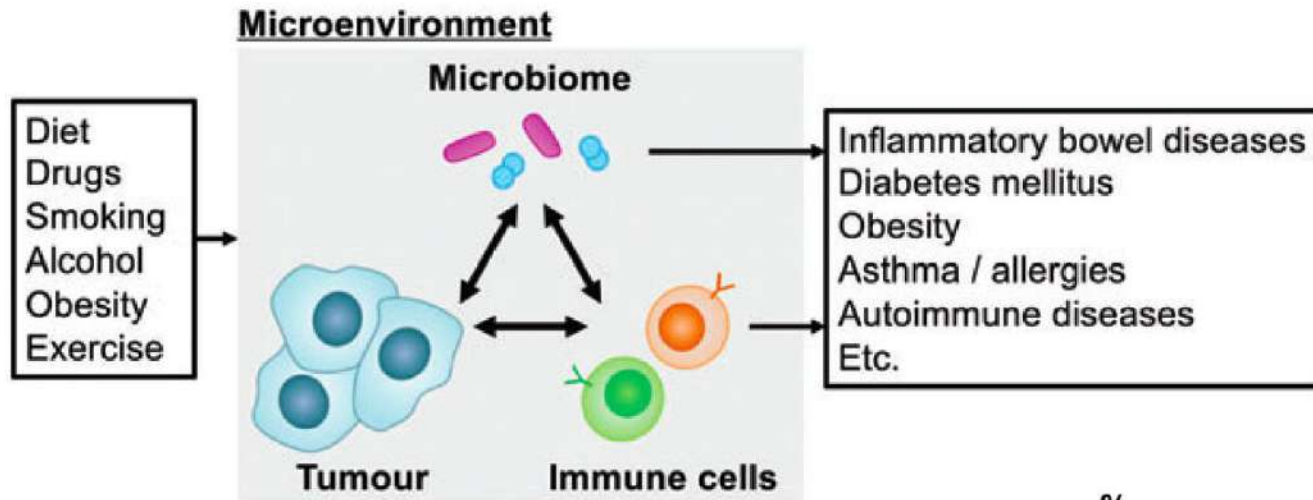
Acceso a biomarcadores y a ensayos clínicos

Calidad analítica

Entorno colaborativo de estudio y validación de dianas y biomarcadores

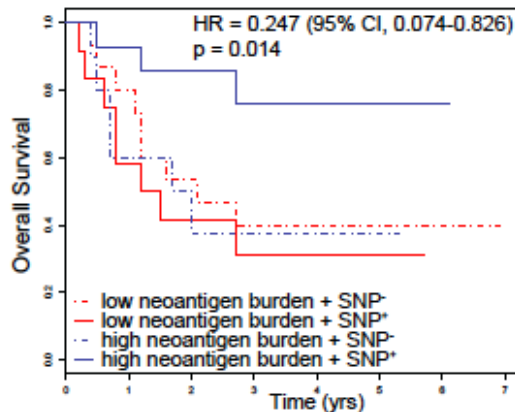
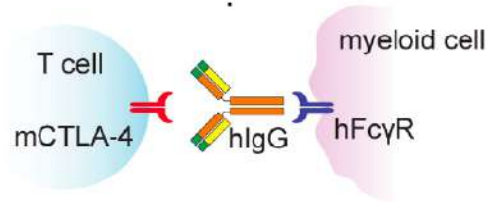
Gestión de la información: investigación y asistencia

