

2019 KOPANA 18th Spring Seminar

Update in liver cancer pathology: stemness and tumor microenvironment

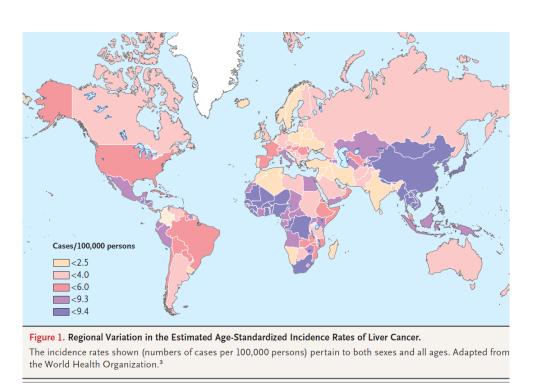
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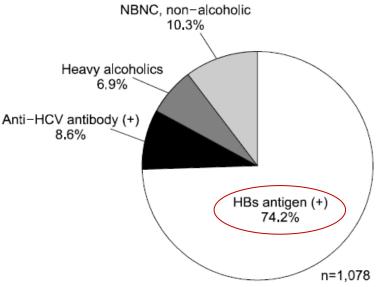


Global burden of liver cancer

- The fifth most common neoplasm in the world
- The third mortality rate among all cancers
- ✓ One million new cases and 700,000 death worldwide annually.

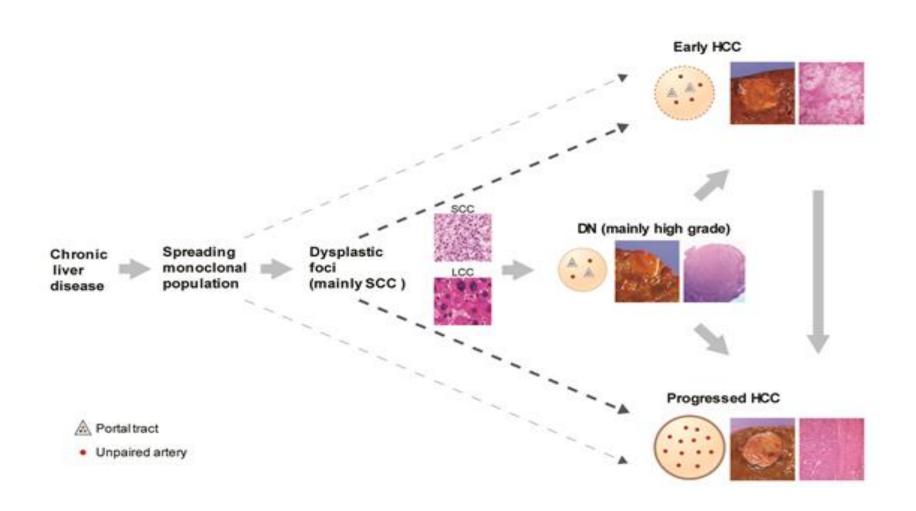


Etiology of HCC in Korea



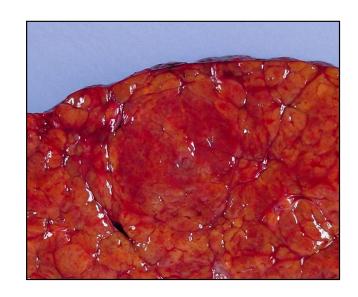
HBsAg (+) rate in Korean : 3% in adult, 0.2% in children

Human hepatocarcinogenesis is multistep procress

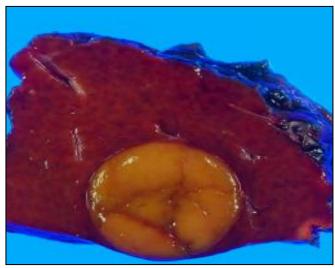


Small HCC (< 2cm)

Early HCC vs. Small progressed HCC

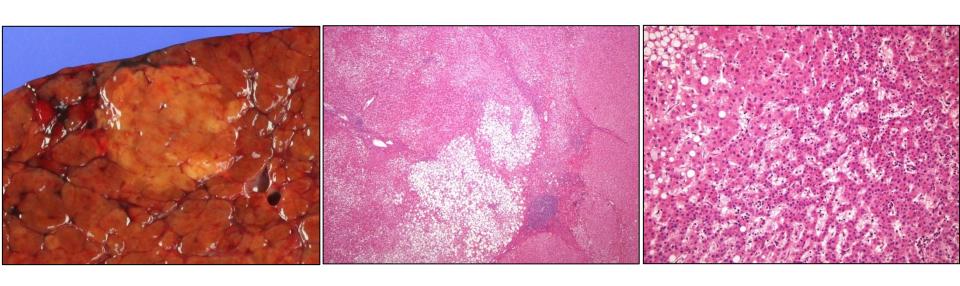


Indistinct margin



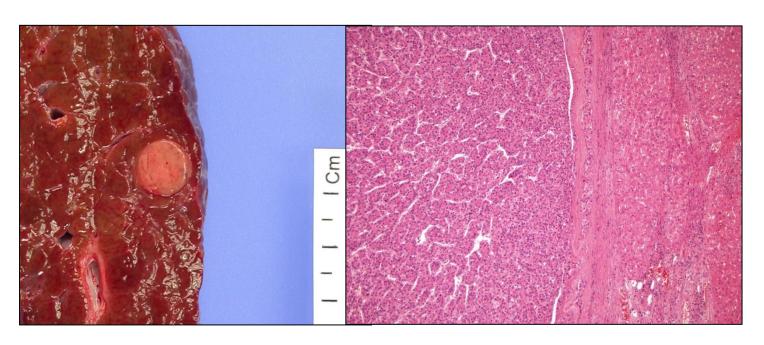
Distinct margin

Early HCC



- Small HCC (11.9 \pm 3.3mm) with indistinct margin
- Very well to well differentiated HCC
- Portal vein invasion: < 5%, Intrahepatic metastasis: 0%
- · "Carcinoma in situ"
- Best prognosis (5yr survival rate > 90%)
- Recurrence rate: 80% at 4yrs after surgery
 - ✓ Metachronous multicentric occurrence

Small and progressed HCC (< 2cm)



- Well defined mass with distinct margin
- Moderately differentiated HCC; 60%
- Tumor invasion in portal vein; 27%
- Intrahepatic metastasis; 10%

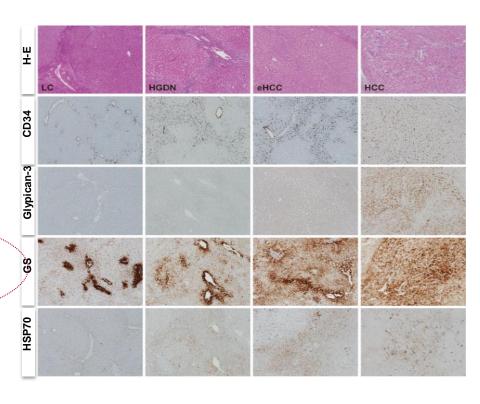


Sequential transcriptome analysis of human liver cancer indicates late stage acquisition of malignant traits

Jens U. Marquardt^{1,2,†}, Daekwan Seo^{1,†}, Jesper B. Andersen^{1,†}, Matthew C. Gillen¹, Myoung Soo Kim⁴, Elizabeth A. Conner¹, Peter R. Galle², Valentina M. Factor¹, Young Nyun Park³, Snorri S. Thorgeirsson^{1,*}

Table 1. Clinicopathological information and HCC marker expression.

