

# Targeting the PI3K/AKT/mTOR Pathway in Renal Cell Carcinoma

# Signalling Pathways in Cancer 2014



James Larkin PhD FRCP Royal Marsden Hospital

### **Disclosures**

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### Overview

- Progress in advanced RCC 2007-2014
- Randomised trials of mTORi in RCC
- How can the role of mTORi in RCC be expanded?
- Predictive biomarkers for mTORi
- Intratumour heterogeneity: implications for predictive biomarkers

# Progress in Advanced Kidney Cancer 2007-2014

Neoadjuvant / Pre-operative



**Adjuvant** 



1st Line Relapse

**SUNITINIB** 

**PAZOPANIB** 

IFN-α + BEVACIZUMAB

**TEMSIROLIMUS** 

Median PFS 9 months

2<sup>nd</sup> Line Relapse

EVEROLIMUS (post-VEGFR-TKI)

AXITINIB (post-VEGFR-TKI/ immunoRx)

SORAFENIB (post-immunoRx)

SUNITINIB (post-immunoRx)

PAZOPANIB (post-immunoRx)

Median PFS 4-5 months

3<sup>rd</sup> Line Relapse

SORAFENIB (post-VEFGR-TKI + mTORi)

EVEROLIMUS (post-VEGFR-TKI x2)

Median PFS 4-5 months

- TEM vs IFN vs TEM + IFN in poor risk 1<sup>st</sup> line
- EVE vs sunitinib 1st line
- EVE + BEV vs IFN + BEV 1<sup>st</sup> line
- TEM + BEV vs IFN + BEV 1st line
- EVE vs placebo post sunitinib/sorafenib
- TEM vs sorafenib post sunitinib

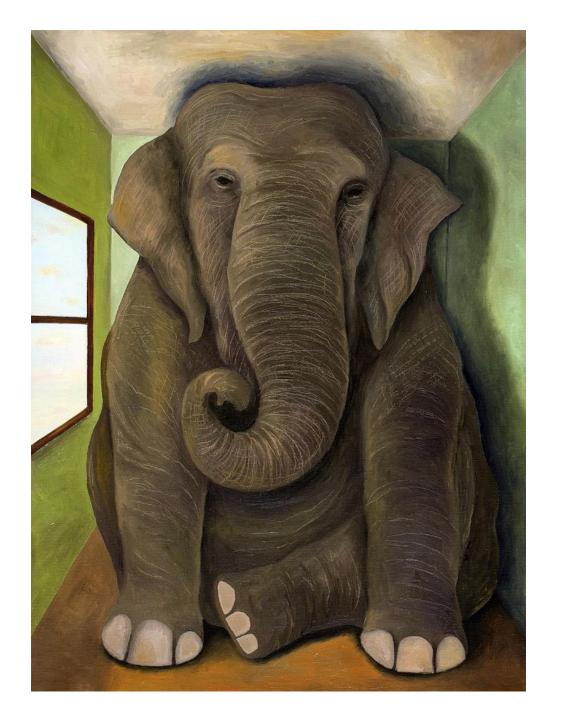
- TEM vs IFN vs TEM + IFN in poor risk 1<sup>st</sup> line
- EVE vs sunitinib 1st line ATIVE
- EVE + BEV vs IFN + BEV 1st lines ATIVE
- TEM + BEV vs IFN + BEV 1st linegative
- EVE vs placebo post sunitinib/sorafenib
- TEM vs sorafenib post sunitinib

- TEM vs IFN vs TEM + IFN in poor risk 1<sup>st</sup> line
- EVE vs sunitinib 1st line ATIVE
- EVE + BEV vs IFN + BEV 1st lines ATIVE
- TEM + BEV vs IFN + BEV 1st linegative
- EVE vs placebo post sunitinib/sorafenib
- TEM vs sorafenib post sunitinib on TEM os WORSE on TEM

- TEM vs IFN vs TEM + IFN in poor risk 1<sup>st</sup> line
- Choice of comparator arm controversial
- No other trials in poor risk group
- No yardstick for anti-VEGF activity
- EVE vs placebo post sunitinib/sorafenib
- Placebo control arm reasonable when trial recruited

