

A UK Perspective on the CUPISCO Trial The Agony and the Efficacy

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Disclosures

Remuneration reasons: attendance at advisory boards; chairing educational meetings; giving invited lectures; travel, accommodation and registration at national/international meetings, consultancy

Companies:

Amgen, BMS, BTG, Guardant Health, Merck Group, MSD, Roche, Sirtex, Servier

Funding for UCLH trials and research:

Amgen, BMS, Guardant Health, Merck Group, MSD, Roche

Focus on 3 main strategies for CUP patients

STRATEGY

HYPOTHESIS

1) Find the molecular primary

CONVERSION



Primary-specific therapies will be more effective

IHC
MIRNA
METHYLATION

2) Find the therapeutic target

ACTIONABLE

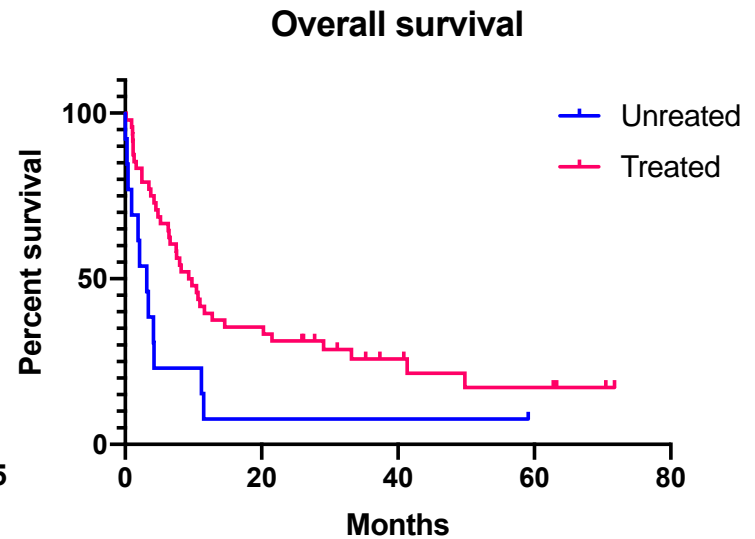
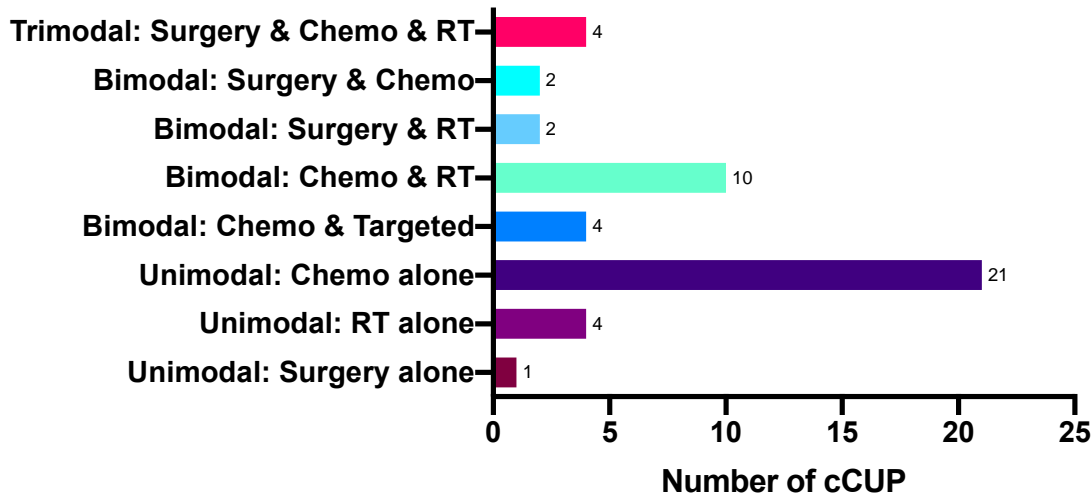


Targeted therapy is feasible, safe and efficacious

IHC
MRNA
ACTIONABLE MUTATIONS/ALTERATIONS
(WHOLE GENOME MUTATION)
(EXOME SEQUENCE)