| | Clinicopathological information | | | | | |
|--|---------------------------------|-------------|----------------------------|-------------------|--------|------------------|
| Patient No. | Sex | Age (yr) | Intrahepatic metastasis | Vascular invasion | Lesion | Size (cm) |
| 1 | М | 68 | No | No | LGDN | 0.8 x 0.8 |
| | | | | | HGDN | 1.5 x 1.4 |
| 2 | М | 54 | No | No | HGDN | 0.8 x 0.8 |
| | | | | | HGDN | 0.8×0.7 |
| | | | | | eHCC | 1.2 x 1.0 |
| | | | | | pHCC | 3.0 x 2.0 |
| 3 | F | 42 | No | No | HGDN | 1.0 x 0.9 |
| 4 | M | 64 | No | No | HGDN | 1.5 x 1.3 |
| 5 | М | 61 | No | No | LGDN | 1 x 0.8 |
| ************ | | | | | LGDN | 0.8 x 0.8 |
| | | | | | LGDN | 1.2 x 1.1 |
| | | | | | HGDN | 1.0 x 1.0 |
| | | | | | HGDN | 1.3 x 0.9 |
| The same of the sa | | | | | HGDN | 1.0 x 1.1 |
| The second second | | | | | eHCC | 1.6 x 1.4 |
| | | | | | pHCC | 3.8 x 3.2 |
| 6 | М | 61 | No | No | eHCC | 2 x 1.9 |
| 7 | M | 50 | No | No | eHCC | 1 x 1.3 |
| 8 | F | 60 | No | No | HGDN | 1.0 x 1.0 |
| | | | | | eHCC | 1.1 x 1.0 |
| | | | | | pHCC | 1.2 x 1.0 |







Sequential transcriptome analysis of human liver cancer indicates late stage acquisition of malignant traits



- Glutathione metabolism
 - NRF2 signaling
- Apoptosis

HGDN

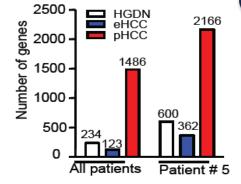
Malignant progression

eHCC

- Proliferation
- Cell cycle control
- Immune reponse
- ECM production

- Cell adhesion
 - **Cytoskeleton remodeling**
- EMT/ Invasion/ Metastasis
- Protein degradation
- TGFb signaling
- WNT / NOTCH signaling
- PI3K signaling
- MYC activation

fHCC



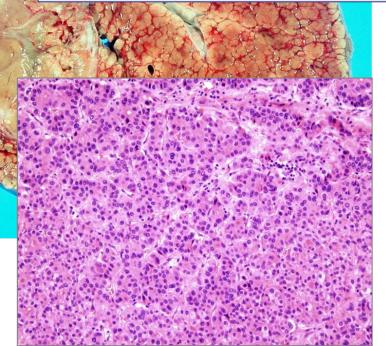
LGDN

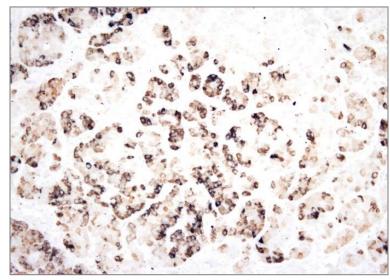
rrogressed rus alterations of Extensive genetic alteration of and subsequent activation of Progressed HCCs prognostic adverse signaling

Puriwuyses the molecular 14869enes the molecular 14869enes the molecular Highlighting the molecular

Early HCC & modest changes in promess
Homogenous & modest changes in promess
transcriptomes
transcriptomes , 123 genes

Cellular heterogenity in HCC





K19: blue/ Brown: HepPar1

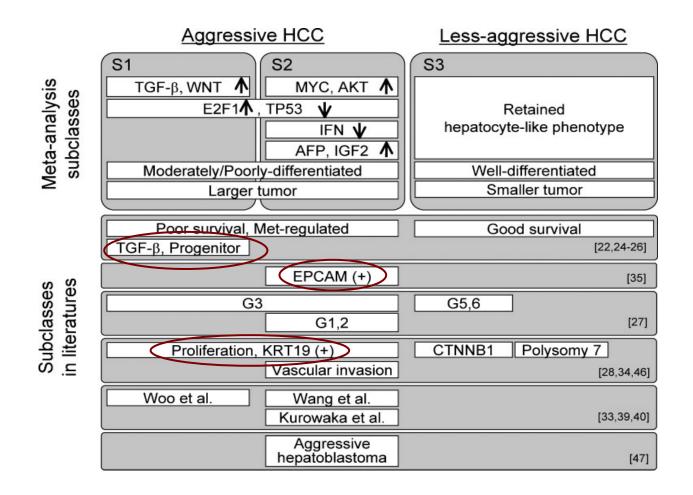
Cancer cell expressing stem cell marker

"Cancer stem (like) cell"

"Cancer stem cell"

- Two ways to be used
- 1 'stem or progenitor cells from which some cancers derive'
- 2 'cancer cells, regardless of origin, which have stem cell-like functions'.
- "Cancer stem cell' to those malignant cells within a cancer that perform stem cell like functioning
 - whether developing these functions de novo during malignant transformation or maintaining them as progeny of transformed stem/progenitorcells.

? Molecular classification might be mirrored by tumor morphology and phenotype





HCC with stem cell markers

1) Pathological characteristics

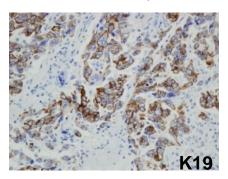
- 2) Tumor microenvironment
 - (1) Fibrous stroma
 - 2 K19 and its regulation mechanism
 - 3 Response to locoregional treatment (TACE)

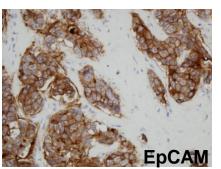
1-1) Pathological characteristics of HCC with stem cell markers

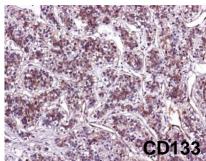
Human HCC cohort 1 (n=137, HBV+ 67.2%)

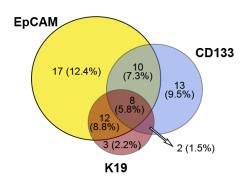
·Stem/progenitor cell marker expression

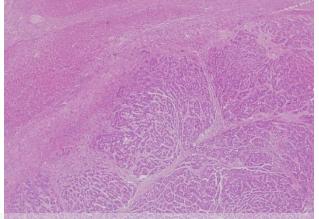
K19 (18%), EpCAM(35%), c-kit (34%), CD133(25%)



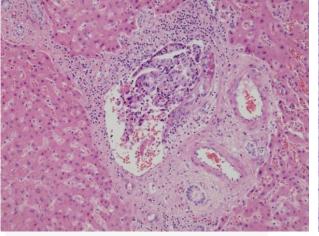




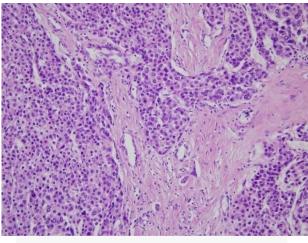




Infiltrative growth without tumor capsule

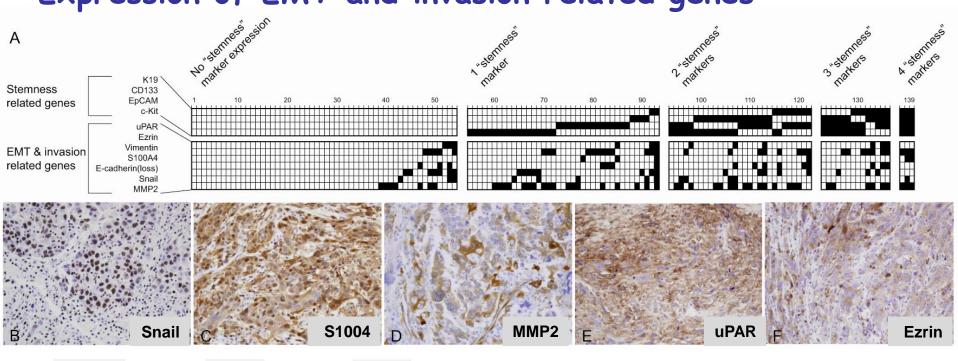


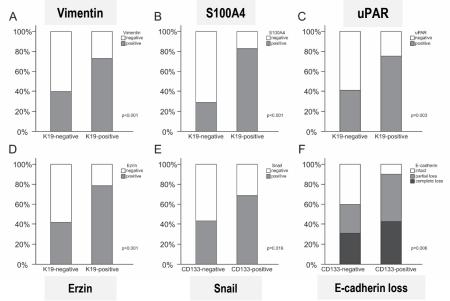
Vascular invasion



Fibrous stroma

·Expression of EMT and invasion related genes





| | Overall survival | Disease-free survival |
|-------|------------------|-----------------------|
| K19 | 0.018 | 0.007 |
| CD133 | 0.057 | 0.552 |
| EpCAM | 0.777 | 0.302 |
| c-kit | 0.642 | 0.562 |

