#### AHCC07

**Precision Medicine in Liver Cancer across an Asia-Pacific Network** 

## ADDRESSING AN URGENT UNMET CLINICAL NEED: the NMRC Flagship Program in Liver Cancer

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Regional Variation in the Estimated Age-Standardized Incidence Rates of Hepatocellular carcinoma.

El-Serag HB. N Engl J Med 2011;365:1118-1127.

## HCC: A Global Un-met Clinical Need mortality-to-incidence ratio of 0.98

#### Men: 2<sup>nd</sup> cause of cancer deaths (previously 3rd)



Estimated age-standardised incidence and mortality rates: men

#### Women: 5<sup>th</sup> cause of cancer deaths (previously 6th)

Estimated age-standardised incidence and mortality rates: women



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## Central challenge in HCC currently: poorly efficacious systemic therapy

- More than 1 million new cases a year, 80% in the Asia-Pacific, <u>but</u> few efficacious systemic therapies
  - 20% of patients are diagnosed at an <u>early stage</u> and benefit from potentially curative therapies – *resection, transplantation, radiofrequency ablation* - recurrences common because of absence of efficacious adjuvant therapy that limits long term survival
- Poorly efficacious systemic therapy for <u>advanced HCC</u> because there are still no validated predictive bio-markers
  - best response rate in 2016 first-line < 10% (sorafenib then standard- of-care)
  - best response rate in 2021 first-line 30% (Atezo+ Bev current standard- of-care)
  - No useful <u>adjuvant</u> therapy after surgery in <u>early/intermediate HCC</u>. High recurrence rates
    - 5-year survival of 67% for early stage
    - 5-year survival of 38% in intermediate stage
  - Highly heterogeneous genome

# Standard approach to drug development in HCC has not been useful

- Most drug development programs depends on single samples to elucidate molecular mechanisms:
  - assumes tumor is homogenous
  - only considers the *presence/ absence* of a driver alteration,
    not their clonal/sub-clonal
    dominance. (Swanton 2015)



#### Schulze Nat Gen 2015 PATIENTS. AT THE HE RT OF ALL WE DO.

# The importance of intra-tumor heterogeneity(ITH)

# THE ELEPHANT METAPHOR OF REALITY spear hose fan wall pole rope

Solid tumors and their metastases are intrinsically complex. Single biopsy often reflects part of the tumor.

Understanding tumor heterogeneity can provide a more holistic picture of the tumor.

Tumor heterogeneity is the genetic basis of tumor evolution, treatment resistance and metastasis.

#### **Example: Renal Cell Carcinoma**

Genetic Intra-tumor Heterogeneity and

Phylogeny: multi-region sampling.



#### Gerlinger M et al. N Engl J Med 2012;366:883-892.

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Clonal heterogeneity

Tumor heterogeneity

**Courtesy: Zhai WW** 

#### few cancers are homogeneous

## A more rational approach to HCC



- multi-region sampling
- Whole exome/whole genome sequencing

**Surgical Cohort:** AJCC Stages I and II HCC - Followed up longitudinally

nature		
COMMONICATIONS		

#### ARTICLE

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OPEN DOI: 10.1038/ncomms14565

#### The spatial organization of intra-tumour heterogeneity and evolutionary trajectories of metastases in hepatocellular carcinoma

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Zhai Nat Comm 2017



of Singapore

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## Prospective data - Evolutionary Patterns in HCC



## Precision Medicine in Liver Cancer Asia-Pacific Network



## AHCC07 - The PLANet Study: Asia-Pacific HCC Trials Group



#### **Precision Medicine in Liver Cancer across the Asia-Pacific Network**



## **Multi-region sampling of HCC tumor**

Tumour (transverse); Venous phase 11-28



Version 1.0 2016

#### High logistical and cultural barrier to entry

Highly integrated process – sample collection involves surgeons, anesthetists, clinical coordinators, pathologists, couriers, RAs, post-docs, PIs – about 15 people from 5 institutions involved



## opportunity for **Vertical and Horizontal integration**

additional grants:



NMRC CS-IRG: epigenomics



#### Integration of Data from the same patient/sample

## PLANet 1.0 Cohort and the wealth of resources generated

PLANET study patient follow-up v X SingHealth N = 90 NUH × N = 18 UMMC N = 13 NCIT N = 15 Total number of patients = 147 Patients reached >=24 months follow-up/dead/recurred = 132 Total number of patients with recurrent HCC = 74 with WGS data = 130, RNAseq data = 119, TMC Immunomics data = 37. Metabolomics data = 55. N = 10Epigenomics data = 51 Duke (Generated by: Singapore Clinical Research Institute) Rurham 12 30 36 42 72 78 0 18 24 48 54 66 60 Time since resection surgery (months)

Last follow-up × Tumor reccurence ▲ Death

- Matched recurrent samples were collected in 35 out of 74 recurrent patients.
- ✓ No. of patients with WGS data: 130
- ✓ No. of patients with RNAseq data: 119
- ✓ No. of patients with Immunomics data: 37
- No. of patients with Metabolomics data:
  55
- ✓ No. of patients with Epigenomics data: 51
- No. of PDP lines successfully established:
  24 lines from 16 patients (Success rate of 20%)
- ✓ No. of PDX lines successfully established: 38 lines from 20 patients (Success rate of HCC-PDX: 11.2%; Success rate of CCA-PDX xenograft: 28.5%).

