

Predictive markers of Sorafenib sensitivity of HCC



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Semmelweis Symposium, Budapest

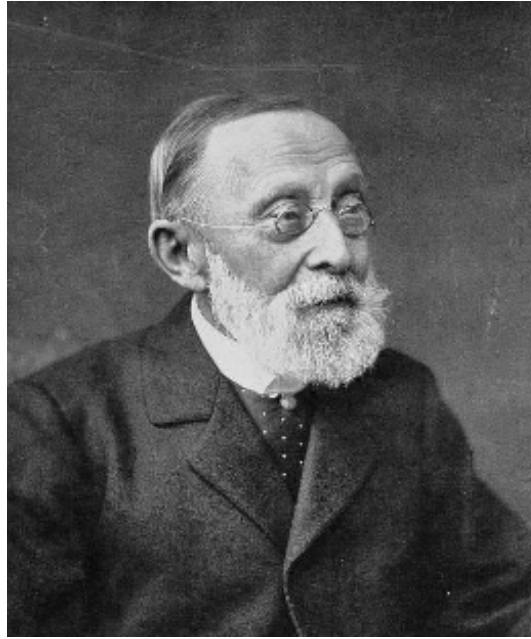
November 06.

2015



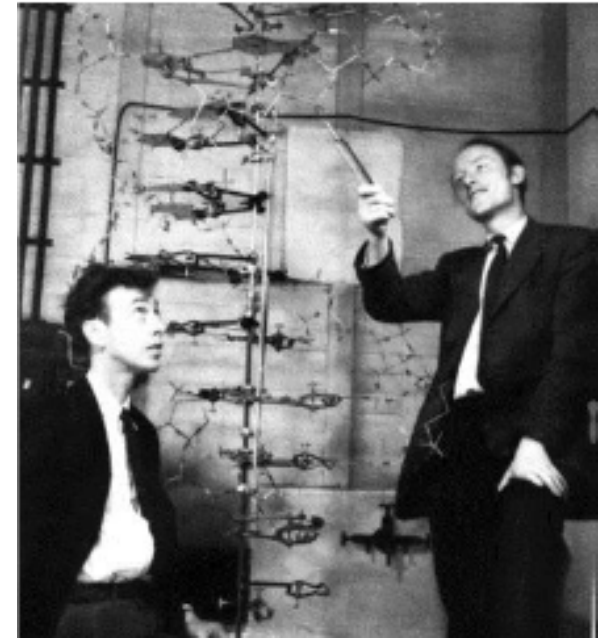
Morgagni, 1761

GI Diseases
erkezete



Virchow, 1858

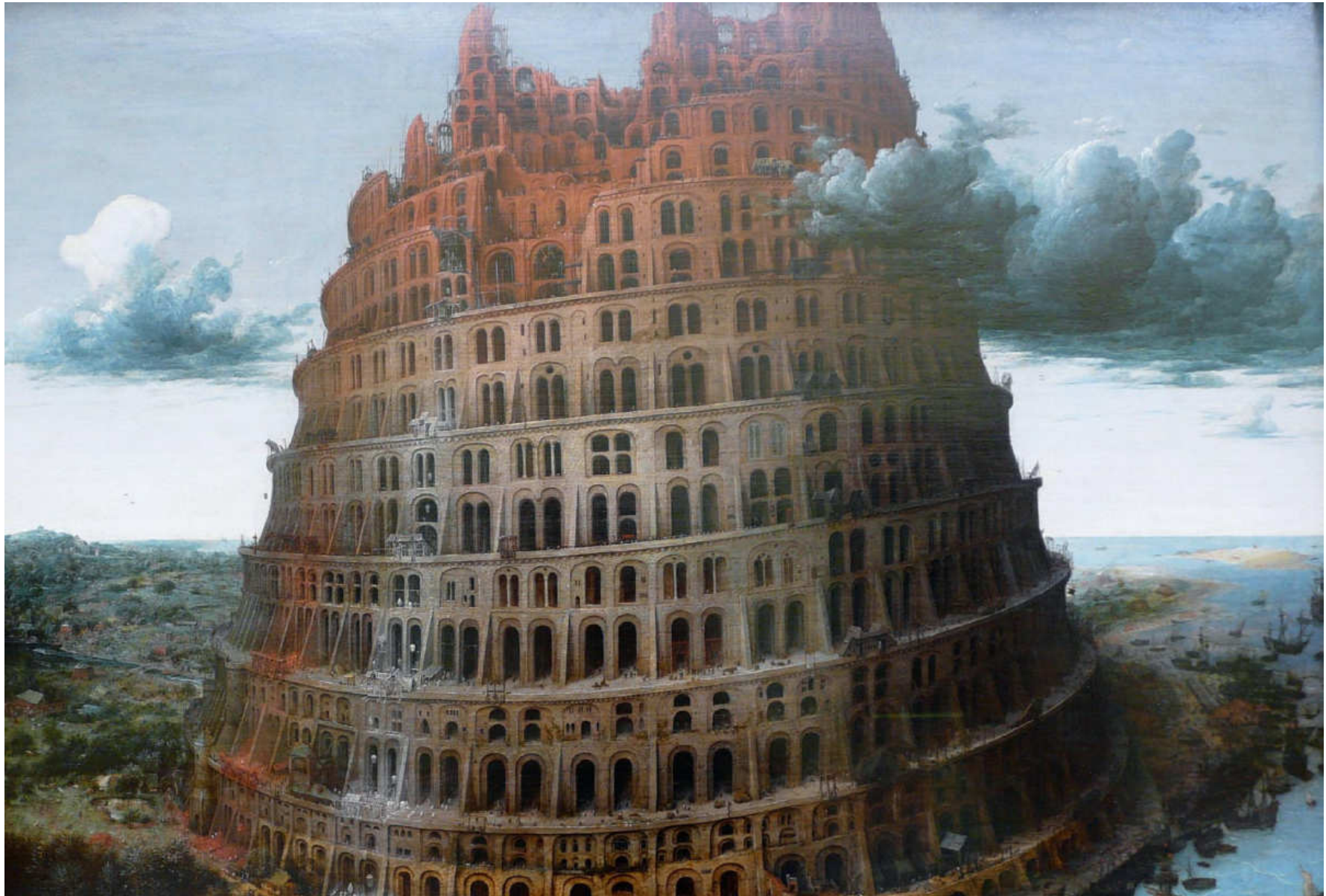