HCC Cohort 2 (n=237, HBV+ 80.2%)

Table 2. Comparison of Clinicopathologic Features Between K19-Positive and K19-Negative HCCs*

| Clinopathologic Features | K19-Positive Group (n = 68) | K19-Negative Group (n = 169) | P Value |
|-----------------------------|--------------------------------|---------------------------------|---------|
| Age (years, mean ± SD) | 52.0 ± 10.2 | 56.2 ± 10.0 | 0.004 |
| Gender (male:female) | 42:26 | 147:22 | < 0.001 |
| HBs antigen (%) | 57 (83.8) | 133 (78.7) | 0.371 |
| Serum ALT (IU/L, mean ± SD) | 36.4 ± 21.3 | 37.3 ± 22.5 | 0.777 |
| Serum AST (IU/L, mean ± SD) | 46.0 ± 19.0 | 44.7 ± 34.6 | 0.780 |
| Serum albumin | 4.3 ± 0.5 | 4.4 ± 0.5 | 0.033 |
| (g/dL, mean ± SD) | | | |
| Serum alpha-fetoprotein | 25 (36.8) | 18 (10.7) | < 0.001 |
| >1,000 IU/mL (%) | | | |
| Cirrhosis (%) | 41 (60.3) | 82 (48.5) | 0.101 |
| Tumor size (cm, mean ± SD) | 3.92 ± 2.02 | 3.88 ± 2.58 | 0.911 |
| Microvascular invasion (%) | 50 (73.5) | 96 (56.8) | 0.017 |
| Major vascular invasion (%) | 6 (8.8) | 9 (5.3) | 0.317 |
| Multiple tumors (%) | 12 (17.6) | 26 (15.4) | 0.688 |
| Poor differentiation* (%) | 35 (51.5) | 92 (54.4) | 0.679 |
| Tumor-capsule formation (%) | 11 (16.2) | 51 (30.2) | 0.027 |
| Fibrous stroma (%) | 12 (17.6) | 12 (7.1) | 0.015 |
| Operation | • | | |
| Minor/major resections | 33/35 | 81/88 | 0.933 |

^{*}n = 237, cohort 2.

Abbreviations: K19, keratin 19; SD, standard deviation; ALT, alanine aminotransferase; AST, aspartate aminotransferase.

Human Hepatocellular Carcinomas With "Stemness"-Related Marker Expression: Keratin 19 Expression and a Poor Prognosis

Haeryoung Kim, ¹ Gi Hong Choi, ² Deuk Chae Na, ³ Ei Young Ahn, ³ Gwang Il Kim, ³ Jae Eun Lee, ³ Jai Young Cho, ⁴ Jeong Eun Yoo, ³ Jin Sub Choi, ² and Young Nyun Park ^{3,5,6}

Hepatology 2011

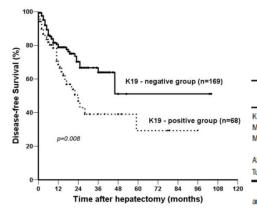
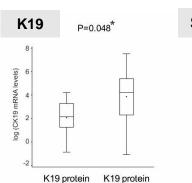


Table 4. Independent Prognostic Factors for Disease-Free Survival by Multivariable Analysis (Cohort 2)

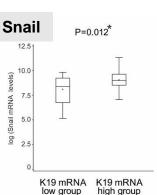
| | | Standard | | |
|------------------|-------------|----------|---------|------------------------|
| Variable | Coefficient | Error | P Value | Relative Risk (95% CI) |
| K19 expression | 0.522 | 0.243 | 0.032 | 1.685 (1.046-2.716) |
| Multiple tumors | 0.883 | 0.278 | 0.002 | 2.417 (1.401-4.172) |
| Major vascular | 0.798 | 0.365 | 0.029 | 2.221 (1.085-4.545) |
| invasion | | | | |
| AST >50 IU/L | 0.786 | 0.313 | 0.012 | 2.194 (1.187-4.054) |
| fumor size >5 cm | 0.672 | 0.263 | 0.010 | 1.958 (1.170-3.277) |

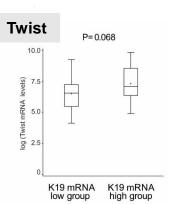
Abbreviations: 95% CI, 95% confidence; K19, keratin 19; AST, aspartate aminotransferase.

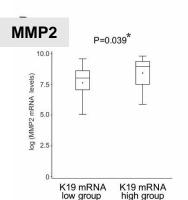


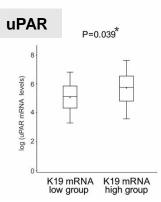
positive

negative









[†]Edmondson-Steiner grades III or IV.

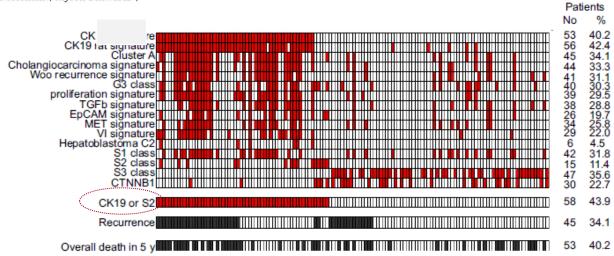


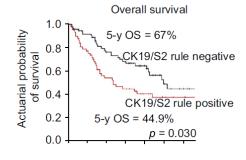


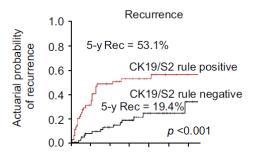
Progenitor cell markers predict outcome of patients with hepatocellular carcinoma beyond Milan criteria undergoing liver transplantation

Oriana Miltiadous¹, Daniela Sia^{1,2}, Yujin Hoshida¹, Maria Isabel Fiel¹, Andrew N. Harrington¹, Swan N. Thung¹, Poh Seng Tan^{1,3}, Hui Dong⁴, Kate Revill¹, Charissa Y. Chang¹, Sasan Roayaie⁵, Thomas J. Byrne⁶, Vincenzo Mazzaferro², Jorge Rakela⁶, Sander Florman¹, Myron Schwartz¹, Josep M. Llovet^{1,7,8,*}

Positive for signature Positive event Rest Positive event





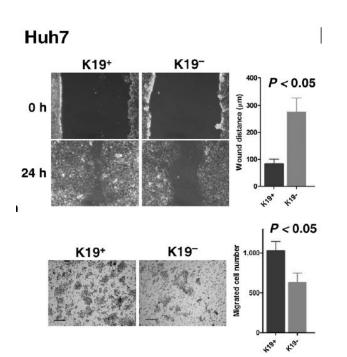


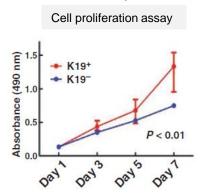
Clinical Cancer Research

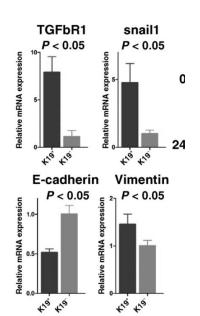
Keratin 19, a Cancer Stem Cell Marker in Human Hepatocellular Carcinoma

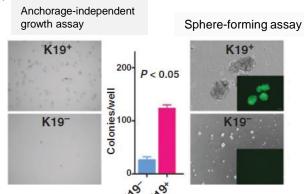
Takayuki Kawai¹, Kentaro Yasuchika¹, Takamichi Ishii², Hokahiro Katayama¹, Elena Yukie Yoshitoshi¹, Satoshi Ogiso¹, Sadahiko Kita¹, Katsutaro Yasuda¹, Ken Fukumitsu¹, Masaki Mizumoto¹, Etsuro Hatano¹, and Shinji Uemoto¹

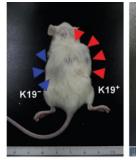
- HCC cell lines were transfected with a K19 promoter—driven enhanced green fluorescence protein gene
- FACS-isolated K19+/K19 cells.