Retos: no solo tratamiento, también prevención

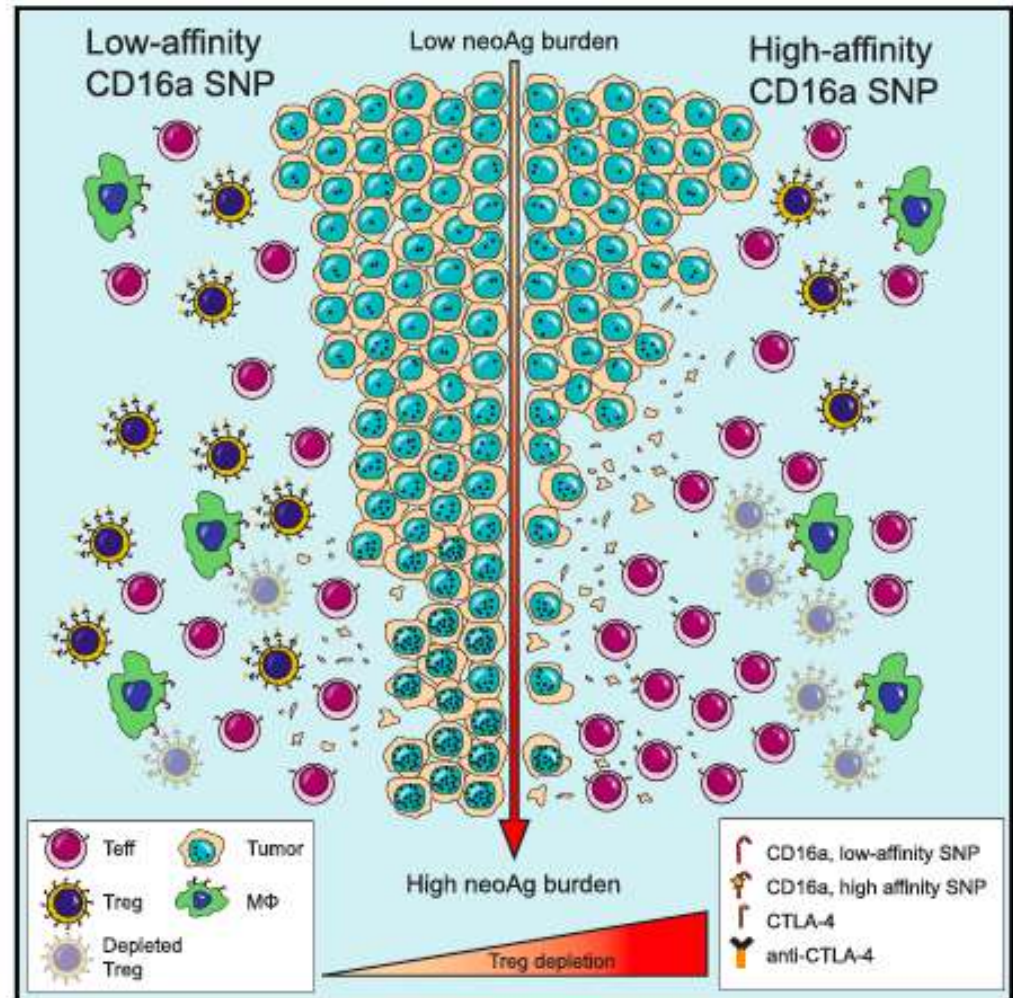


Retos: ¿Algo más de precisión también en el paciente?

Variación genética hereditaria en respuesta inmune tumoral



	Number at risk							
low + SNP-	15	12	8	4	3	2	2	0
low + SNP+	12	7	5	3	1	1	0	0
high + SNP-	10	6	4	1	1	1	0	0
high + SNP+	14	13	11	6	6	1	1	0



Retos: acceso a biomarcadores



Gestión
Hospitalaria

La Sociedad Española de Oncología Médica
está analizando el acceso a los
biomarcadores



