

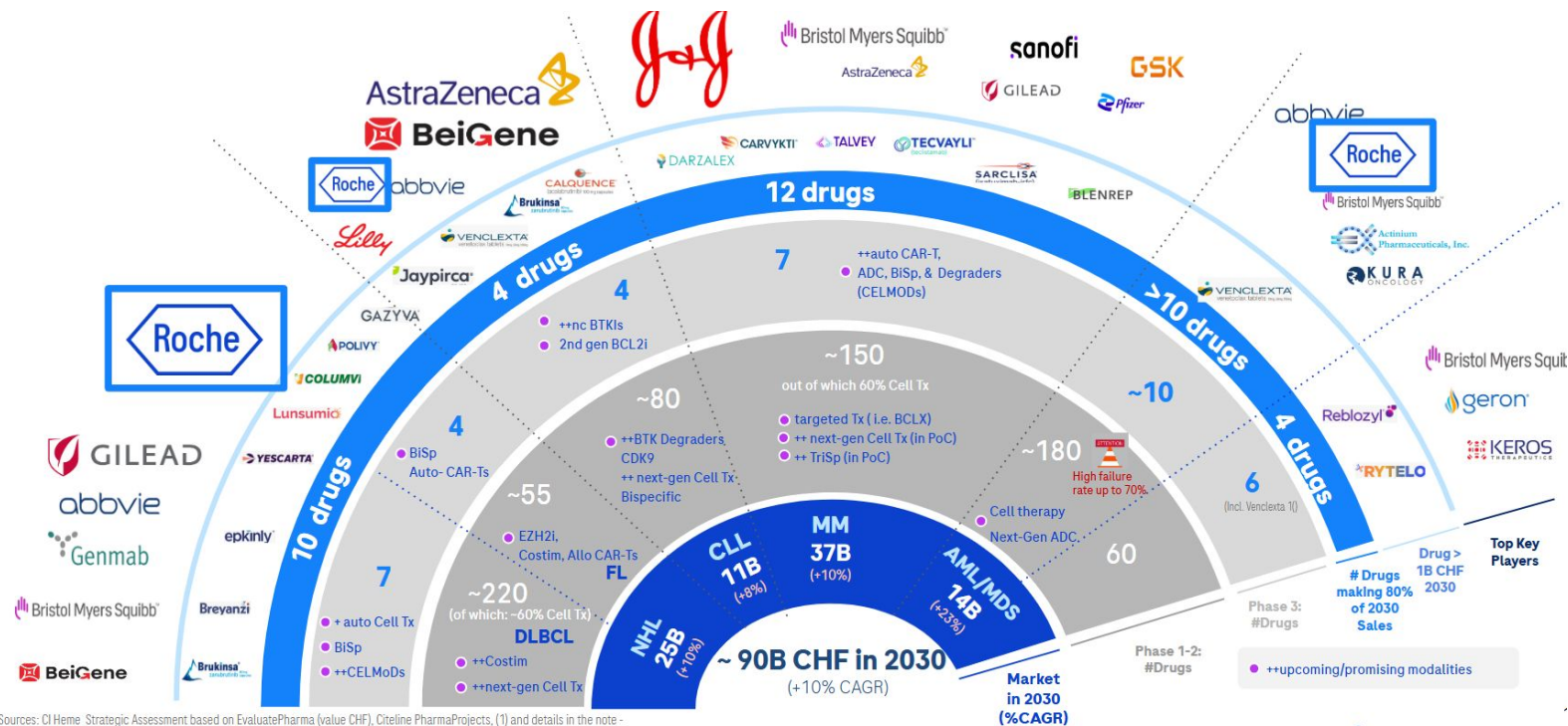
OPERATING CHARACTERISTICS OF M-PROTEIN DYNAMIC METRICS TO SUPPORT EARLY DECISIONS IN MULTIPLE MYELOMA

Pascal Chanu, Mathilde Marchand (Certara), Federico Mattiello, Mark Yan, Tom Chambers, Felipe Castro, Monica Susilo, Divya Samineni, Dale Miles, Chunze Li, Jin Jin

Clinical Pharmacology - Modeling & Simulation

September 19, 2025, Pharmacometrics in France

MULTIPLE MYELOMA (MM) REMAINS AN APPEALING MARKET



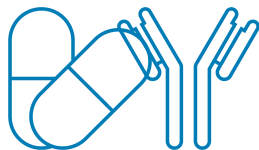
Sources: C1 Heme Strategic Assessment based on EvaluatePharma (value CHF), Cyteline PharmaProjects, (1) and details in the note - High level analysis - not exhaustive - no vaccine included,

Sources [used for the data](#)

Oct 2024

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EARLY DEVELOPMENT SITUATION IN MULTIPLE MYELOMA (MM)



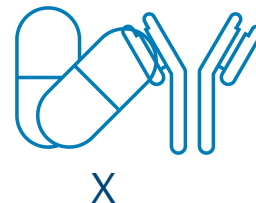
Combination therapy X in
multiple myeloma
Phase 1b data, N=30,
2 dose levels, no control,
endpoint:
ORR i.e. VGPR rate

External data from YODA



RWD  flatiron

MM enabling decision
framework



X



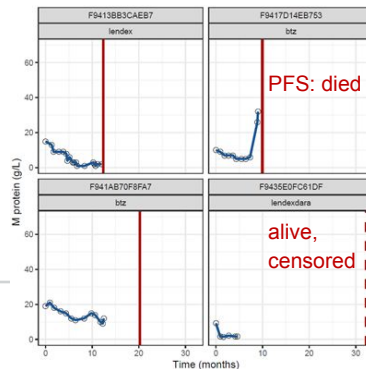
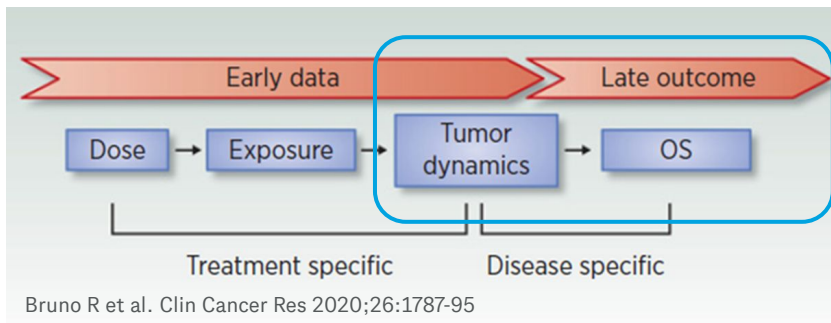
vs