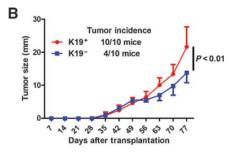












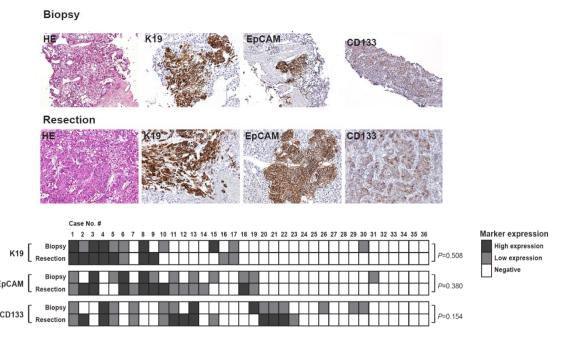


N.D. Theise V.P. Curado S. Franceschi P. Hytiroglou Y.N. Park M. Sakamoto M. Torbenson A. Wee

Poor prognostic marker for HCC

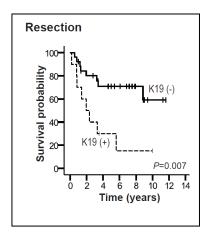
? Can K19 expression be useful maker in biopsied HCCs

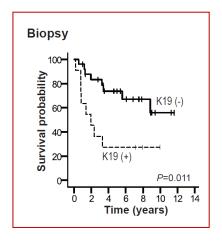
Stemness markers in matched biopsied and resected HCCs (n=36)



| Immunomarkers | Sensitivity | Specificity | Accuracy |
|---------------|-------------|-------------|----------|
| K19 | 80% | 88% | 86% |
| EpCAM | 64% | 86% | 78% |
| CD133 | 71% | 82% | 78% |

Immunoprofiles of resected HCCs as standard of references





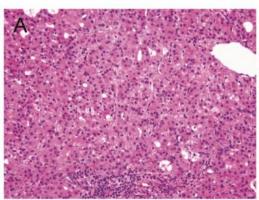


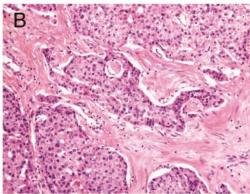
HCC with stem cell markers

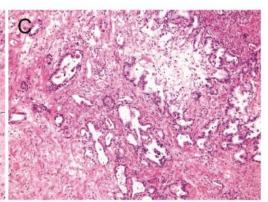
- 1) Pathological characteristics
- 2) Tumor microenvironment
 - 1 Fibrous stroma
 - 2 K19 and its regulation mechanism
 - ③ Response to locoregional treatment (TACE)

2. TME: Fibrous tumor stroma

Scirrhous HCC (HCC with fibrous stroma)







HCC

Tumor cell morphology:
resembling hepatocyte
(polygonal cells having central
round nuclei and abundant
eosinophilic granular cytoplasm)

Architectural pattern: trabecular, pseudoglandular, compact

Stroma: mainly sinusoid-like blood spaces with no or little fibrosis

Scirrhous HCC

Tumor cell morphology: hepatocyte like tumor cell population + small, oval shaped tumor cell population mimicking liver stem/progenitor cells

Architectural pattern: trabecular, nesting (small, oval shaped tumor cell arranged at the periphery of tumor nests facing fibrous stroma)

Stroma: abundant fibrosis≥ 50% of tumor area

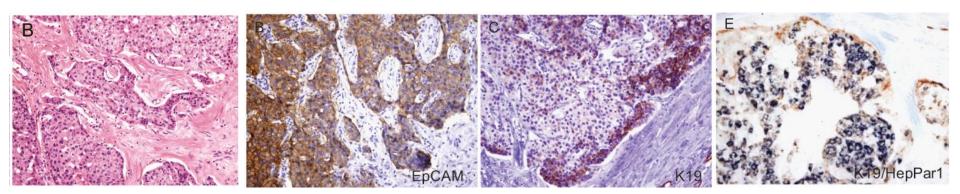
Cholangiocarcinoma

Tumor cell morphology: resembling cholangiocyte (cuboidal or columnar cells having intracytoplasmic mucin)