infosalus / asistencia

**SEOM pide que la Estrategia de Medicina de Precisión
esté "dotada de recursos, coordinada y mantenida en el
tiempo"**

Retos: calidad y metodología común

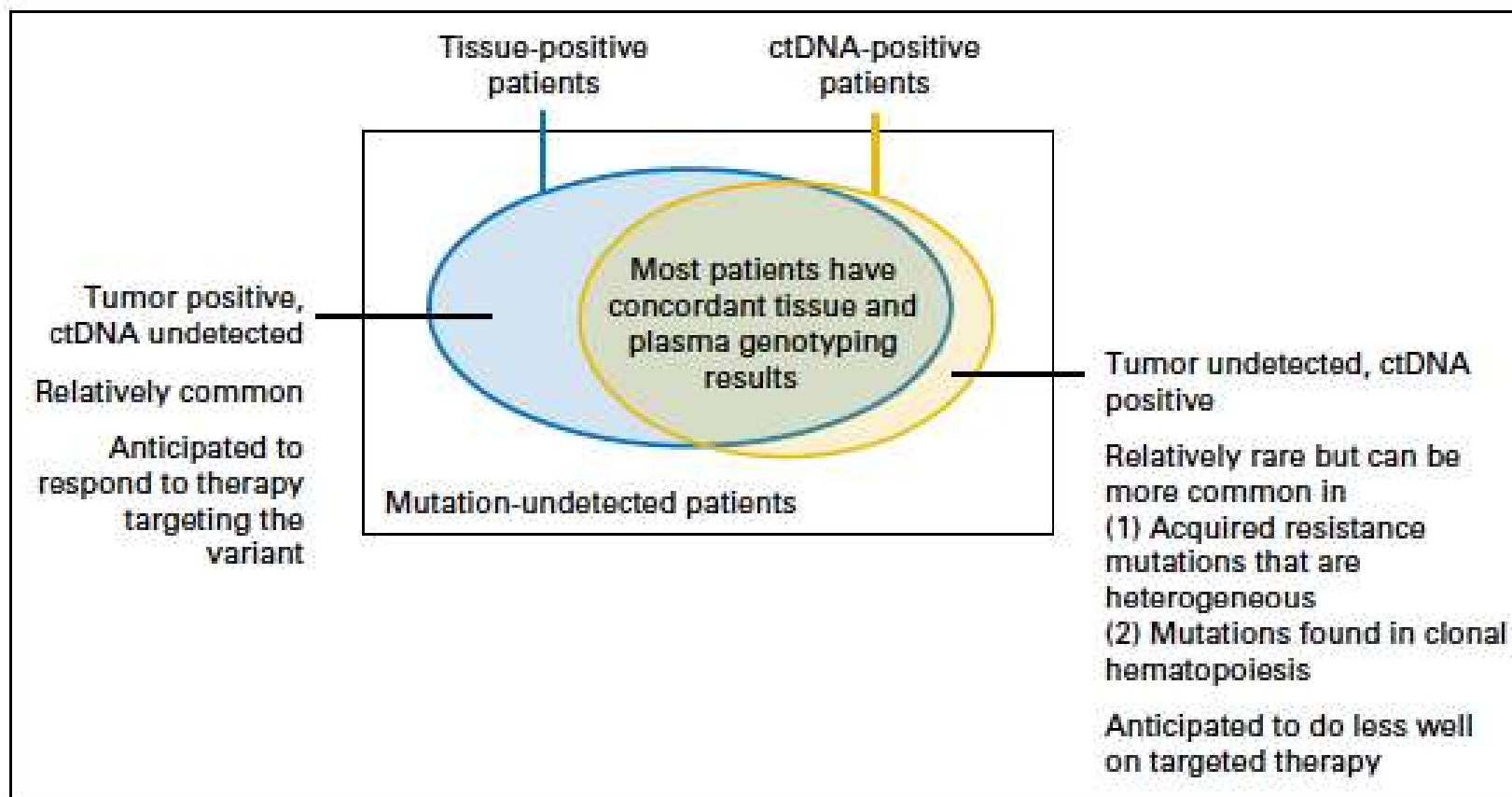
VOLUME 36 • NUMBER 16 • JUNE 1, 2018

JOURNAL OF CLINICAL ONCOLOGY

ASCO SPECIAL ARTICLE

Circulating Tumor DNA Analysis in Patients With Cancer: American Society of Clinical Oncology and College of American Pathologists Joint Review

Jason D. Merker, Geoffrey R. Oxnard, Carolyn Compton, Maximilian Diehn, Patricia Hurley, Alexander J. Lazar, Neal Landman, Christina M. Lockwood, Alex J. Rai, Richard L. Schilsky, Apostolia M. Tsimberidou, Patricia Vassilos, Brooke L. Billman, Thomas K. Oliver, Suanna S. Bruinooge, Daniel F. Hayes, and Nicholas C. Turner



Retos: colaboración multicéntrica

The GENIE registry is a tool that can be used in many ways:

To confirm or refute that mutation X or mutations X, Y, and Z predict patient response to drug A or that the patient's disease is likely to do better or worse over time.