„Zellulärpathologie“



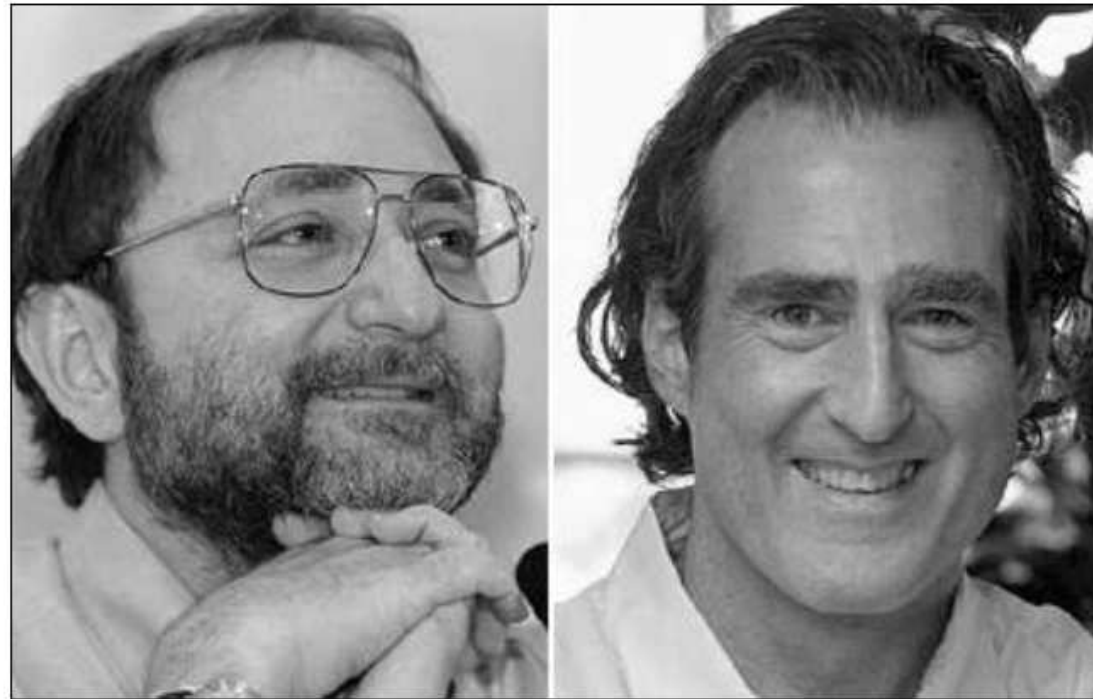
Watson & Crick, 1953

DNA structure

World of non-coding RNAs



World of interference . . .



Andrew Z. Fire

Nobel prize 2006

Craig C. Mello

...reported a potent gene silencing effect after injecting **double stranded RNA** into *C. elegans*...