Architectural pattern: glandular formation

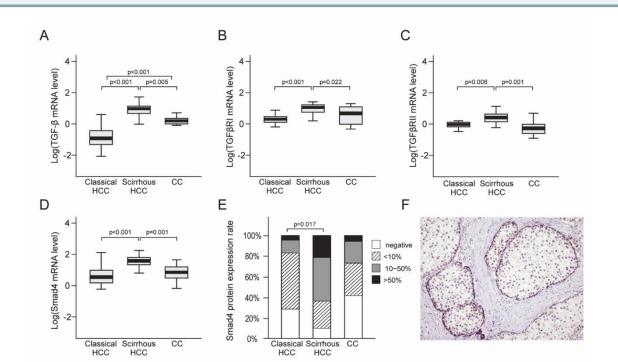
Stroma: marked fibrous stroma

The expression pattern of liver stem cell markers in scirrhous HCCs



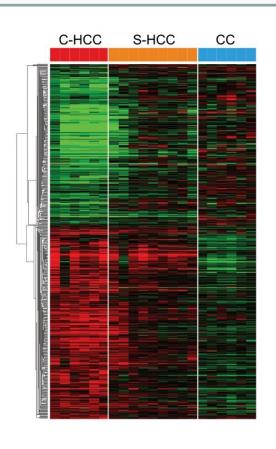
K19: brown/ Hepar1: blue

Expression of TGF-β signaling molecules in S-HCCs

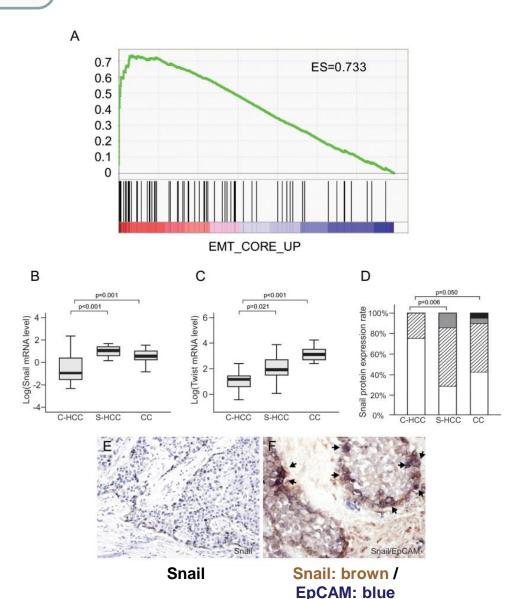


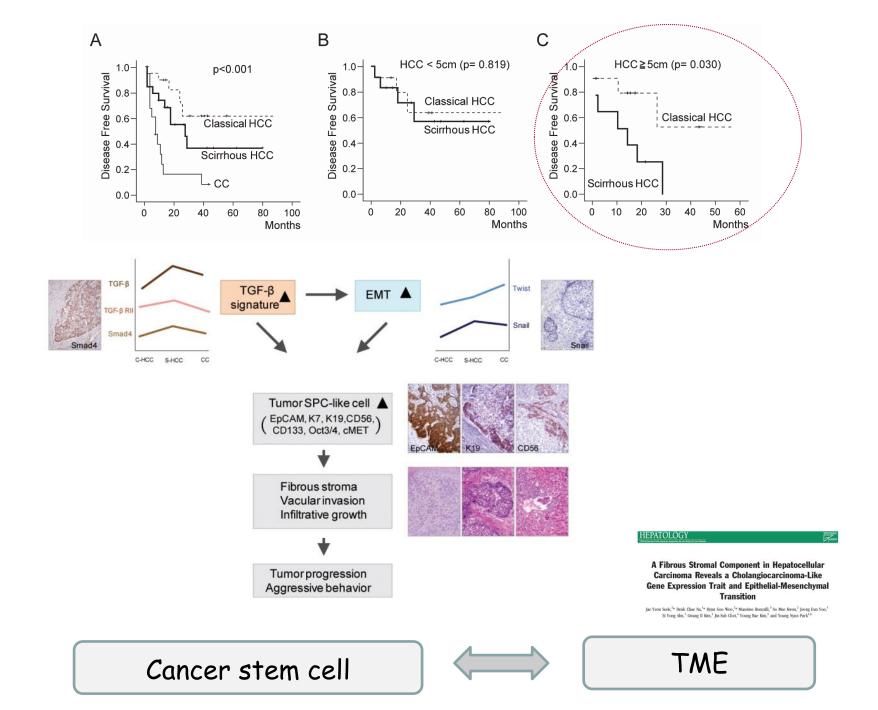
Gene expression profiles of the 617 differentially expressed gene features among C-HCCs, S-HCCs, and CCs

Expression of EMT molecules in S-HCC



Up-regulation of cell adhesion, development, migration, and proliferation-related gene functions in S-HCC



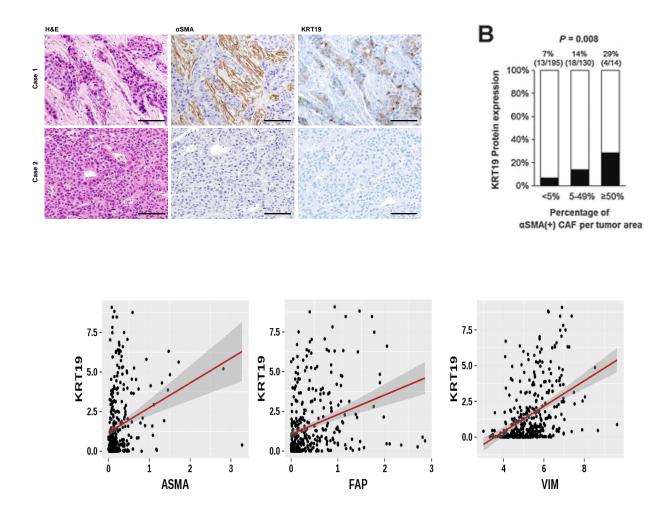




HCC with stem cell markers

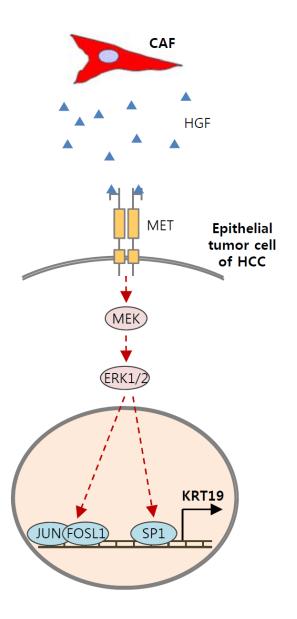
- 1) Pathological characteristics
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 - ③ Response to locoregional treatment (TACE)

\checkmark Correlation between the α SMA-positive CAFs and KRT19 protein expression.

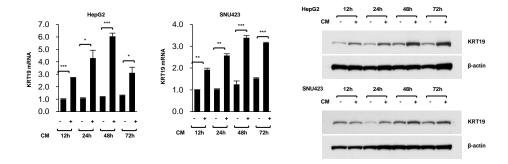


Correlation between the gene expression level of KRT19 and fibrous stromal markers including ASMA, FAP, and VIM in HCC data from TCGA(n = 371).

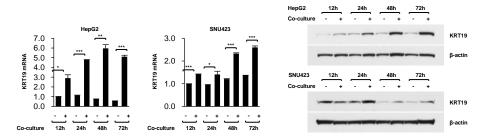
Keratin 19 expression in hepatocellular carcinoma is regulated by fibroblast-derived HGF via MET-ERK1/2-AP1 and SP1 axis



✓ KRT19 expression in HCC is upregulated by paracrine factors from hepatic stellate cells

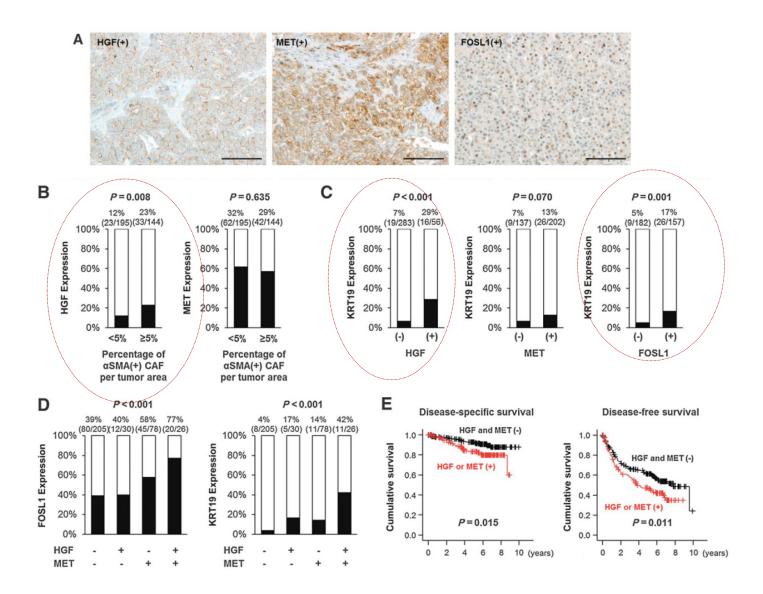


mRNA and protein expression levels of KRT19 after treatment with hTERT-HSC CM.

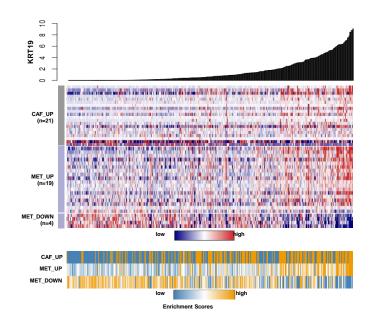


mRNA and protein expression levels of KRT19 after coculture with hTERT-HSC

✓ In clinical specimens of human HCC (n=339), HGF and/or MET expression correlates with a higher KRT19 and FOSL1 expression.

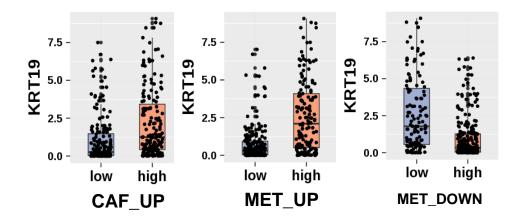


✓ Analysis of HCC data from TCGA revealed KRT19 expression was closely associated with CAF and MET-mediated signaling activities.



Expression heatmap of CAF_UP (n=21), MET_UP (n=19), and MET_DOWN gene signatures (n=4) according to the KRT19 gene expression in the HCC data of TCGA (n=371).

✓ These findings reveal KRT19 expression in HCC is regulated by cross-talk between cancerassociated fibroblasts and HCC cells, illuminating new therapeutic targets for this aggressive disease.