Drug B is approved for patients with mutation Y1. The GENIE registry indicates that patients with mutation Y2 can also be successfully treated with drug B.



Drug C is approved for lung cancer patients with mutation W. The GENIE registry indicates that many blood cancers, colorectal cancers, and stomach cancers also have mutation W.

- Novel disease-causing proteins could be identified and become new drug targets.
- Novel mutation signatures could be uncovered that predict drug sensitivity or patient outcomes.



New clinical trial(s) are opened to test drug C in blood, colorectal, and stomach cancers.



Enough blood, colorectal, or stomach cancer patients in the GENIE data set have already been treated with drug C, showing that it is an effective treatment for these patients.



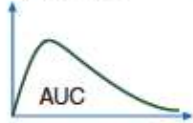
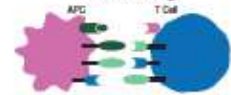
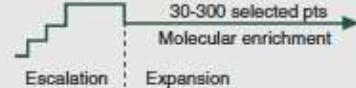
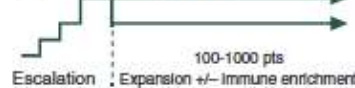
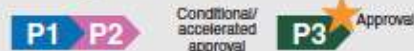
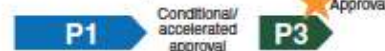
The GENIE registry could provide the evidence necessary to support reimbursement for next-generation sequencing by payers, opening this technology to all patients.



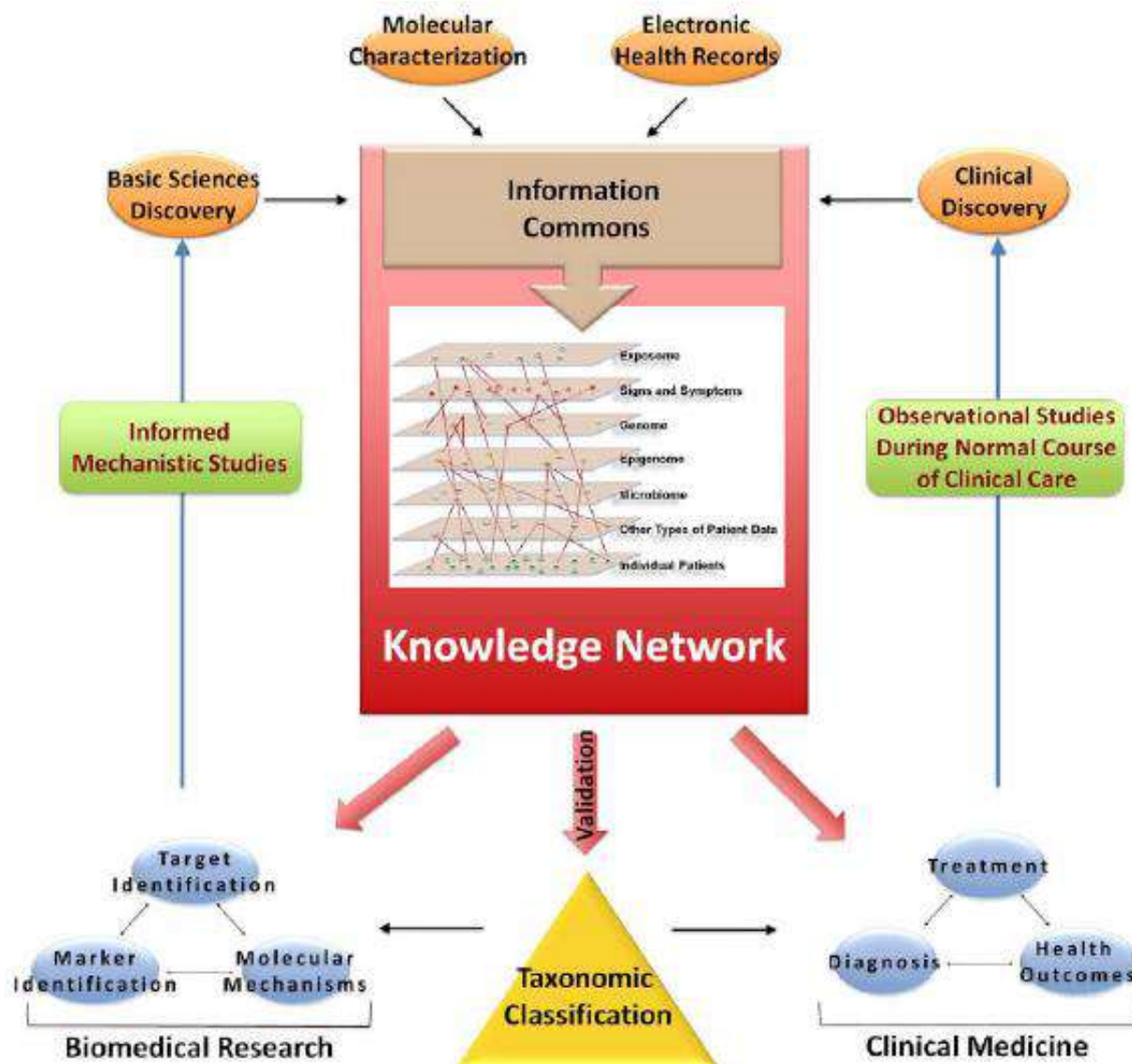
Lessons learned from the assembly and operation of GENIE could benefit other global consortia and vice versa.