Standard of Care

Phase 3 study:
X
versus
Standard of Care:
daratumumab+polamidomide+
dexamethasone (DPd),
endpoint: PFS

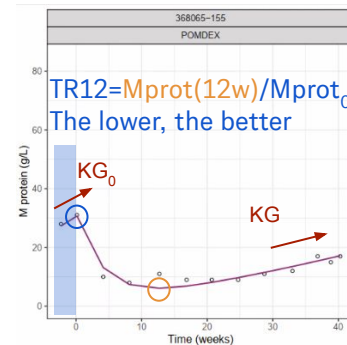
MODELING & SIMULATION FRAMEWORK IN MULTIPLE MYELOMA

Model-based tumor dynamics metrics are biomarkers capturing treatment effect



KG, TR12...
linked to PFS

Application to Multiple Myeloma

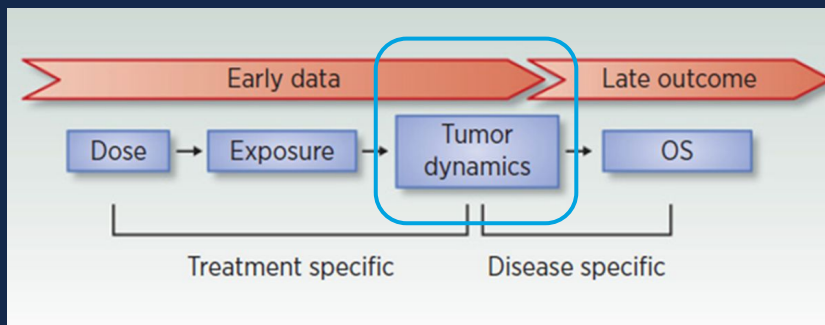


$$t < 0 \quad Mprot(t) = Mprot_0 \cdot e^{KG_0 \cdot t}$$

$$t \geq 0 \quad Mprot(t) = Mprot_0 \cdot (e^{KG \cdot t} + e^{-KS \cdot t} - 1)$$

Stein et al. Clin Cancer Res 2011;17:907-17

OPERATING CHARACTERISTICS OF M-PROTEIN DYNAMIC METRICS



OPERATING CHARACTERISTICS OF TGI METRICS

Tumor Dynamic Model-Based Decision Support for Phase Ib/II Combination Studies: A Retrospective Assessment Based on Resampling of the Phase III Study IMpower150

René Bruno¹, Mathilde Marchand², Kenta Yoshida³, Phyllis Chan³, Haocheng Li⁴, Wei Zou⁵, Francois Mercier⁶, Pascal Chanu⁷, Benjamin Wu³, Anthony Lee⁵, Chunze Li³, Jin Y. Jin³, Michael L. Maitland^{8,9}, Martin Reck¹⁰, and Mark A. Socinski¹¹



ABSTRACT

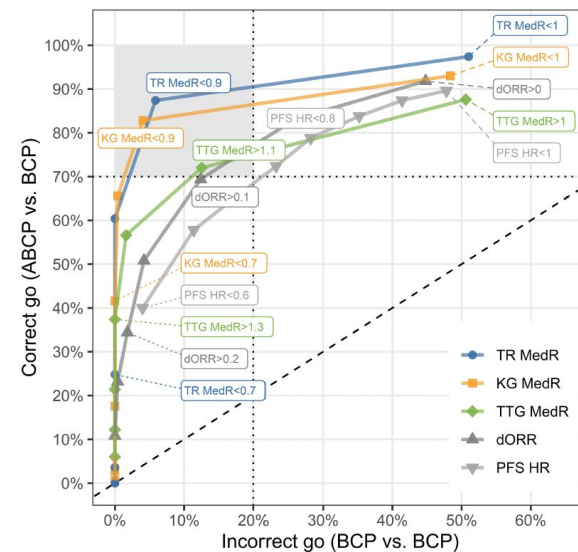
Purpose: Model-based tumor growth inhibition (TGI) metrics are increasingly incorporated into go/no-go decisions in early clinical studies. To apply this methodology to new investigational combinations requires independent evaluation of TGI metrics in recently completed Phase III trials of effective immunotherapy.

Patients and Methods: Data were extracted from IMpower150, a positive, randomized, Phase III study of first-line therapy in 1,202 patients with non-small cell lung cancer. We resampled baseline characteristics and longitudinal sum of longest diameters of tumor lesions of patients from both arms, atezolizumab+bevacizumab+chemotherapy (ABCP) versus BCP, to mimic Phase Ib/II studies of 15 to 40 patients/arm with 6 to 24 weeks follow-up. TGI metrics were estimated using a bi-exponential TGI model. Effect sizes were calculated as TGI metrics ratio of medians (MedR), objective response rate (ORR) difference (d),

and progression-free survival (PFS), hazard ratio (HR) between arms. Correct and incorrect go decisions were evaluated as the probability to achieve desired effect sizes in ABCP versus BCP and BCP versus BCP, respectively, across 500 replicated subsamples for each design.

Results: For 40 patients/24 weeks follow-up, correct go decisions based on probability tumor growth rate (KG) MedR < 0.90, dORR > 0.10, and PFS HR < 0.70 were 83%, 69%, and 58% with incorrect go decision rates of 4%, 12%, and 11%, respectively. For other designs, the ranking did not change with TGI metrics consistently overperforming RECIST endpoints. The predicted overall survival (OS) HR was around 0.80 in most of the scenarios investigated.

Conclusions: Model-based estimate of KG MedR is an exploratory endpoint that informs early clinical decisions for combination studies.