Published OnlineFirst January 23, 2018; DOI: 10.1158/0008-5472.CAN-17-0988

Cancer Research

Keratin 19 Expression in Hepatocellular Carcinoma
Is Regulated by Fibroblast-Derived HGF via a

MET-ERK1/2-AP1 and SP1 Axis

Hyungjin Rhee 1 , Hye-Young Kim 1 , Ji-Hye Choi 2,3 , Hyun Goo Woo 2,3 , Jeong Eun Yoo 1 , Ji Hae Nahm 1 , Jin-Sub Choi 4 , and Young Nyun Park 1,5



HCC with stem cell markers

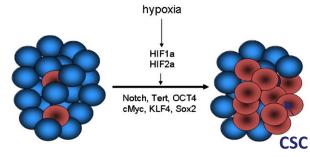
1) Pathological characteristics

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Hypoxic tumor microenvironment

- Hypoxia
 - Most solid tumors
 - Rapid tumor growth and relative lack of blood supply
- The cancer stem cell population is expanded through HIF1/HIF2 pathway under hypoxia (in vitro study).



Nat Rev Cancer. 2011 Jun;11(6):393-410

√ TACE (Transarterial chemoembolization)

- One of most popular loco-regional therapies in HCC
- TACE induces tumor hypoxia.
- Response to TACE is various and a significant number of HCC (50-86%) recurs.





The hypoxic TME may serve as a niche for cancer stem cell.

? Does TACE induced hypoxia affect outcome of HCC patients with stemness marker expression

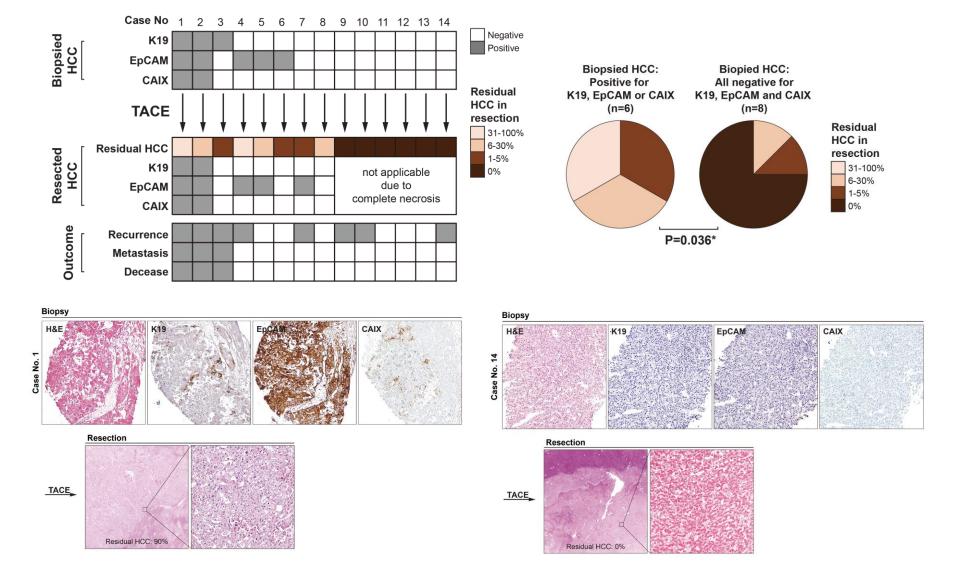
Cohort 1: Biopsy-TACE (1 session)-curative resection matched HCCs (n=14)

Cohort 2: Explanted HCCs with preop locoregional Tx (60%) (n=68)

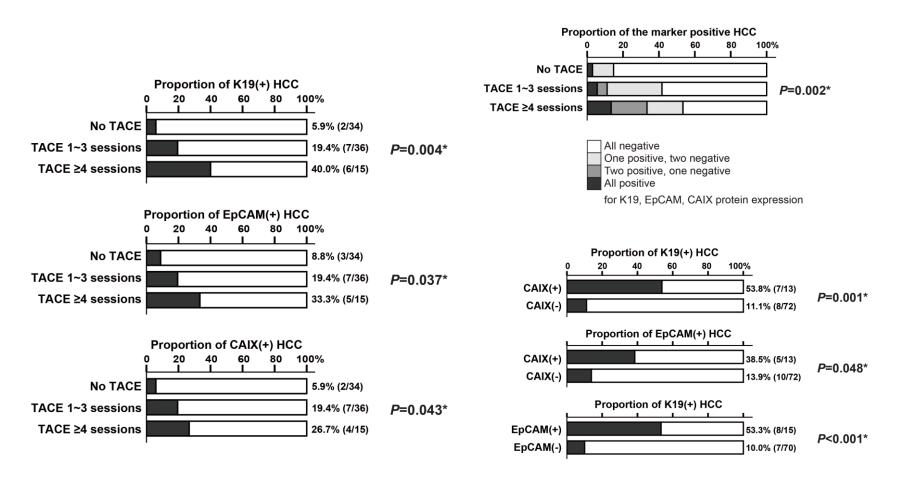
Cohort 3: Resected HCCs without preop locoregional $T \times (n=100)$

Cohort 1: Biopsy-TACE (1 session) - curative resection matched HCCs (n=14)

✓ Single nodular HCC



- •Total necrotic HCCs were excluded as immunoprofiles could not be evaluated.
- •Stemness markers (K19, EpCAM) and hypoxia marker (CAIX) expression were frequently found in HCCs underwent multiple TACE sessions.



Clinicopathological features of hepatocellular carcinomas in cohort 2 according to the CAIX protein expression status

| Clinicopathologic features | CAIX positive $n = 13 (15\%)$ | CAIX negative $n = 72$ (85%) | P-value |
|--|-------------------------------|--------------------------------|-----------------|
| Age (year) | 52 (45–56) | 54 (50–60) | 0.067 |
| Gender (male/female) | 10 (77%)/3 (23%) | 59 (82%)/13 (18%) | 0.670 |
| Etiology (hepatitis B/hepatitis C/alcohol/unknown) | 11 (85%)/1 (8%)/1 (8%)/0 (0%) | 59 (82%)/8 (11%)/4 (6%)/1 (1%) | 0.941 |
| Cirrhosis | 13 (100%) | 70 (97%) | 1.000 |
| Serum aspartate transaminase (IU/l) | 42 (35–75) | 46 (35–68) | 0.779 |
| Serum alanine transaminase (IU/l) | 31 (13–58) | 32 (20–40) | 0.883 |
| Serum albumin (g/dl) | 3.0 (2.6-3.8) | 3.3 (2.8–3.6) | 0.399 |
| Serum platelet (1000/μl) | 66 (41–101) | 79 (54–118) | 0.173 |
| Serum alpha-fetoprotein (IU/ml) | 29.0 (2.9–246.2) | 10.9 (4.8–60.9) | 0.502 |
| Serum PIVKA-II (AU/ml) ^a | 76.0 (24.0–402.3) | 37.5 (18.3–96.0) | 0.131 |
| Tumor pathology | | | |
| Diameter of largest tumor (cm) | 3.0 (2.3–3.5) | 2.2 (1.6–3.5) | 0.319 |
| Total tumor diameter (cm) | 3.5 (2.4–5.5) | 3.6 (2.4–6.4) | 0.665 |
| Differentiation (Edmonson–Steiner grades I/II/III) | 1 (8%)/11 (85%)/1 (8%) | 27 (38%)/40 (56%)/5 (7%) | 0.104 |
| Capsule formation (absent/partial/complete) | 0 (0%)/9 (69%)/4 (31%) | 22 (31%)/32 (44%)/18 (25%) | 0.063 |
| Microvascular invasion | 8 (62%) | 13 (18%) | $0.002^{\rm b}$ |
| Number of the lesion $(1/2 \text{ or } 3/ \ge 4)$ | 6 (46%)/6 (46%)/1 (8%) | 23 (32%)/35 (49%)/14 (19%) | 0.466 |
| Milan status (in/out) | 9 (69%)/4 (31%) | 48 (67%)/24 (33%) | 1.000 |
| K19 protein expression | 7 (54%) | 8 (11%) | $0.001^{\rm b}$ |
| EpCAM protein expression | 5 (39%) | 10 (14%) | 0.048^{b} |

Variables are expressed as median (interquartile range) or number (%).