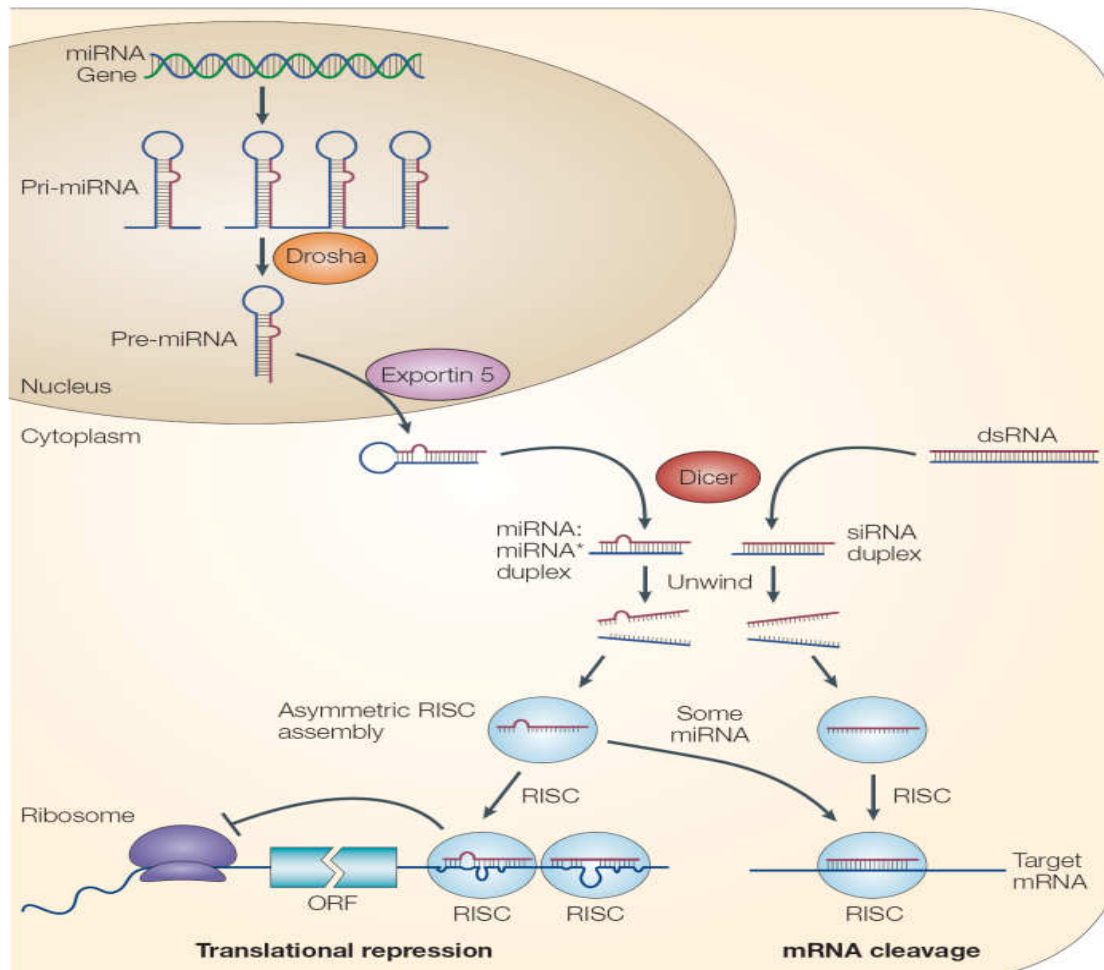
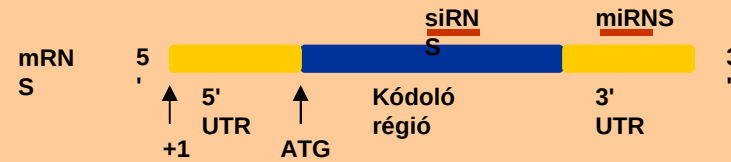
Fire A, et al - Nature 1998