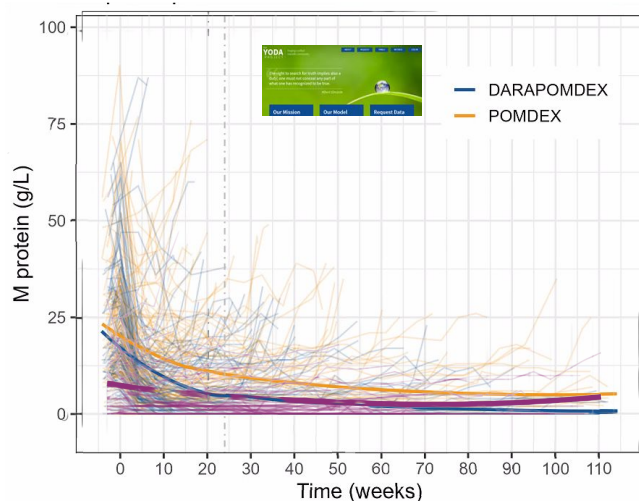
APOLLO PATIENT POPULATION IS REPRESENTATIVE

APOLLO: model development, DPd versus Pd

Dimopoulos et al. Lancet Oncol 2021;22:801-12

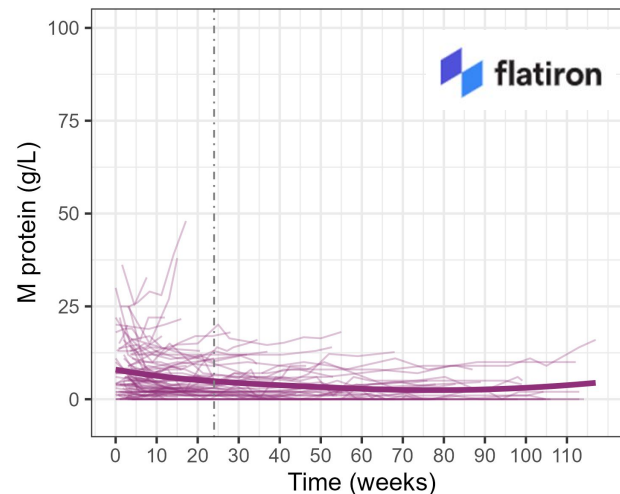
Daratumumab plus pomalidomide and dexamethasone versus pomalidomide and dexamethasone alone in previously treated multiple myeloma (APOLLO): an open-label, randomised, phase 3 trial

Meleis A, Dimopoulos, Evangelos Terpos, Mario Boccadoro, Soana Delimpasi, Meral Bekas, Evrim Karadimitou, Philippe Moreau, Luca Baldoni, Agnieszka Symeonidis, Jelena Bili, Albert Oriol, Maria Victoria Mateos, Hermann Einsele, Ioannis Orfanidis, Tahamtan Ahmadi, Joni Kropac, Tobias Kampferkel, Jordan M Schuster, Yanying Qiu, Hamed Amin, Jessica Vermaulen, Robin Carson, Pieter Sonneveld, for the APOLLO Trial Investigators*



DPd in APOLLO considered as a relevant control for X assessment

RWD of the population of interest shows a good match with DPd arm from APOLLO



RWD from Flatiron Health, an oncology-based electronic health record (EHR)-derived de-identified database

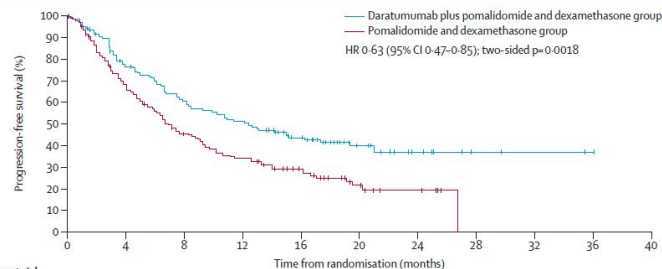
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DATA: APOLLO & CASTOR CLINICAL TRIALS

APOLLO: model development, DPd versus Pd
Dimopoulos et al. Lancet Oncol 2021;22:801-12

Daratumumab plus pomalidomide and dexamethasone versus pomalidomide and dexamethasone alone in previously treated multiple myeloma (APOLLO): an open-label, randomised, phase 3 trial

Meletios A Dimopoulos, Evangelos Terpos, Mario Boccadoro, Sosana Delimpasi, Meral Beksac, Eirini Katodritou, Philippe Moreau, Luca Baldini, Argiris Syreoniadis, Jdema Bika, Albert Oriol, Maria-Victoria Mateos, Hermann Einsele, Ioannis Orfanidis, Tahamtan Ahmadi, Jon Ukropce, Tobias Kampfenkel, Jordan M Schechter, Yangping Qiu, Himan Amin, Jessica Vermaelen, Robin Carson, Pieter Sonneveld, for the APOLLO Trial Investigators*



Number at risk (number censored)

Daratumumab plus pomalidomide and dexamethasone group	151	111	87	74	48	20	8	3	2	1	0
	(0)	(6)	(7)	(7)	(24)	(48)	(59)	(64)	(65)	(66)	(67)
Pomalidomide and dexamethasone group	152	93	61	46	27	12	5	0	0	0	0
	(0)	(11)	(15)	(15)	(27)	(37)	(43)	(47)	(0)	(0)	(0)

CASTOR: validation, DVd versus Vd
Palumbo et al. N Engl J Med 2016;375:754-66

THE NEW ENGLAND JOURNAL OF MEDICINE

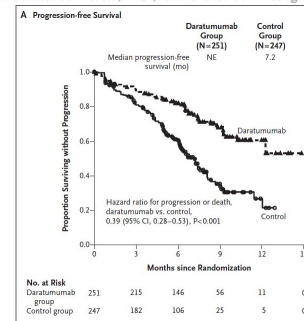
ORIGINAL ARTICLE

Daratumumab, Bortezomib, and Dexamethasone for Multiple Myeloma

Antonio Palumbo, M.D., Asher Chanan-Khan, M.D., Katja Weisel, M.D., Ajay K. Nooka, M.D., Tamas Masszi, M.D., Meral Beksac, M.D., Ivan Spicka, M.D., Vania Hungria, M.D., Markus Munder, M.D., Maria V. Mateos, M.D., Torner M. Mark, M.D., Ming Qi, M.S., Jordan Schechter, M.D., Himan Amin, B.S., Xiang Qin, M.S., William Deraedt, Ph.D., Tahamtan Ahmadi, M.D., Andrew Spencer, M.D., and Pieter Sonneveld, M.D., for the CASTOR Investigators*