Retos: colaboración multicéntrica

	Cytotoxic chemotherapy	Molecularly targeted agents	Immuno-stimulatory antibodies
Patients number	 30-50 unselected patients Target enrichment	 30-200 molecularly selected patients Immune enrichment	 100-1000 immunologically selected patients Pts # Unselected
Route of administration	IV > Oral 	Oral > IV 	Novel routes of administration (intra-tumoral) 
Toxicity	MTD quasi-systematically reached	MTD unconstantly reached	MTD rarely reached → MAD
PK/PD - biomarkers	Traditional PK limited PD  OIB	Traditional PK with potential for PK - based dose recommendation Biomarker-driven PD for target assay validation and molecular enrichment  	PK and pD-based dose recommendation? repeated PD for dynamic biomarkers and immunological monitoring 
Design	Traditional 3 + 3 dose-escalation design  Escalation Expansion 20-30 pts	3 + 3 dose-escalation design with large expansion cohorts in selected populations  Escalation Expansion 30-300 selected pts Molecular enrichment	Accelerated titration/adaptive design multiple parallel expansion cohorts long-term follow-up + drug rechallenge  Escalation Expansion +/- Immune enrichment 100-1000 pts
Drug approval	Based on later phase 2 or 3 trials 	Conditional of accelerated approval based on large molecularly selected expansion cohorts 	Conditional of accelerated approval based on histology and immune-biomarker selected expansion cohorts 
Drug development timeframe	10 years	5-8 years	<5 years