# mTORi have a diminishing role in RCC

- How can this be reversed?
- Increase dose? Neither EVE or TEM are given at MDT in RCC so possible, but not likely
- Use other inhibitors of pathway e.g. PI3K or dual TORC inhibitors: also possible and RP2 studies of GDC0980 and AZD2014 open
- Combinations? In RCC to date these result in increased toxicity and reduced dose



# mTORi have a diminishing role in RCC

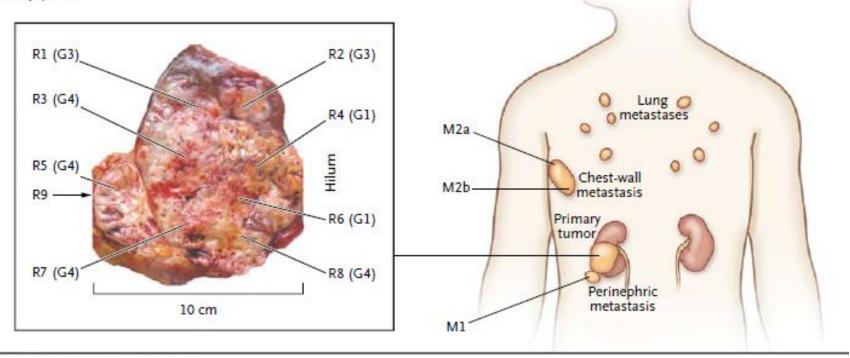
- How can this be reversed?
- Define predictive biomarkers
- Non-clear cell histology is a clinical candidate
- This is not homogeneous: papillary, chromophobe, medullary, collecting duct etc
- Sunitinib is active in papillary / chromophobe
- Our group became interested in trying to develop predictive markers in clear cell RCC for anti-VEGF and mTORi a few years ago...

# The Intratumour Heterogeneity Question

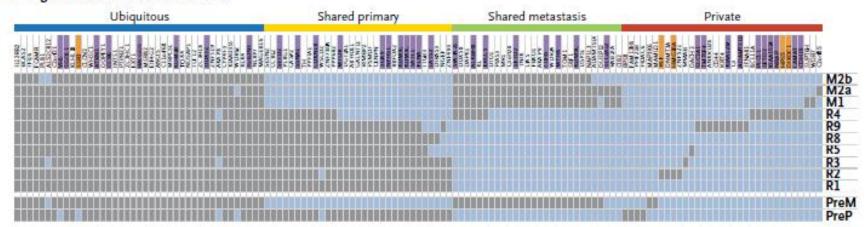
- A fundamental question for personalised medicine:
- Does the putative driver identified from tissue x at time y really drive the metastatic disease in the patient in front of you in the clinic?
- Are image-guided biopsies of large tumours representative of the entire primary, never mind metastatic disease?
- We set out to investigate this

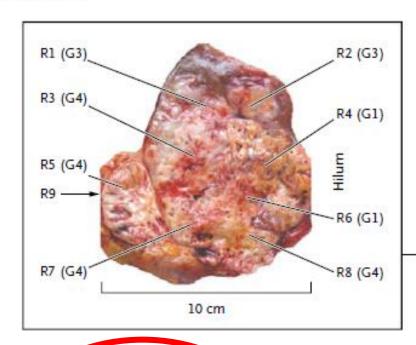
# Radiographic Intratumour Heterogeneity