DPd in APOLLO considered as a relevant control for X assessment

For assessing operating characteristics of M-protein dynamics: DPd will be the experimental arm and Pd the control



MODEL SELECTION TO ASSESS OPERATING CHARACTERISTICS (OC) ON APOLLO DATA

Model development performed in **nlmixr²**

$$t < 0 \quad M_{\text{prot}}(t) = M_{\text{prot}_0} \cdot e^{KG \cdot t}$$

$$t \geq 0 \quad M_{\text{prot}}(t) = M_{\text{prot}_0} \cdot (e^{KG \cdot t} + e^{-KS \cdot t} - 1)$$

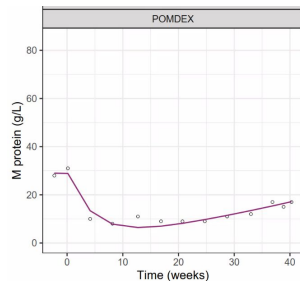
Estimating a different KG0 before treatment improves the model

$$t < 0 \quad M_{\text{prot}}(t) = M_{\text{prot}_0} \cdot e^{KG_0 \cdot t}$$

$$t \geq 0 \quad M_{\text{prot}}(t) = M_{\text{prot}_0} \cdot (e^{KG \cdot t} + e^{-KS \cdot t} - 1)$$

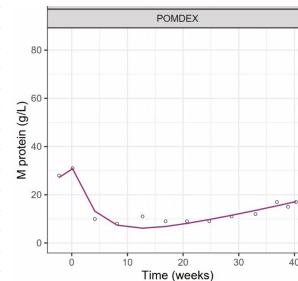
Parameter	Estimate	SE	RSE (%)	Back-transformed	Unit	Shrinkage (%)
Fixed Effects						
ln(KG_DPd)	-7.50	0.0107	0.1	0.000553	day ⁻¹	
ln(KG_Pd)	-6.49	0.0118	0.2	0.00152	day ⁻¹	
ln(KS_DPd)	-3.78	0.0114	0.3	0.0228	day ⁻¹	
ln(KS_Pd)	-4.33	0.0107	0.2	0.0132	day ⁻¹	
TS0	2.80	0.00544	0.2	16.4	g/L	
Random Effects						
KG	82				%CV	66.8
KS	81				%CV	6.1
TS0	81				%CV	0.6
Residual variability						
Res add.	2.78				g/L	

Run: noKG0 objective function value: 13070.03



Parameter	Estimate	SE	RSE (%)	Back-transformed	Unit	Shrinkage (%)
Fixed Effects						
ln(KG0)	-6.79	0.157	2	0.00112	day ⁻¹	
ln(KG_DPd)	-7.02	0.0808	1	0.000894	day ⁻¹	
ln(KG_Pd)	-6.36	0.0852	1	0.00173	day ⁻¹	
ln(KS_DPd)	-4.23	0.123	3	0.0146	day ⁻¹	
ln(KS_Pd)	-4.36	0.127	3	0.0128	day ⁻¹	
TS0	2.82	0.0893	3	16.8	g/L	
Random Effects						
KG0	165				%CV	48.5
KG	82				%CV	61.3
KS	80				%CV	6.4
TS0	81				%CV	3.9
Residual variability						
Res add.	2.93				g/L	

Run: KG0IV objective function value: 13041.53



False GO: Pd vs. Pd

Bootstrapped **Pd** n=151, max FU

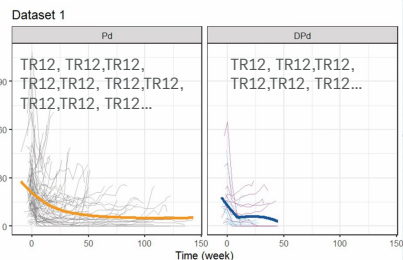
- Fit models, derive metrics and compute GMR

Repeat 1000 times

Bootstrapped **Pd** n=149, max FU

- Fit models, derive metrics and compute GMR

Repeat 1000 times



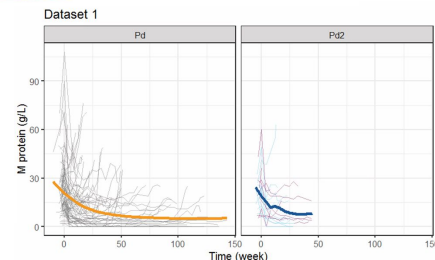
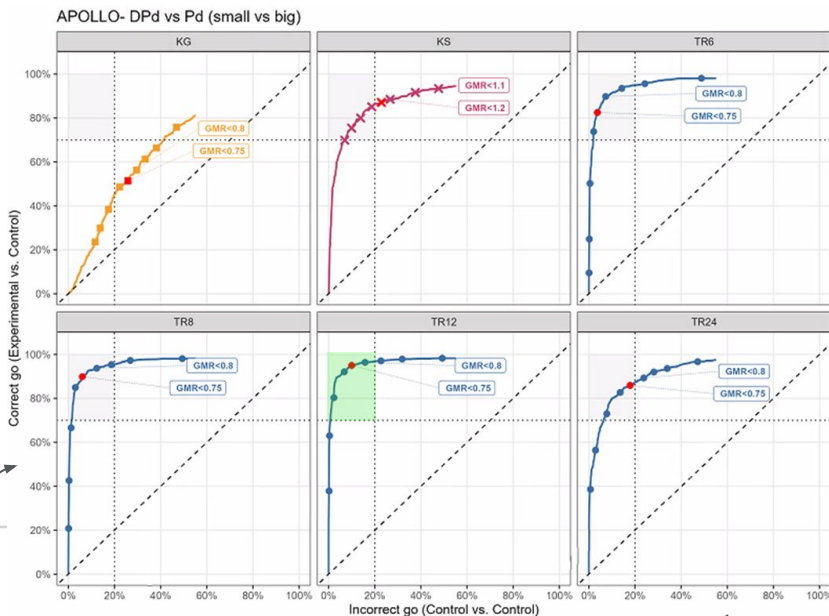
1 GM of TR12 1 GM of TR12

1 GMR exp/control
The lower, the better

X 1000

% of achieving a certain target GMR
e.g. <0.75

Marchand et al. PAGE 2025



- KG has poor OCs, **what's wrong?**
- TR8, TR12 are good metrics (better than TR6 and TR24)
- $p(\text{TR GMR} < 0.75)$ or $p(\text{TR GMR} < 0.80)$ as gating criteria