Retos: la gestión de la información

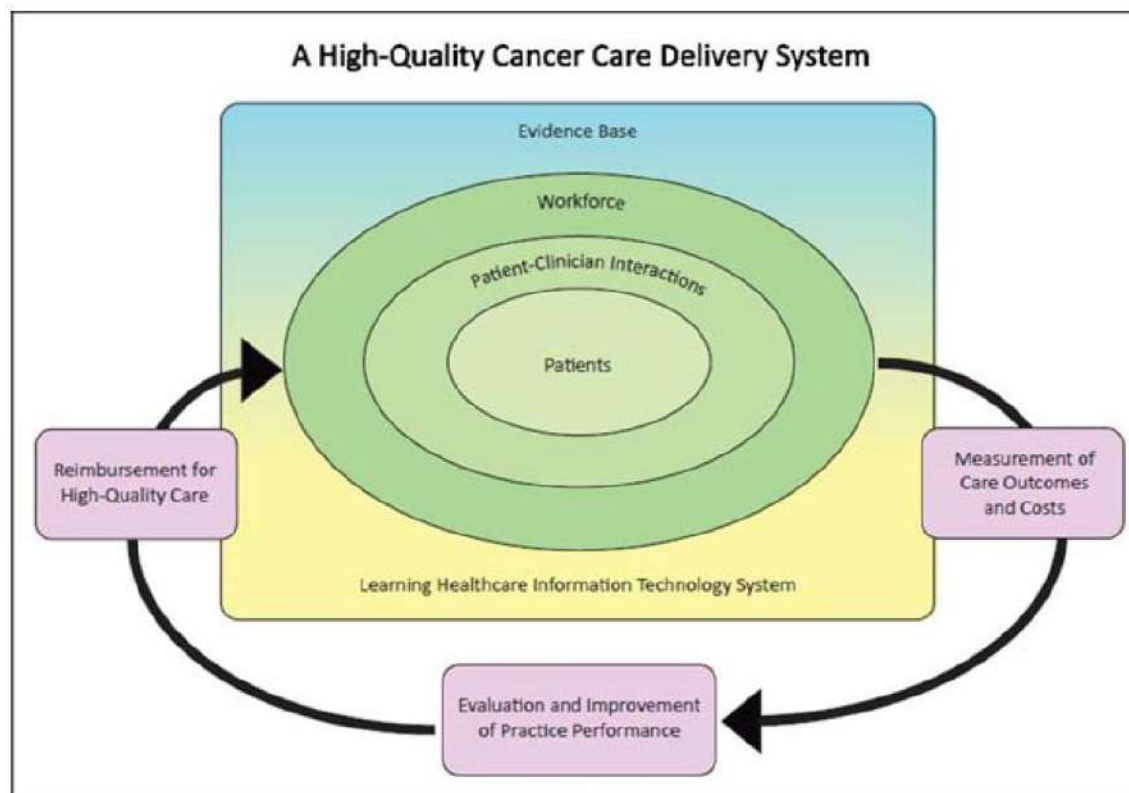


Improving the quality of cancer care in America through health information technology

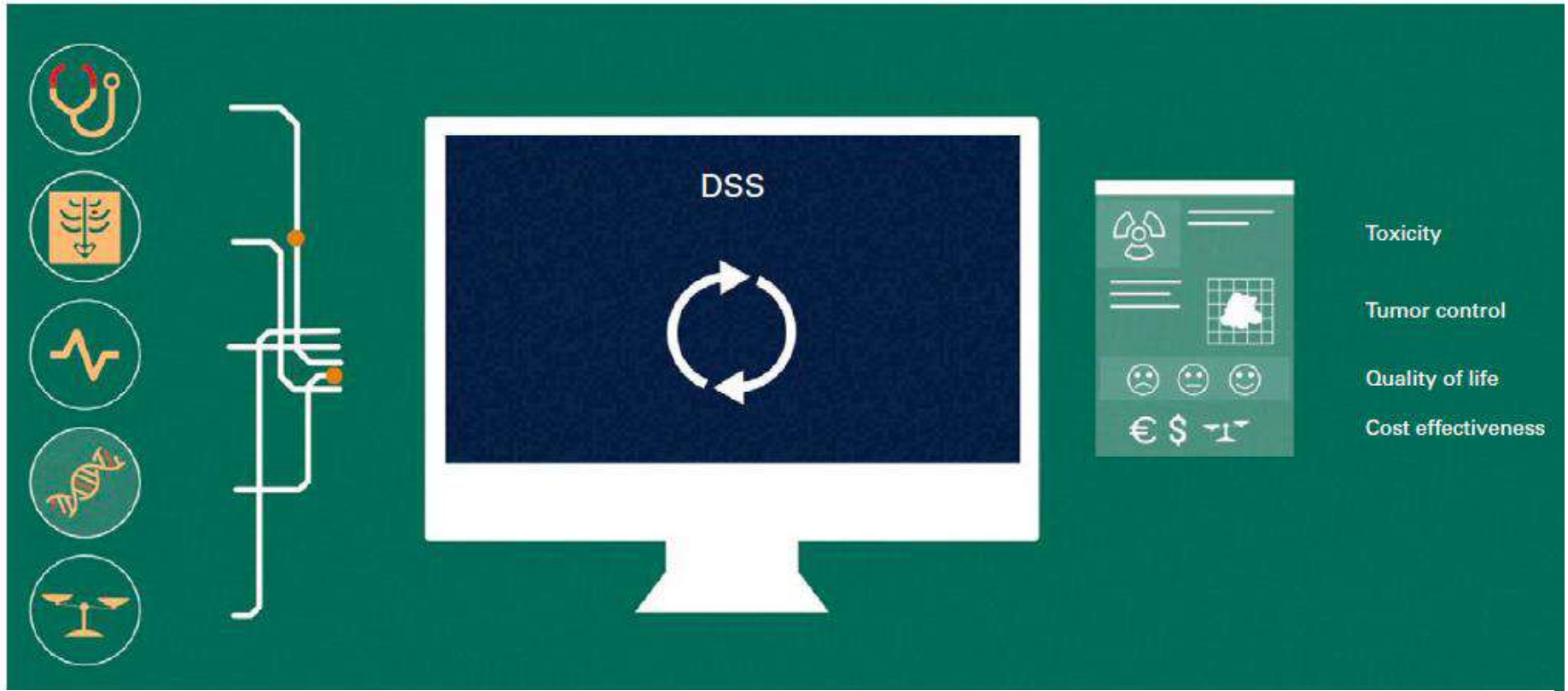
Thomas W Feeley,¹ George W Sledge,² Laura Levit,³ Patricia A Ganz^{4,5}