3) Access a clinical trial

UCLH CUP MDT 2013-2017: cCUP patients who embark on therapy (n= 48/61)



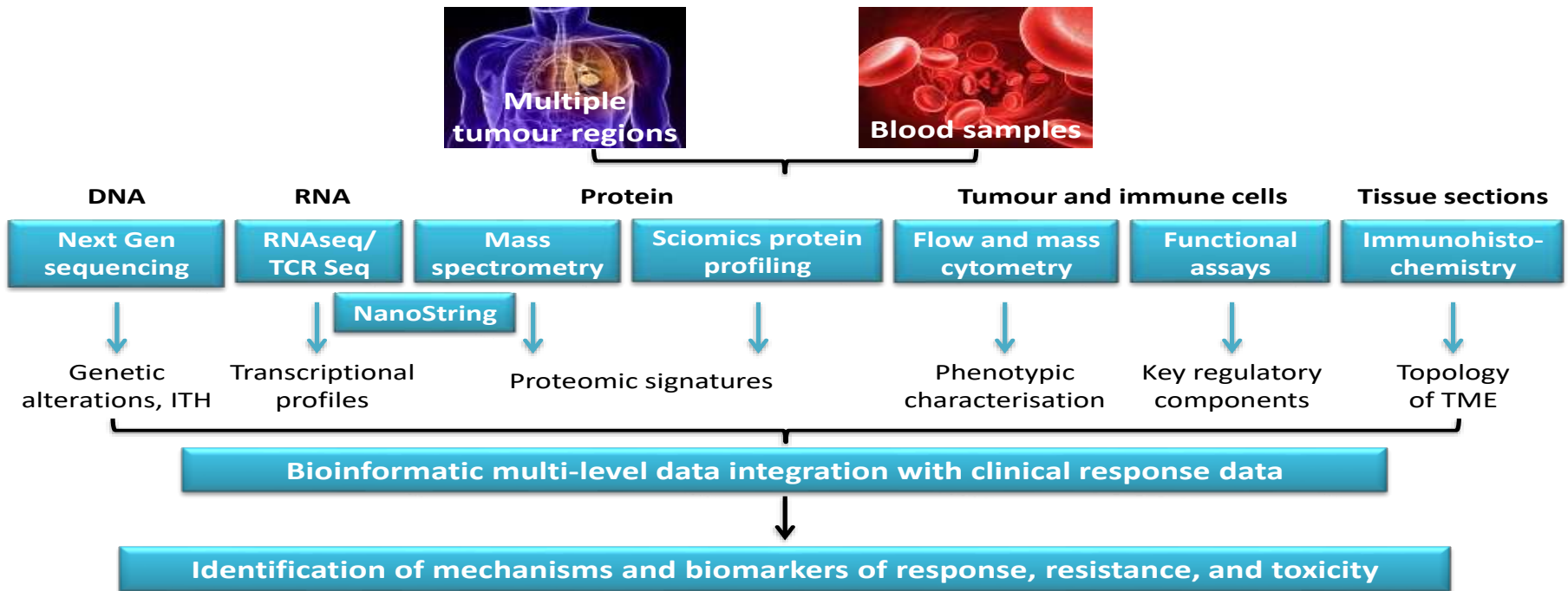
Mean Performance Status 1.5 (0-4)

Median OS 9.5 months, 1 year survival 40%

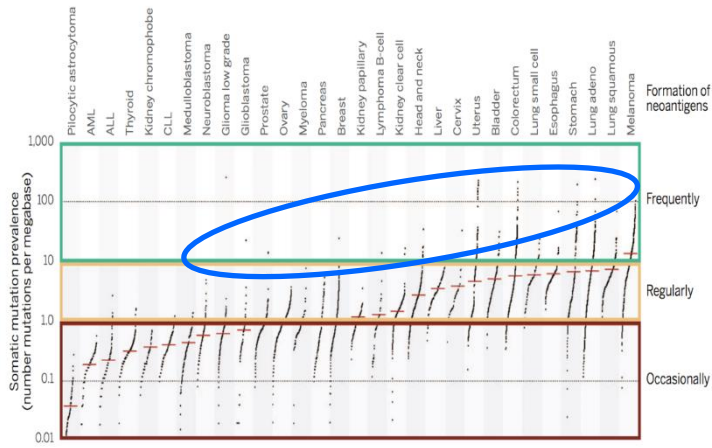
On a trial? 1 in first 4 years, now 4 in last 6 months

