

#### Precision-Panc: The Next Generation Therapeutic Development Platform for Pancreatic Cancer

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## Pancreatic Cancer

- 3<sup>rd</sup> cause of cancer death (2<sup>nd</sup> within a decade)
- 5% alive at 5 years
- Average survival ~6 months
- 90% die within a year
- Surgery only cure (~20%)
- Mortality not significantly changed for 50 years
- Chemotherapy modestly effective but some significant responses in undefined subgroups
- Majority metastatic chemotherapy and targeted therapy. However therapeutic development has been challenging





### "Precision Medicine"

- Matching the Right Treatment to the Right Patient
- Cancer subtype responds to treatment 'X'





#### **Challenges of Therapeutic Developments in PDAC**

- Not enough patients
  - relatively rare cancer, but high mortality
  - Rapid deterioration of PS
  - Need collaboration/consortium approach

#### • No drugs made specifically for PDAC

- (Apart from PEGPH20)
- Need to "repurpose" or "rescue"
- Need to make PDAC "attractive" investment for pharma
- No strong well validated biomarkers
  - Needs better understanding of molecular pathology
  - Needs stronger pre-clinical evidence (clear line of sight)
  - Needs novel clinical trial design to seek signals
- No molecular assay made specifically for PDAC
  - (Apart from HA)
  - Need custom build





## **PRECISION-Panc**

Improving outcomes through a dynamic research & development platform for Precision Medicine



## **Precision-Panc UK (Global)**

Dynamic therapeutic development platform taking advantage of a continuous loop of discovery, learning, refinement, and implementation











### **Precision-Panc Master Protocol**



Clinical CI: Juan Valle Translational CI: David Chang

### The Master Protocol: what does it do





Lots of opportunities for complimentary, non-competing trials Therapeutic and biomarker development A platform for all to use Pharma & industry buy ins

Adjuvant

Biomarker validation/development....

## **Molecular Profiling**

#### Harmonised molecular profiling platform **designed specifically** for pancreatic cancer

#### **Clinical Sequencing (real time)**

- 1) GPOL Clinical Cancer Genome
- 2) Integration with histopathology

#### **Research Sequencing (batched)**

- 1) WGS (when possible)
- 2) Transcriptome Sequencing
- 3) Liquid biopsy (Manchester)





### Assay design: platform selection

# Targeted capture sequencing is the platform of choice for a **clinically-focussed assay**

Genomic assay requirement	TCS	WGS	WES
Detect clinically significant events	Yes	Yes	No
Real-world compatible (FFPE, low input DNA/tumour cellularity)	Yes	No	±
Cost efficient (data production, analysis and archiving)	Yes	No	±
Clinically meaningful turnaround time (sample to report)	Yes	No	No



### **Clinical Cancer Genome**

- Bespoke design for PDAC
- Agilent baits
- Illumina sequencing
- ~ 300 500X coverage



#### 2. TCS delivers high quality data on all classes of clinically-relevant alteration



3. Assay content informed by expert data analysis & curation



Susie Cooke, Philip Beer





Patient ID: Tamour type: Pancreatic adenocarcinoma Sample source: Sequencing date: 04 FEB 2018 Sample type: Pancreatic resection (macrodissected) Test requester:

#### Tumour cellularity was estimated at 40% by pathology and 36% by sequencing.

This sample harbours pathogenic mutations in ARAS and TPS3, has less of CORNZA/28 and SMAD4, amplifications of COMD1 and ART2 and a samen of structural variants consistent with homologous recombination deficiency (HRD). This spectrum of mutations is consistent with Pancreatic Ducial Adenocarcineme (NOS), HRD h associated with response to platinum-based chemotheregy or PAP Inhibition.

Somatic driver alteration	Potential therapies, scials or biomarkers			
BRAS G12Y, WAF 18%, 4634 coverage	Potential clinical trial (MIX inhibitor, URK inhibitor)			
1953 Franciskih, VAF 1996, S60x coverage	No current therapeutic options			
SMAD4 Homesygous deletion	No current therapeutic options			
CDKN2A/28 Horsegon deinter	Potential clinical trial (CDK4/4 inhibitor)			
COND1 Amplification Tecopies	Potential clinical trial (CDK4/6 inhibitor)			
AKT2 Amplification 9+ copies	Potential clinical trial (AKT inhibitor/MTOR inhibitor)			

Renalogous Recombination Delicionary Present	Not detected	<12 mutations per Mb
HA Typing	Tumour-Nermal pair penotype match	Somple Contamination
Indeedgewest	score	None

Possenger mutations and Variants of Unknown Significance: NIL

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Metric	Score	Merric	Score/	Metric	Sare	Metra	Scare	
DI	200		-2.31%	6	101	Geore	718	
.LC	740	DP	1.19%	0	64.2	5MP	505	
01	*	54.	8.28%	87	0.70%	Cite-	387	
97/0	19.3/43%	-55	100%	149	167	NOM	1/1	

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Patient ID: Tamour type: Pancreatic adenocarcinoma Sample source: Sequencing date: 04 FEB 2018 Sample type: Pancreatic resection (macrodissected) Test resulter:

Sequencing was certed per ecceeding to the Good Clercal Laboratory Pacific (SCUP) standard at the Gleggy Pacific Decision Decision, Unkerstary GPCO, Norther & Decision Decision, Unkerstary of Stagew. The Laboratory Decision Decision, The methodology send was targeted capture reasoning. Casterna was performed using MM-Abati Stagiliert lengthering a benche sui of selected generatic factores. The base of the caster have been seen to caster a second caster and the select set of selected generatic factores. The base of the caster is a selected to the caster and a second caster and the selected to the sel

The table at the further of page 1 of the report, marked for interval use any, contains key warries that are used to assess the quarks of the approximg funding report sign off.