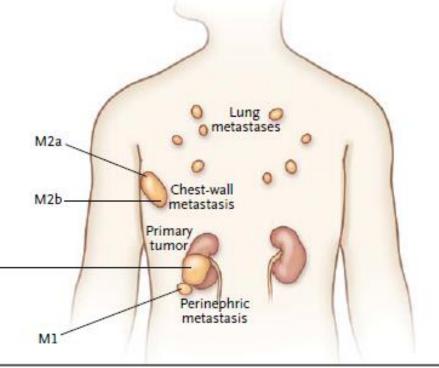


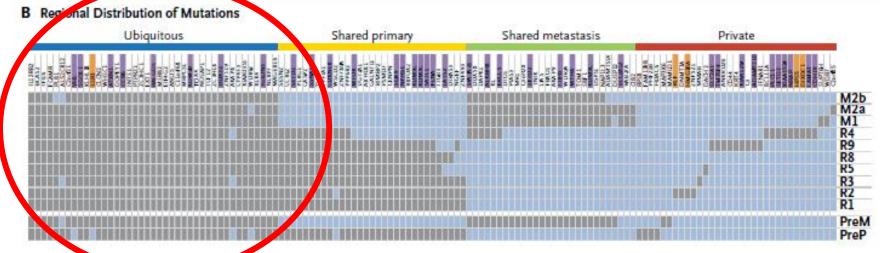


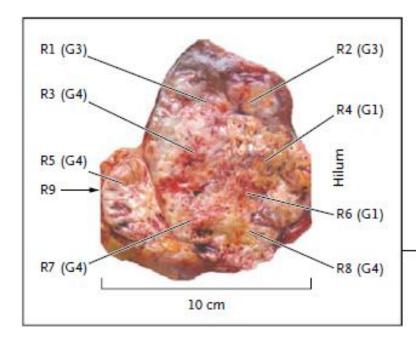
#### **B** Regional Distribution of Mutations