IMPORTANCE OF MODEL'S ROBUSTNESS WHEN ASSESSING OC

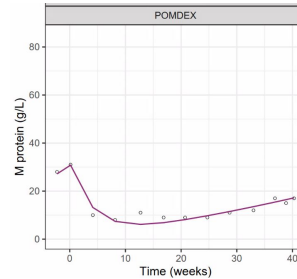
$$t < 0 \quad M_{\text{prot}}(t) = M_{\text{prot}_0} \cdot e^{KG_0 \cdot t}$$

$$t \geq 0 \quad M_{\text{prot}}(t) = M_{\text{prot}_0} \cdot (e^{KG \cdot t} + e^{-KS \cdot t} - 1)$$

Estimating a different KG0 before treatment improves the model

Parameter	Estimate	SE	RSE (%)	Back-transformed	Unit	Shrinkage (%)
Fixed Effects						
ln(KG0)	-6.79	0.157	2	0.00112	day ⁻¹	
ln(KG_DPd)	-7.02	0.0808	1	0.000894	day ⁻¹	
ln(KG_Pd)	-6.36	0.0852	1	0.00173	day ⁻¹	
ln(KS_DPd)	-4.23	0.123	3	0.0146	day ⁻¹	
ln(KS_Pd)	-4.36	0.127	3	0.0128	day ⁻¹	
TS0	2.82	0.0893	3	16.8	g/L	
Random Effects						
KG0	165				%CV	48.5
KG	82				%CV	61.3
KS	80				%CV	6.4
TS0	81				%CV	3.9
Residual variability						
Res add.	2.93				g/L	

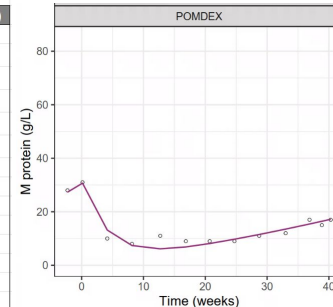
Run: KG0IIV objective function value: 13041.53



On small subsamples, the typical value of KG0 is identifiable but likely not its random effect

Parameter	Estimate	SE	RSE (%)	Back-transformed	Unit	Shrinkage (%)
Fixed Effects						
ln(KG0)	-5.96	0.127	2	0.00258	day ⁻¹	
ln(KG_DPd)	-7.63	0.0792	1	0.000486	day ⁻¹	
ln(KG_Pd)	-6.37	0.0966	2	0.00171	day ⁻¹	
ln(KS_DPd)	-3.80	0.117	3	0.0224	day ⁻¹	
ln(KS_Pd)	-4.32	0.129	3	0.0133	day ⁻¹	
TS0	2.68	0.0769	3	14.6	g/L	
Random Effects						
KG0	NA				%CV	NA
KG	82				%CV	60.3
KS	76				%CV	5.3
TS0	70				%CV	7.9
Residual variability						
Res add.	3.27				g/L	

Run: KG0nollV objective function value: 13326.31



This model makes more sense:

KG0 > KG_Pd > KG_DPd
[0.00201;0.00331] [0.00142;0.00207] [0.000416 ; 0.000567]

Let's redo OCs with this model

False GO: Pd vs. Pd

Bootstrapped **Pd** n=151, max FU

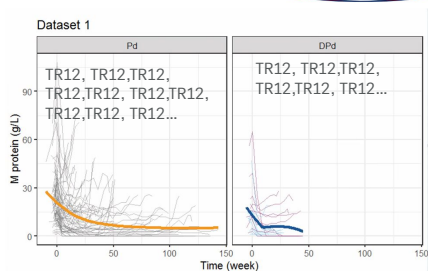
Fit models, derive metrics and compute GMR

Repeat 1000 times

Bootstrapped **Pd** n=149, max FU

- Fit models, derive metrics and compute GMR

Repeat 1000 times



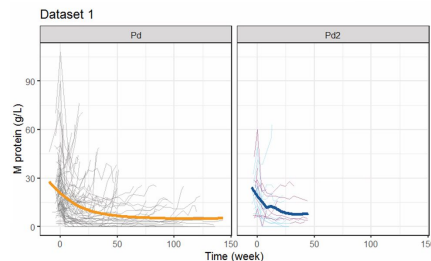
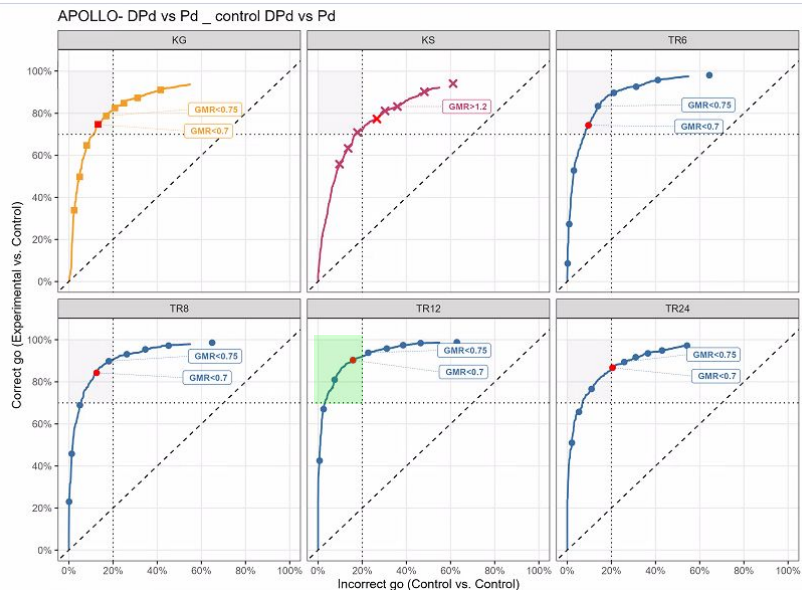
1 GM of TR12