Analysis has been performed to excitations the population of marignant to non-marignant radius in the sample literator calculatory. The variant while thereins for each reduction investees should be interpreted in the context of the transcurpolicitienty, in order to according whether the matching is donal or acclosure (or, present in all or a cabox of the marignant calculator).

The give panel includes 14 priors which are known to furblad infraction (prior produces cancer inspection which. When approxime means has been place to the panels, potentially subagain priorbie relations in these priors will do be returned. It is important to note that this enders will not equal pathogens infracting surrants in genes where then those inducted in tarbalance control approximate variants in the table holes.

If you have any quantizes or require any further assignments with the interpretation of any of the results contained within this report, please contained for Seconda Contained Contained

#### Genes included in sequencing assay and types of alterations reported.

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ACVEDA.	HTM .	04162	160.57	EDHI	MAPSEI	NOTOHI	PPRINTA.	ENP-DR	1097
ALCORA	BUM .	ULLA.	FGFR1	1042	MARKI	1001015	PPTOR3	10801	1012
ARTS	1001	CTARIES.	POPER	6005	Anables .	NOV	ReixJ	ROBERT	TOFIERS.
AKT2	BRCAS	BARK	FGP#5	6962	NONE	MARS	PTOP1	PPAL	107082
ANTO	BRCK3	DAMITIA	ALC: NO.	alesa.	Millel	INFORT.	PTEN.	RINKS	1953
ALR.	Clientin	1044	PLTS	10.01	MIT	INTERE.	#162	NETTER	THES.
WORLDN-	COMP1	TREAD	FOR J	1943	MINT	WINES.	PIPPLE	942802	7562
ALCOSING	CEMPS	1000.0	64148	a povea.	MISHER	PAUM	88823	NUTZ	LED MY
400	00000	(8304	GADIG	#DH	Alcast	PERMIT	AADGE:	Constants.	AUGER.
ARAF	00463	62540	CHAIL	RIT	NTON	POCOLULE	RATE:	DAMAGES.	ANR.
ANDEA	-00224	FAMILITE	08463	KARDA	MUTH	PERMA	884	SMANCA4	
AR1018	00H1	<b>EANSCA</b>	GNAS	RMR2C	NYC	PECIDA	Wantin	SHO	
ARIES	10066	RENCE	HIPLA	<b>KMTJD</b>	MARK	PROD	881	50.69	
6754	CDH4	F#MCD0	14.6-1	ERAS.	Anth	PBG81	BIVE.	\$1463	
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### **Tissue: Why EUS-guided biopsy?**

- There is always a primary to biopsy (any clinical stage)
- May select patients with low volume metastatic disease (better PS)
- Same setting as ERCP
- Can biopsy some of the liver and nodal lesions at the same time
- Additional research samples can be obtained at the same time
- If we can sequence this, should have no issues with perc biopsy
- Enables precision medicine approach



Stephan Colin Dreyer McKay Fraser Duthie



#### **Study progress: low failure rate**



(failure)



CISION

### **Precision-Panc Clinical Trials**

- **PRIMUS-001:** 1<sup>st</sup> line metastatic (FOLFOX-A Vs AG)
  - Adaptive randomised Phase II/III, up to 460 patients, ongoing
  - DDR biomarker
- **PRIMUS-002:** neoadjuvant (FOLFOX-A & AG)
  - Phase II, up to 250 patients, starts March 2019
  - DDR biomarker
- **PRIMUS-003:** 2<sup>nd</sup> line metastatic (CXCR2 + PDL-1)
  - Phase Ib, 20 patients, complete
  - Immune & Tumor microenvironment
- **PRIMUS-004:** 2<sup>nd</sup> line metastatic umbrella
  - Currently 1 appendix (2 cohorts), 90 patients, start Q2 2019
  - PARPi + ATRi combination over come acquired platinum resistance
- More under plan (neoadjuvant & adj/maintenance umbrella)
  - Preclinical Therapeutic Testing Board
  - NCRI CSG Subgroup / Master Protocol Strategy Board









#### Synthetic Lethality as Therapeutic Strategy in Cancer







McLornan et al NEJM 2014

**PRIMUS-001:** A randomised adaptive Phase II/III study of **FOLFOX-A** versus **AG** in metastatic PC, with integrated **DDR biomarker** evaluation.