^aSerum PIVKA-II levels not available for five patients.

^bIndicates P < 0.05.

Univariate and multivariate analyses of disease-free survival in cohort 2

| | Univariate analysi | S | Multivariate analysis | |
|--|---|---------------------------|---|----------------------|
| Variables | Hazard ratio (95% confidence interval) | e P-value ^a | Hazard ratio (95% confidence interval) | P-value ^a |
| Age (≥60 years) | 0.03 (0.0–8.1) | 0.222 | | |
| Gender (male) | 0.8 (0.2–2.8) | 0.677 | | |
| Etiology (hepatitis B virus) | 2.4 (0.3–18.7) | 0.400 | | |
| Serum alpha-fetoprotein (≥400 IU/ml) | 8.4 (2.6–26.6) | < 0.001 ^b | 6.8 (1.8–26.1) | $0.005^{\rm b}$ |
| Serum PIVKA-II (≥400 AU/ml) | 6.0 (1.8–20.0) | $0.004^{\rm b}$ | 2.0 (0.5–8.7) | 0.358 |
| Microvascular invasion (positive) | 2.4 (0.8–7.5) | 0.138 | | |
| Differentiation (Edmonson–Steiner grade III) | 1.4 (0.2–10.6) | 0.769 | | |
| Milan status (out of Milan) | 2.1 (0.7–6.4) | 0.209 | | |
| Pre-transplantation transarterial | 7.7 (1.0–59.5) | 0.051 | | |
| chemoembolization (one or more sessions) | | | | |
| CAIX protein expression (positive) | 7.4 (2.4–22.9) | 0.001 ^b | 6.4 (1.9–22.0) | $0.003^{\rm b}$ |
| K19 protein expression (positive) ^c | 3.5 (1.4–8.7) | $0.007^{\rm b}$ | | |
| EpCAM protein expression (positive) ^c | 3.6 (1.4–8.8) | 0.006 ^b | | |

^aUnivariate and multivariate analyses were performed using the Cox proportional hazards model.

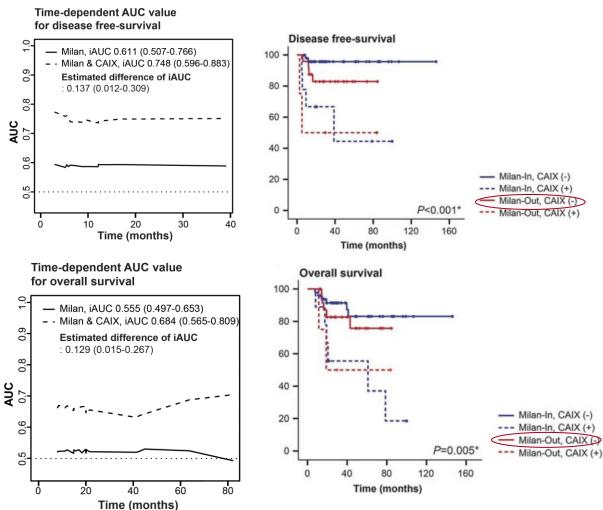
^bIndicates P < 0.05.

^cK19 and EpCAM were not included in the multivariate analysis because of significant associations with CAIX.

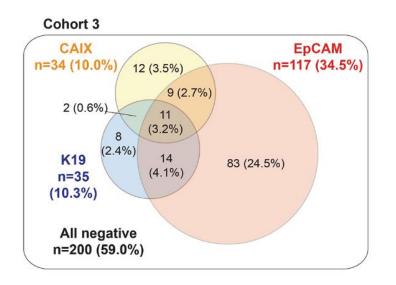
 CAIX was an independent predictor of recurrence/survival after transplantation.

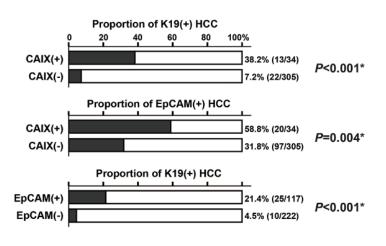
When CAIX is combined to Milan criteria, prediction of recurrence/survival

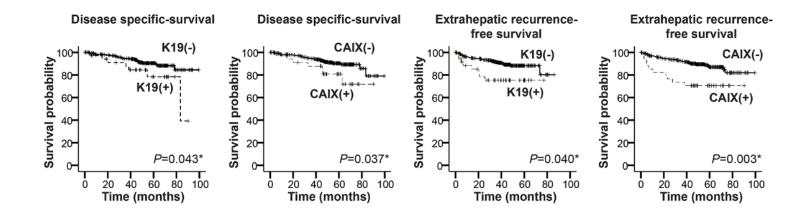
could be improved.



Cohort 3: Hepatic resection HCC cohort without preoperative treatment (n=339)



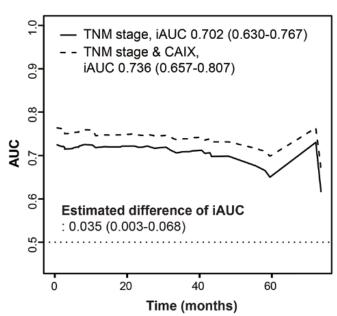




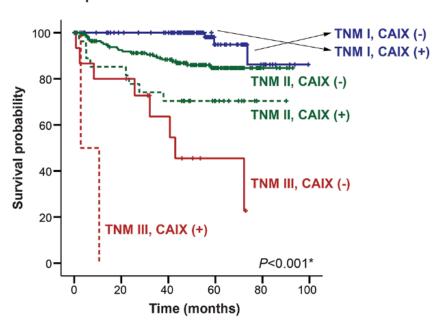
Cohort 3: Hepatic resection HCC cohort without preoperative treatment (n=339)

- Stemness markers (K19) and hypoxia marker (CAIX) were poor prognostic indicator.
- CAIX expression was independent prognostic factor for extrahepatic recurrence.





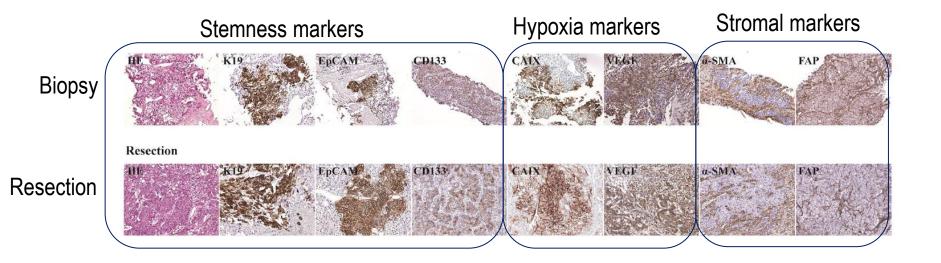
Extrahepatic recurrence-free survival



What happens in cancer stem cell and TME during TACE?