1 GM of TR12

1 GMR exp/control
The lower, the better

X 1000

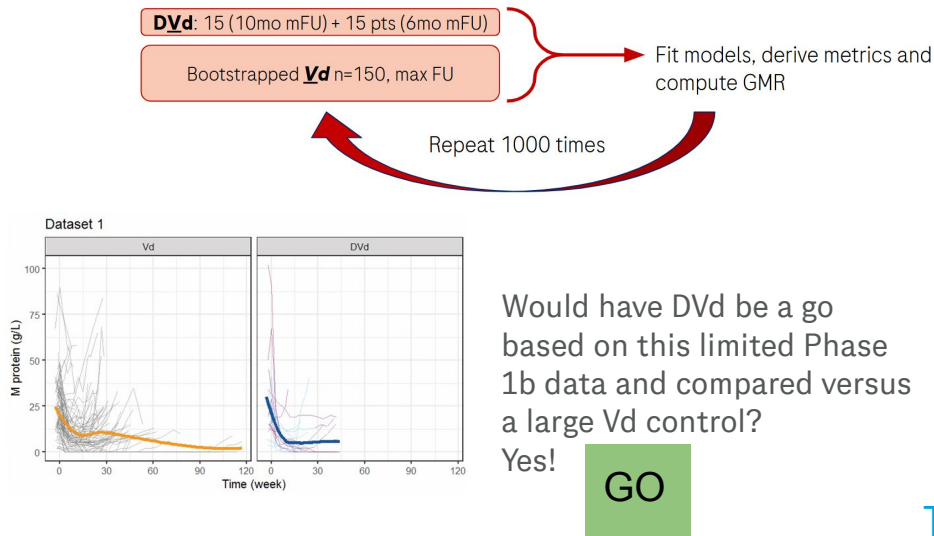
% of achieving a certain target GMR
e.g. <0.75



- Results make sense with a less parameterized model
- KG is now a decent metric
- TR8, TR12 are good metrics
- $p(\text{TR GMR} < 0.70)$ as gating criteria

LET'S TEST THE APPROACH ON THE CASTOR TRIAL

True GO : DVd vs. Vd



Probability of achieving the gating criteria

Experimental (DVd) versus Control (Vd): True GO

Metric	p(GMR<0.70)%	p(GMR<0.75)%
KG	94.1	96.9
TR8	74.3	77.4
TR12	87.5	90.2

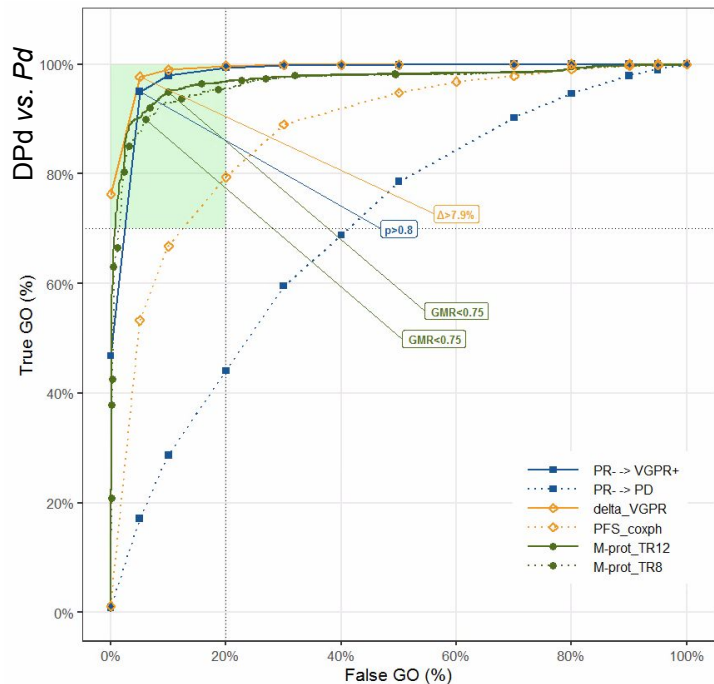
Control (Vd) versus Control (Vd)/ False GO

Metric	p(GMR<0.70)%	p(GMR<0.75)%
KG	11.8	16.3
TR8	3.8	8.2
TR12	7.6	12.1

The metric and the gating criteria are validated
We can use this approach to ungate a Phase 3 with treatment X in comparison to DPd

COMPARISON M-PROTEIN DYNAMICS VERSUS OTHER APPROACHES

Operating Characteristics (OCs) for the various metrics based on APOLLO



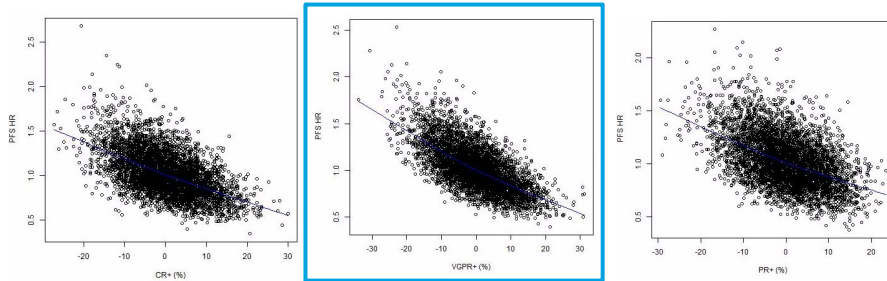
Method	Data	Assessment	Key assets
-VGPR+ (Bayesian approach) -ΔVGPR+	Observed	X	VGPR: Primary analysis - Association between ΔVGPR+ and PFS HR
Multistate model	Model-predicted	X vs control (DPd from APOLLO)	-Leverages longitudinal ORR -Transition PR→VGPR has good OCs
M-protein dynamic model	Model-predicted	X (M-protein evaluable) vs control (DPd from APOLLO)	-Leverages longitudinal continuous M-protein data -M-protein ratios to baseline at weeks 8 & 12 have good OCs

ΔVGPR+ and the 2 model-based approaches demonstrate very good OCs while PFS has relatively poor OCs in early development settings (few subjects, short follow-up)

Courtesy: Mark Yan, Federico Mattiello and MM decision enabling framework
Multistate model and Bayesian analysis

LET'S PRESSURE TEST, WHAT IS THE ASSOCIATION WITH PFS?