#### PRIMUS-002

An umbrella phase II study examining two neo-adjuvant regimens (FOLFOX-A and AG) in resectable and borderline resectable Pancreatic Ductal AdenoCarcinoma (PDAC), focusing on biomarker and liquid biopsy development





- DDR BM evaluation
- Clonal evolution
- Intra-tumoral heterogeneity
- Resistance mechanism
- Feasibility of liquid biopsy



#### PRIMUS-004: 2<sup>nd</sup> line Metastatic Umbrella





### PRIMUS-004 (Appendix 1)



Oncology Lead: Mairead McNamara Translational Lead: Stephan Dreyer





### Precision-Panc / PRIMUS Recruitment (22 Jan 2019)



### **Reasons for Declining PRIMUS-001** (N = 10)

- 2 x wanted to start chemotherapy immediately
- 2 x wanted Standard of Care treatment
- 2 x due to travel
- 2 x declined all treatment
- 1 x chose FOLFIRINOX due to gBRCA carrier
- 1 x chose single agent chemotherapy



#### Lessons Learnt...

- Be as patients and clinicians friendly as possible
  - Patient pathway
    - Embed research activities into SoC
    - o Shorten & simplify
    - Attractive and available trial options (stages & PS)
    - Novel trial designs (adaptive with integrate biological Qs)
  - Tissue pathway
    - o Use "surplus"
    - o Use exist structure/pathway if possible
    - Bring cyto/pathology & biorepository together
    - o Clinically meaningful TAT
- Be pragmatic & realistic (clinical Vs research)
- Help each site set up (strength vs challenges)
- Identify "champions" from each specialty @ each site
- Start small, then grow...
- Ensure "key ingredients" of precision medicine are secured





### **Glasgow Precision Oncology Laboratory**

**Andrew Biankin** 

David Chang Susie Cooke

Judith Dixon-Hughes Anna Morris Sarah Allison Maja Bailey Dario Beraldi Holly Brunton Giusy Caligiuri Euan Cameron Ricky Cunningham Stephan Dreyer Lisa Evers Amanda Ewing James Stuart

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Search: University of Glasgow

in







#### Glasgow Royal Infirmary

Colin McKay Ross Carter Euan Dickson Nigel Jamieson Fraser Duthie Lyn Smith Janet Graham

Derek Grose David McIntosh Abdulla Al-Adhami Elspeth Cowen Kimberley Booth Endoscopy staff

#### Queen Elizabeth University Hospital

Nicola Williams Paul Westwood Clinical Genetics lab Christine Whilshire GGC Biorepository





#### **Patients and families**

#### University of Glasgow CRUK Glasgow Centre

Andrew Biankin David Chang Jeff Evans Susie Cooke Fraser Duthie Judith Dixon Anna Morris Janet Graham Derek Grose Nigel Jamieson Robert Jones Colin McKay **Beatson Institute of Cancer Research** Owen Sansom Jen Morton Catherine Winchester

Cambridge University CRUK Cambridge Institute Duncan Jodrell Bristi Basu Pippa Corrie Tessa Kasia

Glasgow CTU James Paul Jamie Stobo Sarah Bradley Manchester University CRUK Manchester Research Institute Juan Valle Caroline Dive Claus Jorgensen Ged Brady Mairead McNamara Derek O'Reilly

University of Oxford Cancer Research UK Oxford Centre Eric O'Neill Somnath Makerjee

The Institute of Cancer Research, London Chris Lord

#### **Precision-Panc centres around the UK**













Pancreatic Cancer U K



Scottish Genomes Partnership









### Thank you for your attention





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### DNA / RNA Yield sufficient for NGS

		Fresh Frozen		
	Size	DNA Yield (mean, range (ng))	RNA Yield (mean, range (ng))	
Boston Acquire®	22G	1819 (133 – 7350)	191 (30 – 1187)	
Sharkcore®	19G	2170 (11.4 – 6000)	N/A	
Sharkcore®	22G	2939 (1134 – 7595)	481 (40 – 1790)	
Cook Procore®	20G	1745 (290 – 4750)	18 (3.6 – 44)	
		FFI	PE	
	Needle Size	DNA Yield (mean, range (ng))	RNA Yield (mean, range (ng))	
Training set (n = 14)	22G	1819 (133 – 7350)	191 (30 – 1187)	
PRECISION-Panc EUS set (n = 27)	22G	1740 (102 – 2860)	n/a	
PRECISION-Panc Core set (n = 19)	Various	550 (0 – 1730)		



### The discoverable space: novel cancer genes

#### Current knowledge of cancer genes is close to saturation



Lawrence et al. Nature. 2014 January 23; 505(7484): 495–501 Bailey et al. Cell. 2018 Aug 9;174(4):1034-1035



### Assay design: defining content

Commercial and LDT cancer panels show **poor concordance** in gene selection, likely due to lack of objective methodologies



Panel	No. of genes
Ion AmpliSeq comprehensive	409
FoundationOne CDx	309
Caris Molecular Intellegence	593
Illumina TSO500	523
Tempus xT	594
Dana Farber OncoPanel V3	447
MSK-IMPACT 468	468
MD Anderson v1	409



### 2<sup>nd</sup> Highest Cause of Cancer Mortality Soon



Rahib et al Cancer Res 2014