HCC TACE group: Bx-TACE- Resection (n=10)

HCC Non-TACE group: Bx ----- Resection (n=36)



HCC TACE group:

Bx-TACE- Resection (n=10)

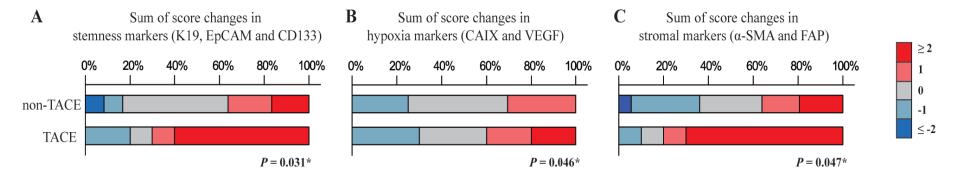
HCC Non-TACE group: Bx ------ Resection (n=36)

| Immunomarker expression in biopsied specimens | | | | | |
|---|---------------------------------|----------|--------|--|--|
| K19 | 5 (50%) | 11 (31%) | 0.283 | | |
| EpCAM | 6 (60%) | 12 (33%) | 0.157 | | |
| CD133 | 3 (300 | 9 (25%) | 0.706 | | |
| CAIX | reference | 10 (28%) | >0.999 | | |
| VEGF | 6 (60%) 3 (30°) 6 (60%) 6 (60%) | 28 (78%) | 0.682 | | |
| α-SMA | 6 (60%) | 25 (69%) | 0.573 | | |
| FAP | 5 (50%) | 19 (53%) | 0.876 | | |
| Immunomarker expression in re | esected specimens | | | | |
| K19 | 5 (50%) | 10 (28%) | 0.257 | | |
| EpCAM | 8 (80%) | 14 (39%) | 0.032* | | |
| CD133 | 6 (60%) | 13 (36%) | 0.277 | | |
| CAIX | 6 (60%) | 10 (30%) | 0.074 | | |
| VEGF | 6 (60%) | 29 (81%) | 0.220 | | |
| α-SMA | 9 (90%) | 15 (42%) | 0.011* | | |
| FAP | 9 (90%) | 19 (53%) | 0.064 | | |

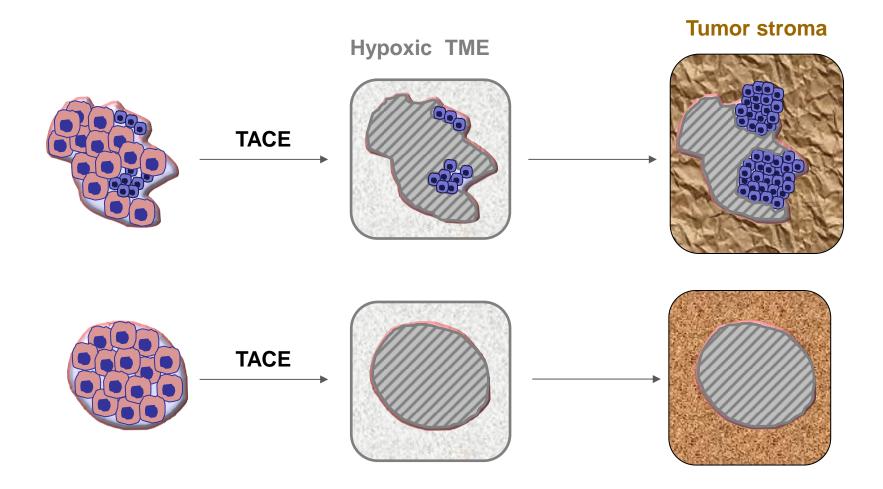
HCC TACE group:



HCC Non-TACE group: Bx ----- Resection (n=36)



Increased expression of stemness markers and altered tumor stroma in HCC under TACE-induced hypoxia: A biopsy and resection matched study



- HCC cells <u>without</u> stemness
 - HCC cells with stemness

- √ The expression of stemness (K19, EpCAM) and hypoxia (CAIX) related markers were correlated each other.
- ✓ HCC with these markers showed resistance to TACE and poorer outcome.
- ✓ Stemness marker expression is considered to be increased along with tumor stromal alteration under TACE-induced hypoxia, which might promote the aggressive biology of HCC.
- ✓ Evaluation of stemness and hypoxia markers may have an additional value in predicting HCC outcome, especially for TACE-treated HCCs.

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Poor outcome of hepatocellular carcinoma with stemness marker under hypoxia: resistance to transarterial chemoembolization www.impactjournals.com/oncotarget/

Oncotarget, 2017, Vol. 8, (No. 59), pp: 99359-99371

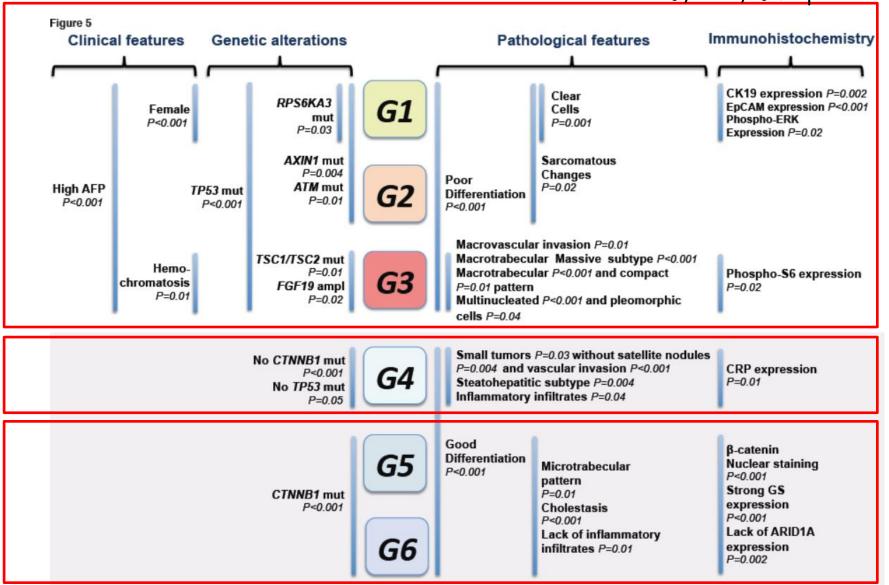
Research Paper

Increased expression of stemness markers and altered tumor stroma in hepatocellular carcinoma under TACE-induced hypoxia: A biopsy and resection matched study

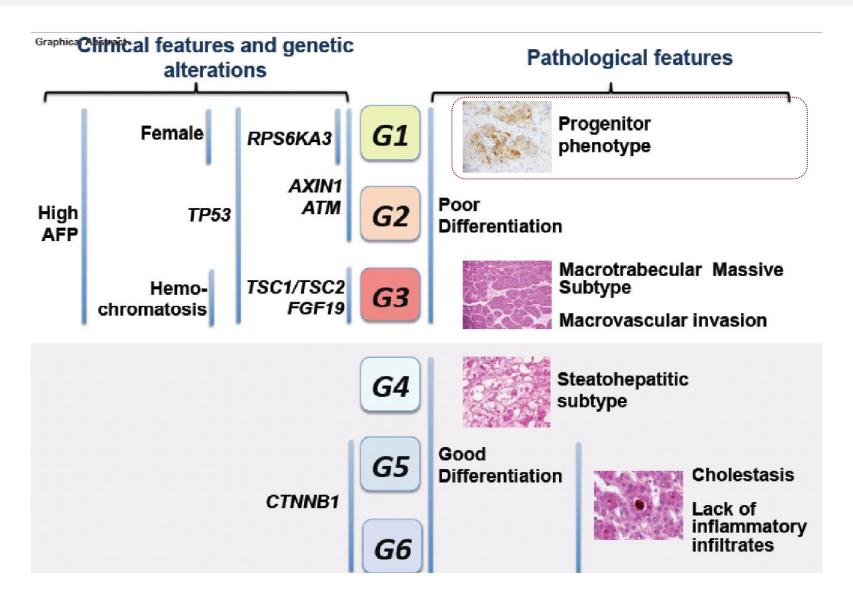
Ji Hae Nahm^{1,*}, Hyungjin Rhee^{2,3,4,*}, Haeryoung Kim⁵, Jeong Eun Yoo^{1,4,7}, Jee San Lee^{1,3,4}, Youngsic Jeon^{1,3,4}, Gi Hong Choi⁶ and Young Nyun Park^{1,3,4,7}

Histological Subtypes of HCC Are Related To Gene Mutations and Molecular Tumour Classification

Calderaro J, et al, J Hepatol 2017



Histological Subtypes of HCC Are Related To Gene Mutations and Molecular Tumour Classification



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Update on Precursor and Early Lesions of Hepatocellular Carcinomas

Young Nyun Park, MD, PhD





139 citation