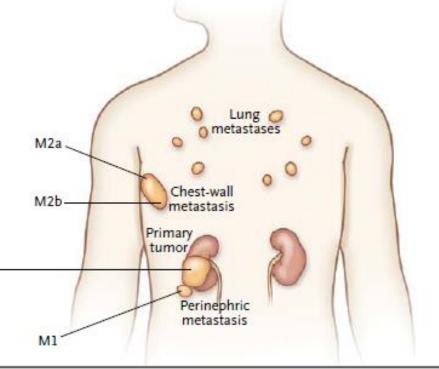


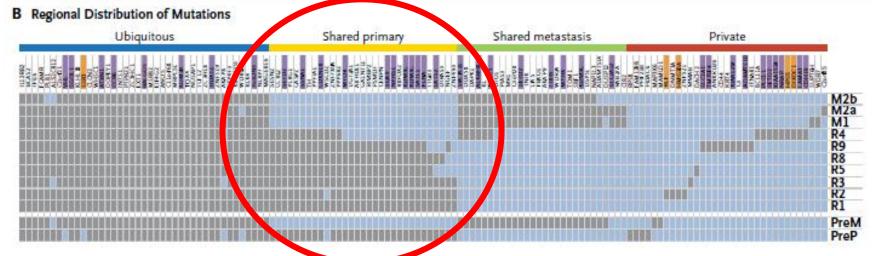


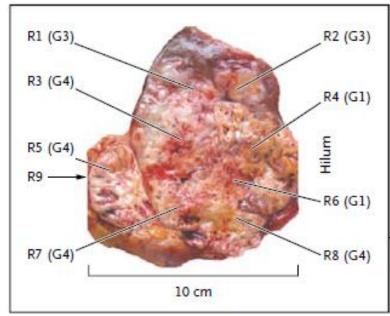


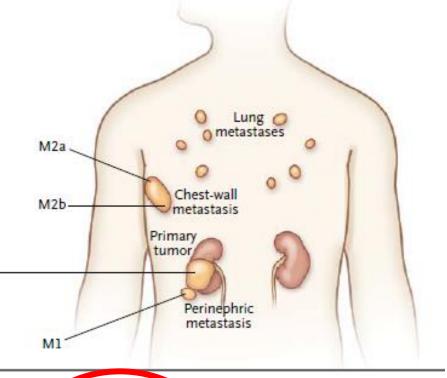


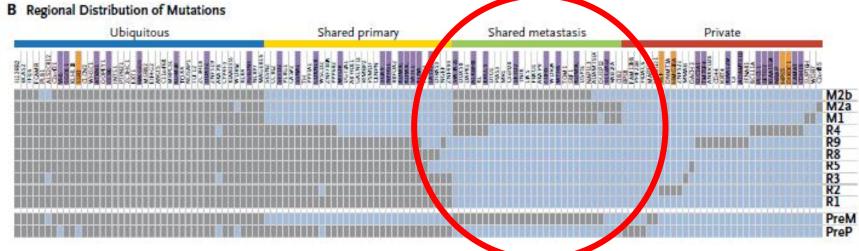


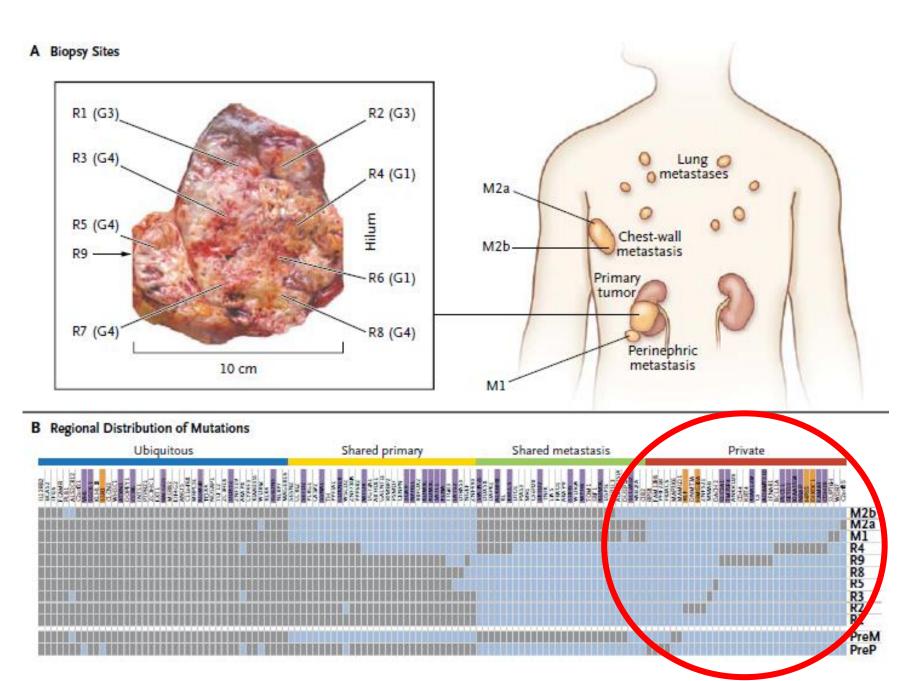






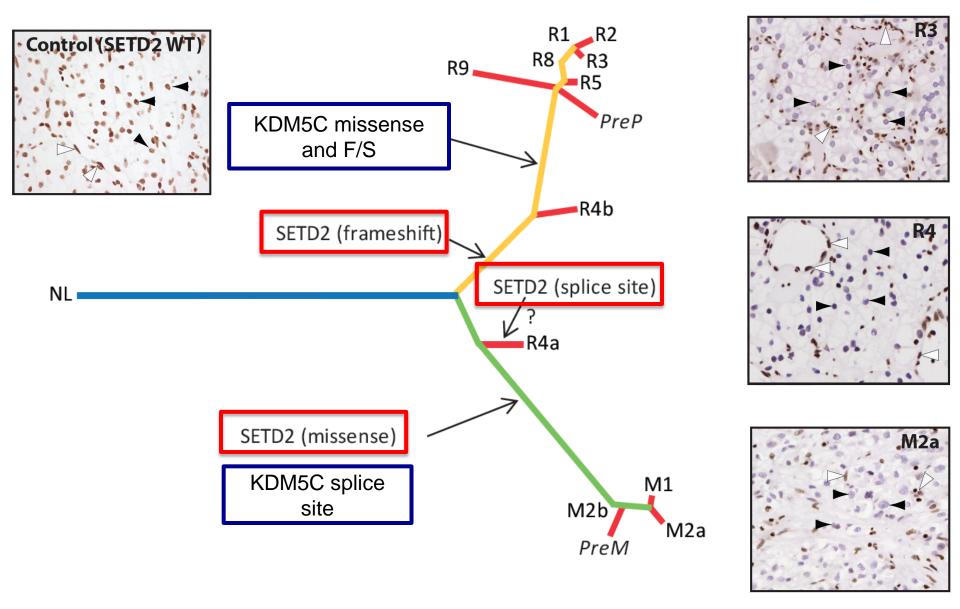




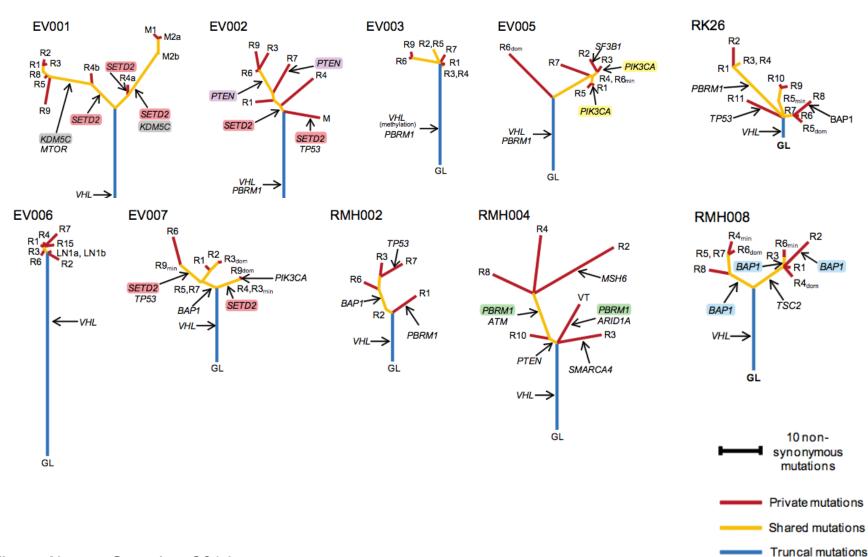


65% mutations are heterogeneous and not present in every biopsy

# Evidence for Parallel Evolution SETD2 Loss of Function: H3K36 tri-methylation



# Branched Evolution in ccRCC



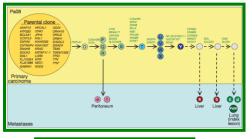
## Branched Evolution in ccRCC

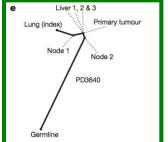
Table 1 Comparison of driver mutation prevalence in ccRCC samples

	Prevalence in TCGA samples	Prevalence in all M-seq samples	Prevalence in cases based on M-seq	Prevalence cases/prevalence M-seq