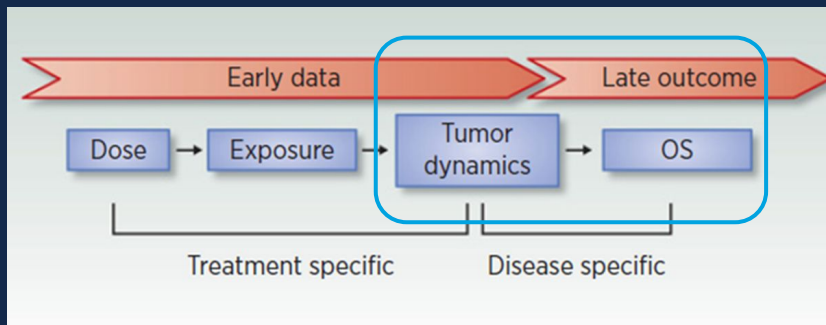
- Meta-analysis based on 21 randomized Ph2/3 trials published after 2014
 - VGPR+ rate has the strongest association (among other response-based endpoints) with median PFS
 - No strong association found between delta in response rate and PFS HR probably due to heterogeneity in patient populations
- Patient-level data from APOLLO (DPd arm, N = 146)
 - Low to moderate correlation between response and PFS; VGPR+ is superior to PR+ and CR+
 - M-protein dynamic metric logKG shows similar association than delta in VGPR+



KG: growth constant,
TR12: Tumor ratio to
baseline at week 12,
TTG: Time To Growth...

Endpoint	APOLLO (DPd)	
	Correlation coef.	R-sq
Delta in VGPR+	-0.68	0.46
logKG	0.66	0.44
KG	0.64	0.41
TR24	0.59	0.34
TR18	0.52	0.27
TTG	-0.49	0.24
TR12	0.40	0.16
TR8	0.31	0.10

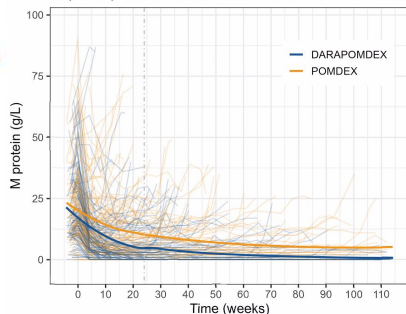
PROBABILITY OF TECHNICAL SUCCESS OF PHASE 3 BASED ON PFS SIMULATIONS



TGI-PFS MODEL DEVELOPMENT ON APPOLO

1. Derive M-protein dynamic metrics

nlmixr²



$$t < 0 \quad M_{\text{prot}}(t) = M_{\text{prot}_0} \cdot e^{KG_0 \cdot t}$$

$$t \geq 0 \quad M_{\text{prot}}(t) = M_{\text{prot}_0} \cdot (e^{KG \cdot t} + e^{-KS \cdot t} - 1)$$

Parameter	Estimate	SE	RSE (%)	Back-transformed	Unit	Shrinkage (%)
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ln(KG_Pd)	-6.37	0.0966	2	0.00171	day ⁻¹	
ln(KS_DPd)	-3.80	0.117	3	0.0224	day ⁻¹	
ln(KS_Pd)	-4.32	0.129	3	0.0133	day ⁻¹	
TS0	2.68	0.0769	3	14.6	g/L	
Random Effects						
KG0	NA			%CV	NA	
KG	82			%CV	60.3	
KS	76			%CV	5.3	
TS0	70			%CV	7.9	
Residual variability						
Res add.	3.27				g/L	

Run: KG0nolIV objective function value: 13326.31

2. Univariate survival analysis

	Score	p.LRT	N	Sign
logKG	230.7	0.0000	239	+
TTG	89.7	0.0000	239	-
KG	77.2	0.0000	239	+
TR6	31.6	0.0000	239	+
pred_BSLD	25.3	0.0000	239	+
TR8	24.5	0.0000	239	+
ALBU	17.1	0.0000	239	-
HGB	15.3	0.0001	239	-
TR12	13.4	0.0003	239	+
iss	11.6	0.0006	239	+
iss1	10.9	0.0010	239	-
Obs_BSLD	10.9	0.0010	239	+
TR18	8.0	0.0047	239	+
cytrisk	7.2	0.0271	175	-
TR24	6.8	0.0090	239	+
iss3	5.9	0.0148	239	+
SECR	5.2	0.0230	239	+
logKS	3.6	0.0590	239	-
rengprn	2.8	0.0948	239	-
LDH	2.4	0.1235	239	+
iss2	2.1	0.1502	239	+
BIL	1.7	0.1882	239	+
ALP	1.4	0.2330	239	+
CRCL	1.3	0.2577	239	-
TPRO	1.2	0.2670	239	+
KS	0.9	0.3479	239	-
ALT	0.7	0.4090	239	+
age	0.5	0.4940	239	-
BECOG0123	0.3	0.5928	239	+
BWT	0.2	0.6596	239	+
AST	0.1	0.7695	239	-
SEX	0.1	0.7386	239	-
racegr1n	0.1	0.7089	239	+

M-protein dynamic metrics

Tested in multivariate survival analysis

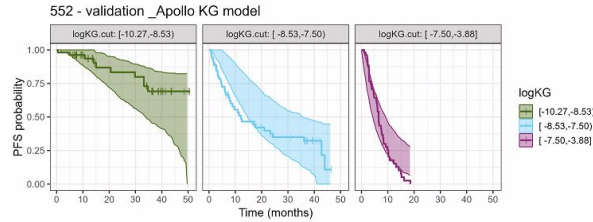
3. Multivariate parametric survival model

Term	Estimate	std.error	Z-value	p-value	Lower CI	Upper CI
(Intercept)	-5.210	0.563	-9.255	<2e-16	-6.313	-4.106
logKG	-0.770	0.051	-15.226	<2e-16	-0.869	-0.671
HGB	0.193	0.041	4.742	0	0.113	0.273
Log(scale)	-0.110	0.055	-2.010	0.0444		