(Hessey, Mcvinnie, Shiu – Poster)

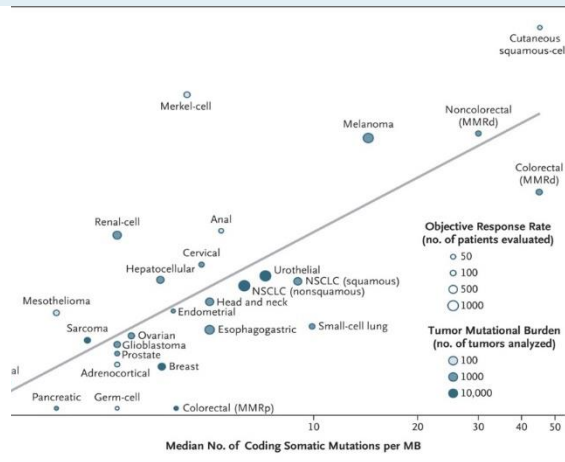
The CITA IMDC* Platform



Is TMB a good immunotherapy biomarker?



Schumacher Science 2015



Yarchoan M et al, N Engl J Med 2017

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Tumor mutation burden as an immunotherapy biomarker

High TMB

- Somatic Mutations
 - Mutations (ubiquitous radiation, smoking, other carcinogens)
 - Hereditary or acquired mismatch repair deficiency (dMMR)
 - Age related DNA replication errors
- Abnormal proteins derived from somatic mutations
- Non-inflamed: decreased neoantigen presentation, poor chemokine expression, dense stroma, MDCs, Tregs
- Inflamed: neoantigens presented on MHC and recognized by CD8 T cells
- Combination immune checkpoint blockade
- PD-(L1) immune checkpoint blockade
- CD8 T cells, PD-L1(+), PD-L1(-)