	(n = 218 samples)	(n = 79 samples)	(n = 10 cases)	samples
PBRM1	42%	39%	60%	1.5
SETD2	18%	27%	30%	1.1
BAP1	21%	24%	40%	1.7
KDM5C	7%	11%	10%	0.9
TP53	5%	5%	40%	8.0
ATM	3%	4%	10%	2.5
ARID1A	6%	1%	10%	10.0
PTEN	5%	10%	20%	2.0
MTOR	9%	8%	10%	1.3
PIK3CA	3%	4%	20%	5.0
TSC2	2%	4%	10%	2.5
PI3K-mTOR pathway	18%	28%	60%	2.2

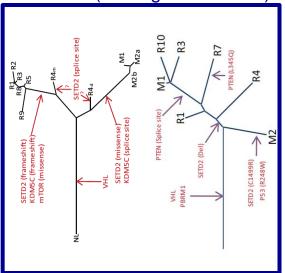
## Branched Evolution in Cancer

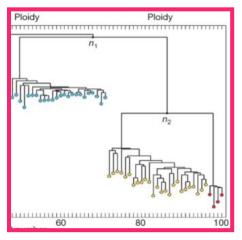
Pancreas (Yachida/Campbell 2010) Breast (Navin 2011. Shah 2009) ALL (Enver and Greaves 2011)

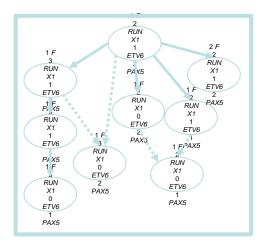




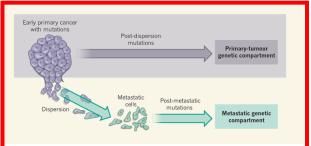
Renal (Gerlinger et al 2012)

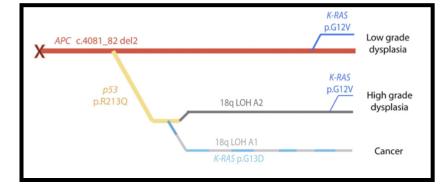






Medulloblastoma (Wu et al 2012)