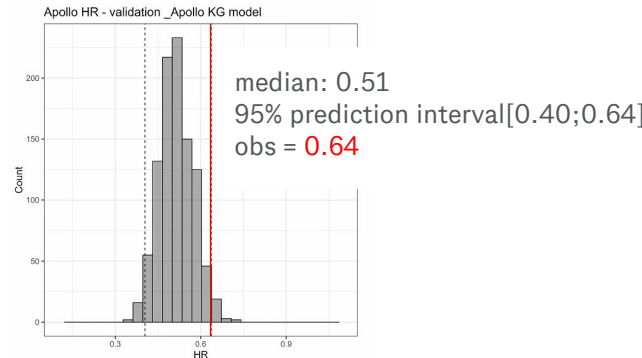
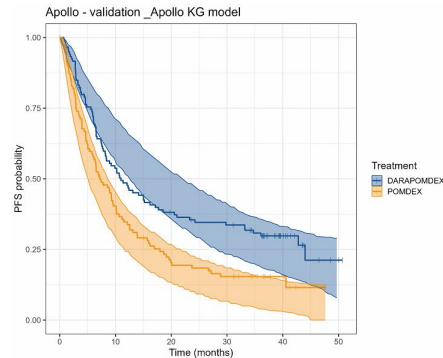
PFS is longer with slower growth rate and higher baseline hemoglobin (HGB)

TGI-PFS MODEL VALIDATION ON APOLLO & CASTOR

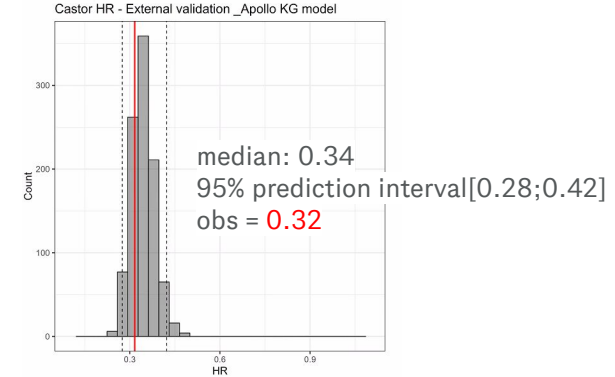
PFS model qualification on APOLLO



The model predicts quite well PFS in the different quartiles of log(KG)



External Validation on CASTOR



PFS model validated, it can be used to simulate Phase 3 trial with treatment X and assess its probability of technical success (PTS)

PROBABILITY OF TECHNICAL SUCCESS OF PHASE 3



Phase 3 study:

X

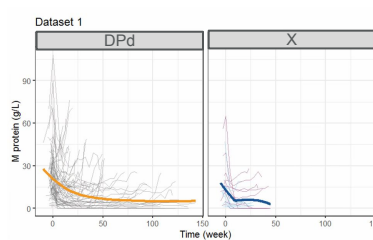
versus

Standard of Care:

daratumumab+polamidomide+
dexamethasone (DPd),
endpoint: PFS

X: 15 (10mo mFU) + 15 pts (6mo mFU)

DPd: complete arm n=120, max FU



Fit M-protein data,
get $\log(KG)$,
add HGB

PFS simulations of Phase 3 design
160 vs. 160 patients

1000 trials

1000 HR, 1000 Logrank tests

- 1 median HR and 95% prediction interval
- 1 probability of Logrank tests with $p < 0.05$
- 1 probability of $HR < \text{target}$

RISK ASSOCIATED WITH DECISION MAKING BASED ON LIMITED DATA

DPd: 15 (10mo mFU) + 15 pts (6mo mFU)

Pd: complete arm n=120, max FU

Distribution of median HR:
median 0.69 [0.25;1.09]
Observed HR: 0.63

Distribution of probability of
success: median 71% [6;100]

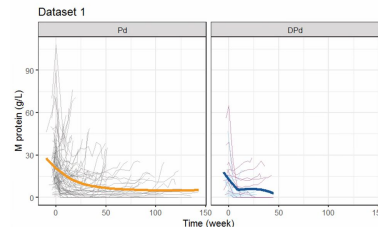
PTS assessment highly
depends on the small
experimental arm data

X500

each with a
different
DPd arm

In early development, we
only have N=1 set of Phase
1b data to make the decision

Fit M-protein data,
get log(KG),
add HGB



PFS simulations of APOLLO design
150 vs. 150 patients

200 trials

200 HR, 200 Logrank tests

- 1 median HR
- 1 probability of Logrank tests with $p < 0.05$

RISK ASSOCIATED WITH DECISION MAKING BASED ON LIMITED DATA

DVd: 15 (10mo mFU) + 15 pts (6mo mFU)

Vd: complete arm n=250, max FU

Distribution of median HR:
median 0.58 [0.20;0.91]
Observed HR: 0.39

Distribution of probability of
success:
median 99.5% [19.0;100.0]

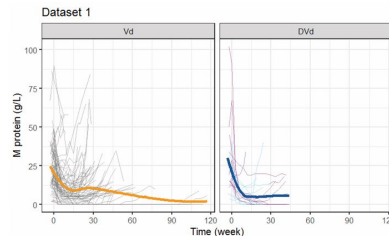
PTS assessment highly
depends on the small
experimental arm data

X500

each with a
different
DPd arm

In early development, we
only have N=1 set of Phase
1b data to make the decision

Fit M-protein data,
get log(KG),
add HGB



PFS simulations of CASTOR design
250 vs. 250 patients

200 trials

200 HR, 200 Logrank tests

- 1 median HR
- 1 probability of Logrank tests with $p < 0.05$

CONCLUSIONS

- Assessing Operating Characteristics is a valuable approach to identify what is the metric, the target and the gating criteria to rationalize early decision making in a quantitative manner
 - Importance of the robustness of the model used to analyze the 1000 subsamples
 - The metric selected should ideally be well associated to the primary endpoint used in the Phase 3 study we want to ungate
- The traditional TGI-PFS (OS) approach can also be used to simulate Phase 3 outcomes and assess its probability of technical success (PTS)
 - As expected, there is a very high weight on the small Phase 1b data on the decision, i.e. the variability of the PTS is huge which leads to risky decision, we should consider larger Phase 1b trials to de-risk Phase 3 Go/No Go decisions

The image features a complex, organic, and textured background in shades of blue and green, resembling a microscopic view of tissue or a marbled paper pattern. A large, solid dark blue rectangle is centered on the page, serving as a backdrop for the text.

THANK YOU

The background of the image is a complex, organic pattern resembling a microscopic view of tissue or a marbled paper texture. It features various shades of blue and green, with intricate, swirling, and cellular-like structures. Overlaid on this background is a large, solid dark blue rectangle that serves as a backdrop for the company logo.

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