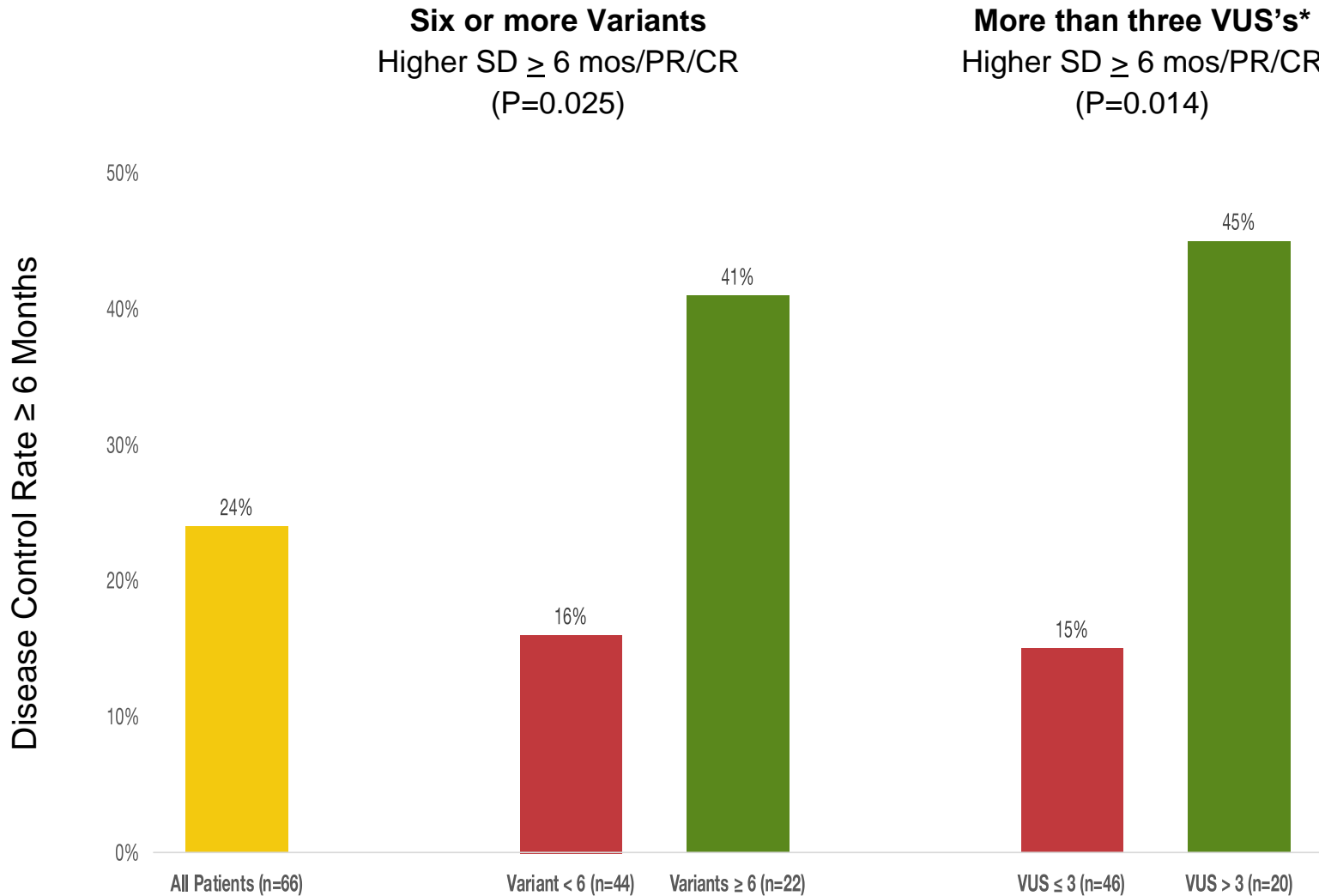
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ESMO

...it can't be as simple as that...
And blood TMB is coming.....

Mutation Burden (Guardant360) Predicts IO Outcomes



* VUS = Variant of Unknown Significance

Circulating Tumour DNA (ctDNA) Experience in Patients with Cancer of Unknown Primary (CUP)

Kai Keen Shiu^{1,2}, Helen Winter¹, Mariana Kushnir¹, Gabriel Mak¹, Carmen Murias¹, Charles Swanton², Richard Lanman³, Iris Faul³, Hendrik-Tobias Arkenau^{1,2}

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The median turnaround time (TAT) from sample collection to report was 10 days (range 6-15).

Seventeen patients had potentially actionable mutations (17/25 = 68%)

4 patients had no mutations detected which might be explained by: 1 patient had post resection; 2 patients were responding to chemotherapy; 1 patient was sampled prior to commencing chemotherapy.

Significant actionable targets included: 2 BRAF^{V600E}; 5 KRAS mutations; FGFR; MYC amplifications; KIT; PIK3CA; *ERRB2*.

Three or more somatic mutations (including variants of uncertain significance (VUS)) were found in 12 patients; six or more mutations were found in 6 patients.

Future Value of IO therapy?

63 year old man: poorly differentiated carcinoma, CK7 focally +ve, all other markers -ve

Good response to 6 cycles of Cisplatin-Capecitabine

Now progression

Taxane?

Irinotecan?

Immunotherapy?

Guardant360 Tumor Response Map

The Guardant360 Tumor Response Map illustrates the mutant allele percentage (% cDNA) of observed somatic variants at each sample submission time point. The "Somatic Alteration Burden" value below refers to the maximum % cDNA detected at each time point. Amplifications are not plotted, and only the first and last four test dates are plotted. Please see the Physician Portal (<https://portal.guardianhealth.com>) for the Tumor Response Map with all test dates.