### Discoveries in the TCR PLANET - Onco-fetal Reprogramming confers immune-escape in HCC (Theme 1)





Sharma 2020 Cell

- Re-emergence of fetal-associated PLVAP+/VEGFR2+ endothelial cells (EC) and embryonic-like FOLR2+/CD163+ tumour-associated macrophages (TAMs)
- immune suppressive environment maintained by VEGF/NOTCH Signaling
- **Hypothesis**: key is niched co-localization of cells and molecular pathways and density
- Provide insights on the immune-escape mechanisms targeted by PD-L1 inhibitor atezolizumab and anti-VEGF antibody bevacizumab (Atezo+Bev).
- Potential value of using onco-fetal profiles to correlate with clinical outcomes with systemic therapeutics and the development of predictive biomarkers in HCC.

## Discoveries in the TCR PLANET – DNA ITH vary a lot across patients and there are diverse evolutionary routes to metastatic tumour (Theme 1)



**Wide range** of Genomic ITH in primary tumour



## Intra-tumour heterogeneity (ITH) of HCC is a major challenge to the treatment of

metastatic tumour.

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## Discoveries in the TCR PLANET – Co-existence of multiple transcriptomic sub-types in 1/2 HCCs and clinical trajectory driven by "Bad Apples" (Theme 1)





Mixed RNA subtypes found in half of the patients

In HCC with mixed subtypes, clinical outcomes are determined by the subtype with the worst prognosis ("bad apple" in the barrel)



Zhai et al. Under minor revision in National Science Review

Chen et al. Manuscript in Preparation

> Potential predictive biomarkers based on "bad apples" signature

### Discoveries in the TCR PLANET – High immune heterogeneity within and between patient tumours (Theme 1 and 2)



While the majority of the tumours were immunologically hot (35%) or cold (33%), a significant proportion (n=18, proportion=33%) of the patients were **immunologically mixed**.



Zhai et al. Under minor revision in National Science Review

Nguyen et al. (2020) Nat Communications

High immune ITH in HCC may account for the differential response to immuno-therapy

#### Discoveries in the TCR PLANET – Establishment of individualized patient-derived cellular models facilitate downstream drug discovery and clinical translation (Theme 3)



Tan et al. (2019) Gastroenterology, 157(6):1615-29 Rashid et al. (2018) Sci. Transl. Med., 10(43).





- Identification of NAD metabolism as a therapeutic vulnerability in a subset of liver cancer (*Theme 3 PI: Tam WL*).
- Application of QPOP across
  PDOs to identify effective
  treatment combinations (*Theme* 3 PI: Chow E)

Highlight the translational value of patient-derived cellular models that properly reflect the heterogeneity of HCC

# A regional and whole-of-nationeffort

#### **NMRC Grants**

#### **Clinical Collaborators**

SGH (Brian Goh) NUH (Glenn Bonney) UMMC (Yoong BK) NCIT (Rawisak) TMC (Vanessa) Duke Durham (Sabino)

#### **Bench Collaborators**

GIS (Patrick Tan, Roger Foo, Tam WL, Zhai WW, Chen JB, Ankur Sharma) STIIC (Valerie Chew) NUS (Edward Chow, Tan Boon) NTU (Yulan Wang) SIgN (Florent Ginhoux)

#### **PLANet patients and their families**



TCR 1<sup>st</sup> Investigator Meeting, 2016



TCR 2<sup>nd</sup> Investigator Meeting, 2017



TCR 3<sup>rd</sup> Investigator Meeting, 2018



TCR 4<sup>th</sup> Investigator Meeting, 2019

# Main scientific discoveries to date

From the large cohort of resected HCC patients annotated with comprehensive clinical trajectory, multi-omics data and representative PDP/PDX models, we have shown that

- ✓ Evolutionary routes to metastatic tumour are highly diversed and recurrence can emerge early/late from the index tumor.
- ✓ Significant proportion of HCCs have mixed transcriptomics subtypes and the worst subtype drives clinical trajectory.
- ✓ Onco-fetal reprogramming is a novel immune-escape mechanism in HCC
  - $\checkmark$  importance of co-localization of molecular pathways

## **Going forward: PLANet2.0**