Box 1 Goals of the 10 recommendations to improve the quality of cancer care in America

1. Provide patients and their families with understandable information about cancer prognosis, treatment benefits and harms, palliative care, psychosocial support, and costs.
2. Provide patients with end-of-life care that meets their needs, values, and preferences.
3. Ensure coordinated and comprehensive patient-centered care.
4. Ensure that all individuals caring for cancer patients have appropriate core competencies.
5. Expand the breadth of data collected in cancer research for older adults and patients with multiple comorbid conditions.
6. Expand the depth of data collected in cancer research through a common set of data elements that capture patient-reported outcomes, relevant patient characteristics, and health behaviors.
7. Develop a learning healthcare information technology system for cancer that enables real-time analysis of data from cancer patients in a variety of care settings.
8. Develop a national quality reporting program for cancer care as a part of learning healthcare system.
9. Implement a national strategy to reduce disparities in access to cancer care for under-served populations by leveraging community interventions.
10. Improve the affordability of cancer care by leveraging existing efforts to reform payment and eliminate waste.



Retos: la gestión de la información



Sistemas de apoyo a la decisión multifactoriales

Nuevos retos: diagnóstico genético DTC

FDA Clears 23AndMe's DTC Breast Cancer Gene Test -- But 'Buyer Beware'



Arlene Weintraub, CONTRIBUTOR

I cover the science and business behind drug development and health.
FULL BIO ✓

Opinions expressed by Forbes Contributors are their own.



Anne Wojcicki, CEO of 23andMe Inc., believes consumers should have better access to BRCA

The direct-to-consumer genetic-test marketer 23andMe celebrated an historic first today, with the first FDA approval of its test for some BRCA1/BRCA2 mutations. The genes that the test covers have been linked to an increased risk of breast, ovarian and prostate cancer.



Find out what your DNA says about your health, traits and ancestry.

add to cart

\$199

see all reports

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MEETS FDA REQUIREMENTS

Genetic Health Risks*

Learn how your genetics can influence your risk for certain diseases.



NOW WITH 150+ REGIONS

Ancestry

Discover where your DNA is from out of 150+ regions worldwide - and more.



Wellness

Learn how your genes play a role in your well-being and lifestyle choices.



MEETS FDA REQUIREMENTS

Carrier Status*

If you are starting a family, find out if you are a carrier for certain inherited conditions.



Traits

Learn how your DNA influences your facial features, taste, smell and other traits.



CONCLUSIONES

Cambio extremadamente rápido

Beneficios reales, pero no siempre y a veces escasos

Retos científicos y logísticos

España: acceso no equitativo y ausencia de planificación

Balance difícil: eficiencia marcador o fármaco / ineficiencia marcador o fármaco

Retos asistenciales