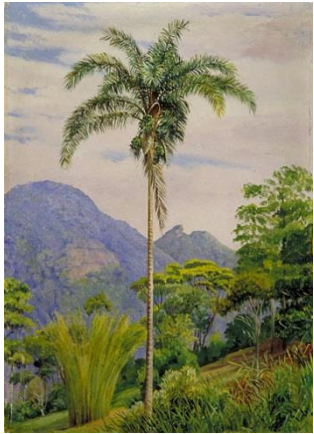
Summary of Somatic Alterations & Associated Treatment Options

The percentage of altered cell-free DNA (% cDNA) circulating in blood is related to the unique tumor biology of each patient. Factors that may affect the % cDNA of detected somatic alterations include tumor growth, turn-over, size, heterogeneity, vascularization, disease progression, and treatment.

Alteration	% cDNA or Amplification	FDA Approved in Indication	Available for Use in Other Clinical Trials
Relevant for Therapy Selection			
<i>TP53</i> <i>W23*</i>	54.0	None	Trials Available
<i>MYC</i> <i>AMP</i>	+++	None	Trials Available
<i>PDGFRA</i> <i>AMP</i>	+	None	Dasatinib, Imatinib, Lenvatinib, Nilotinib, Nintedanib, More drugs available Trials Available
<i>KIT</i> <i>AMP</i>	+	None	Axitinib, Cabozantinib, Dasatinib, Imatinib, Lenvatinib, More drugs available Trials Available
Additional Alterations Detected			
<i>FGFR1</i> <i>Q594L</i>	0.4	The functional consequences and clinical significance of this gene variant are not established. Similar to other alterations in circulating cDNA, the amount (% cDNA) of this variant may reflect disease progression or response to treatment; clinical correlation is advised.	
<i>NF1</i> <i>R262C</i>	0.2	The functional consequences and clinical significance of this gene variant are not established. Similar to other alterations in circulating cDNA, the amount (% cDNA) of this variant may reflect disease progression or response to treatment; clinical correlation is advised.	
<i>MYC</i> <i>R439G</i>	0.1	The functional consequences and clinical significance of this gene variant are not established. Similar to other alterations in circulating cDNA, the amount (% cDNA) of this variant may reflect disease progression or response to treatment; clinical correlation is advised.	

Trunk and branch clonal diversity (& clinical outcome)

Palm



Chestnut



Baobab Tree



Dying Muhly Bush



Successful Predictive Biomarkers and Drug Targets
HER2/EGFR/KRAS/ALK/BRAF

Swanton NEJM 2012
Roylance et al 2011
Birkbak et al 2011

Aim – gently push or big kick?