Colon Adenoma-Carcinoma (Thirlwell et al 2010)

# Clonal Architecture as a Biomarker?

**Palm** 

Chestnut

**Baobab Tree** 





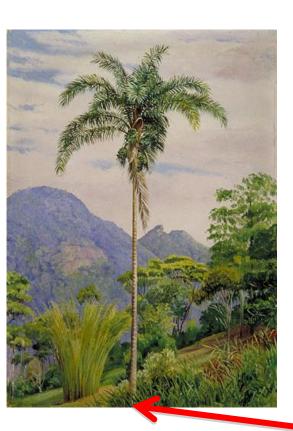


# Clonal Architecture as a Biomarker?

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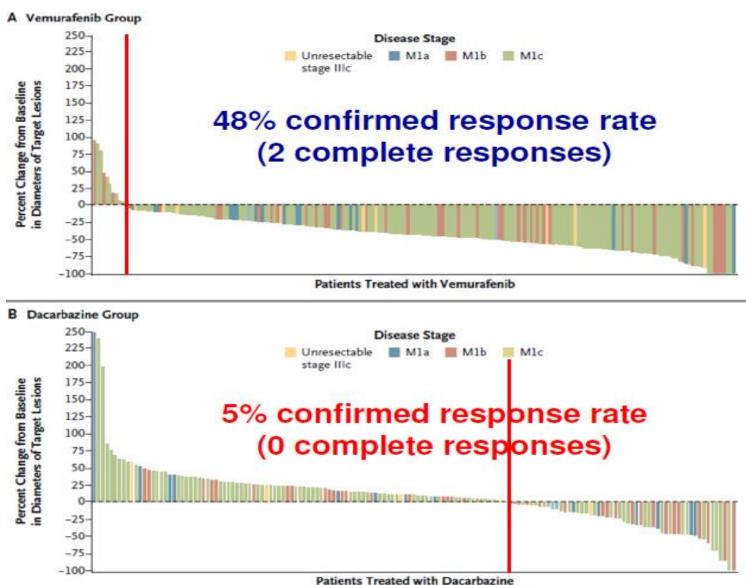




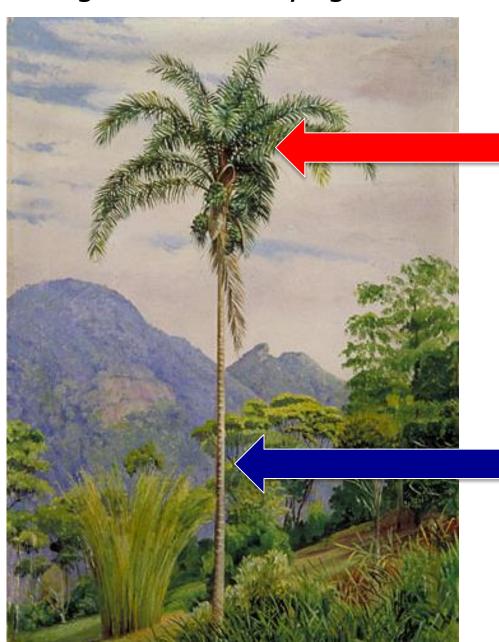


Successful Biomarkers eg EGFR/KRAS/HER2/BRAF Trunk not branches?

# BRAF in Melanoma: 'Truncal Driver'



### Target Tumour Phylogenetic Trunks and Resolve Branches



Branched Genetic Events Present in Some Cancer Cells not others Dynamic during disease course

Monitor subclonal events to define drug resistance mechanisms

Trunk Genetic Events Present in Every Cancer Cell

**DEFINE TRUNK DRIVERS** 

### **Conclusions**

- mTORi active in RCC but less (on average in unselected patients) than anti-VEGF therapy
- No predictive biomarkers for drugs in RCC
- mTOR pathway aberrations not infrequent
- Are they 'truncal drivers' though?
- Further study, particularly of metastatic sites
  / non-invasive technologies needed
- Understanding this could transform the use of mTORi in RCC

# Acknowledgements



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- Our patients and their families



# Thank you