The PEACE (Posthumous Evaluation of Advanced Cancer Environment) consortium

A national post-mortem programme and consortium



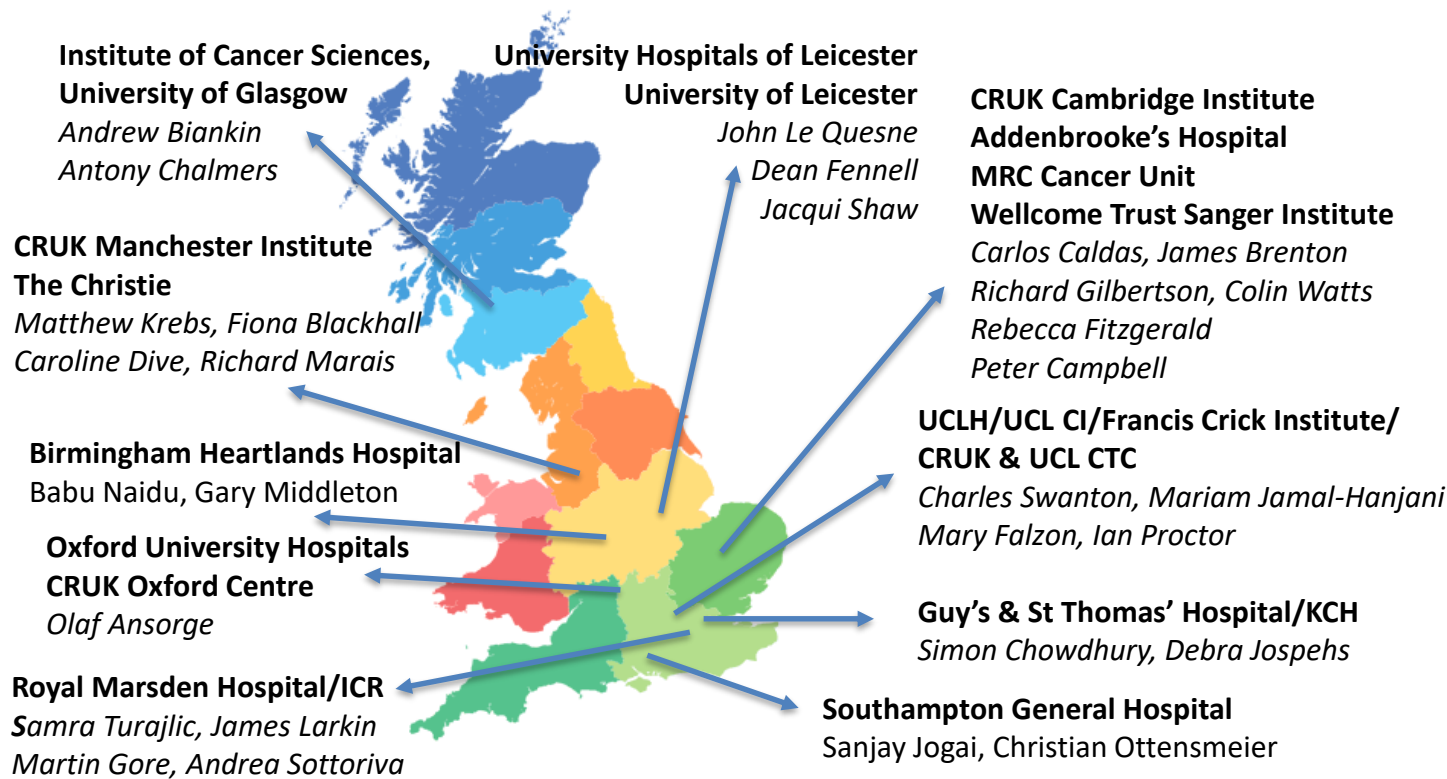
PEACE

National prospective observational study intended to facilitate tissue donation, in metastatic cancer, from multiple tumour sites in the post-mortem setting

Funded by a Cancer Research UK Centre Network Accelerator Award

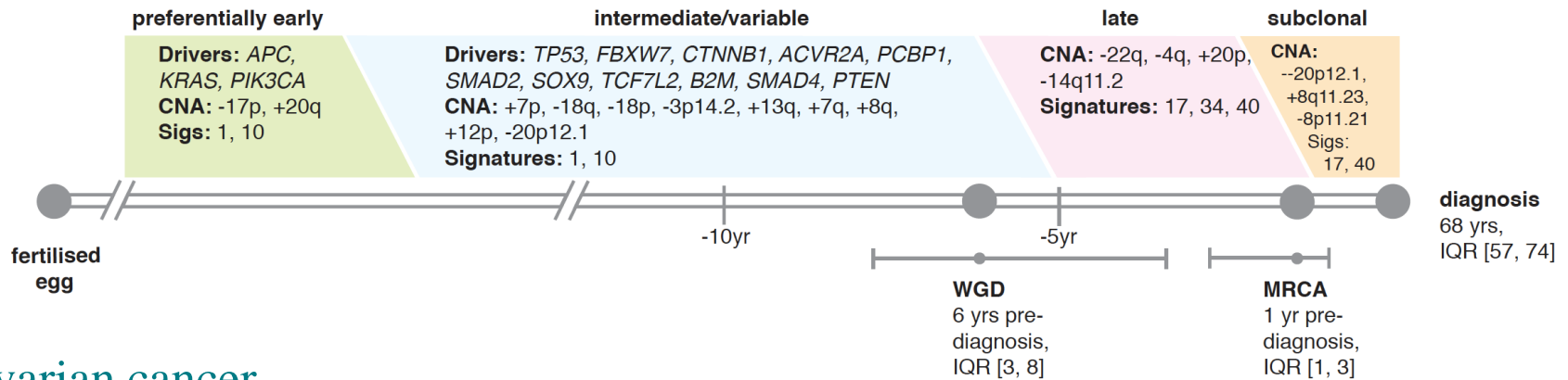
Aim: establish a national PM protocol and a resource of tissue & blood in highly clinically annotated patient cohorts (500 PMs over 5 years) leveraging investment in CRUK-funded clinical studies

Mariam Jamal-Hanjani

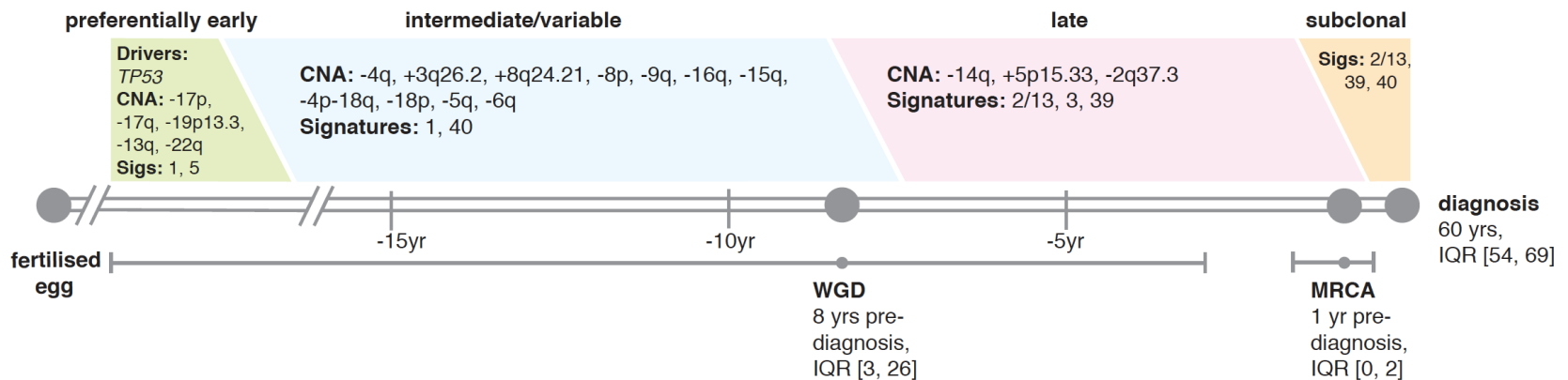


Timelines of cancer development

Colorectal cancer



Ovarian cancer



Perspectives for CUP

- **Molecular archaeology of cancer:** massively parallel sequencing and bioinformatics algorithms can **disentangle the subclonal architecture and life history of tumours**
- **Post-mortem sampling** allows **tracking evolution** of clones and subclones over time and space
- Could answer key questions in CUP:
 - Evolutionary history of CUP: track the **pattern of spread** and the **site of origin**
 - Are **common aetiologies/drivers/pathways** underlying early metastatic dissemination?
 - Can we **identify early events** and develop **early diagnosis approaches**?

Biobank all pCUP/cCUP

STRATEGY

- 1) Find the primary using molecular profiling** **CONVERSION** →
MUO/pCUP
TIMELY
APPROPRIATE
MANAGEMENT
QOL/PROM/PREMS
- 2) Find the therapeutic target** **ACTIONABLE** →
SMDTs
Genomic Boards
Trials for Good
Prognosis cCUP
Poor PS subgroups
QOL/PROM/PREMS
- 3) Access a clinical trial** →

STUDY/TRIAL/ARENA

Primary-specific therapies will be more effective

Targeted therapy is feasible, safe and efficacious

The optimal way to test a treatment strategy

Thank you

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