RNS silencing – RNA interference

PATHOBIOLOGY - EXPRESSION PATTERN

DIAGNOSTICS

THERAPY



siRNS
microRNA
s
piwiRNAs

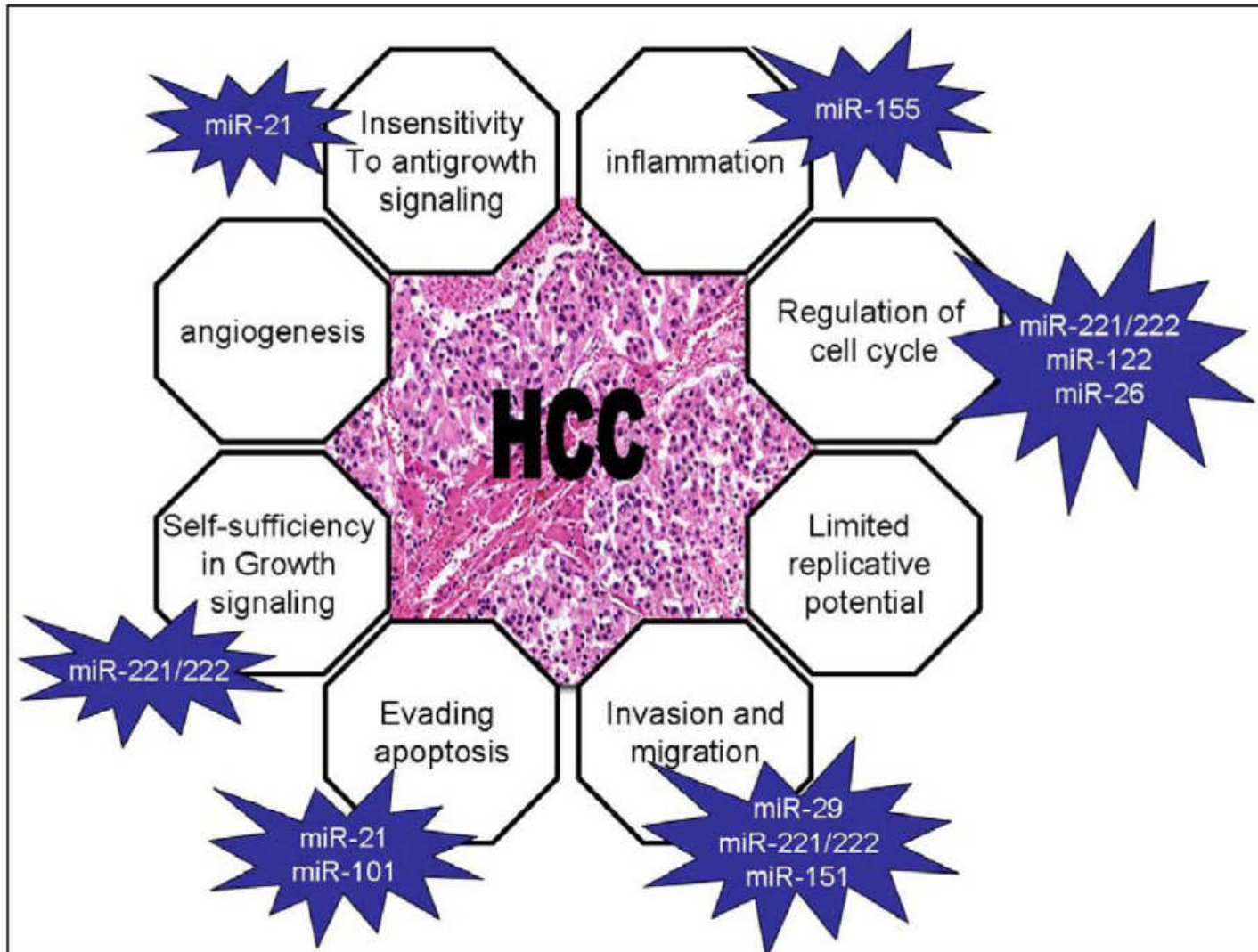
DNA

mRNA

protein

- 20-22 bp RNA
- Negative regulation
- Posttranscription level
- ~ 2000 mikroRNAs
- Normal cell function
- pathologic conditions
- characteristic miR profile





Braconi C. et al., Semin. Oncol., 2014
Cortez et al., Nat Rev Clin Oncol, 2011
Braconi C. et al., Semin. Oncol., 2011

Referen				
Autho				
Murakar				25
Pineau				
Gramant				1,
Li-Fu				1
Jiang				0,
Li				0c,
Su				1, 23,
Wang				
Connolly				6,
		miR-15a, miR-92	let-7a, miR-122	

Braconi C.et al., Semin. Oncol., 2014
 Cortez et al., Nat Rev Clin Oncol, 2011
 Braconi C.et al., Semin. Oncol., 2011

Proved or assumed biological effect of the investigated miRNAs

Oncogenic miRNAs

●	miR-17-5p	Proliferation
●	miR-18a	Proliferation, migration (member of the oncogenic miR-17-92 cluster)
●	miR-21	Proliferation, migration
●	miR-34a	Inhibits p53
●	miR-210	Proliferation, antiapoptotic
●	miR-221	Proliferation, invasion, antiapoptotic
●	miR-222	Proliferation, invasion, antiapoptotic
●	miR-224	Proliferation, migration

Reference miR

miR-140

Tumor suppressor miRNAs

●	miR-195	Proapoptotic
●	miR-214	Inhibits invasion, affects β -catenin pathway
●	miR-223	Inhibits proliferation

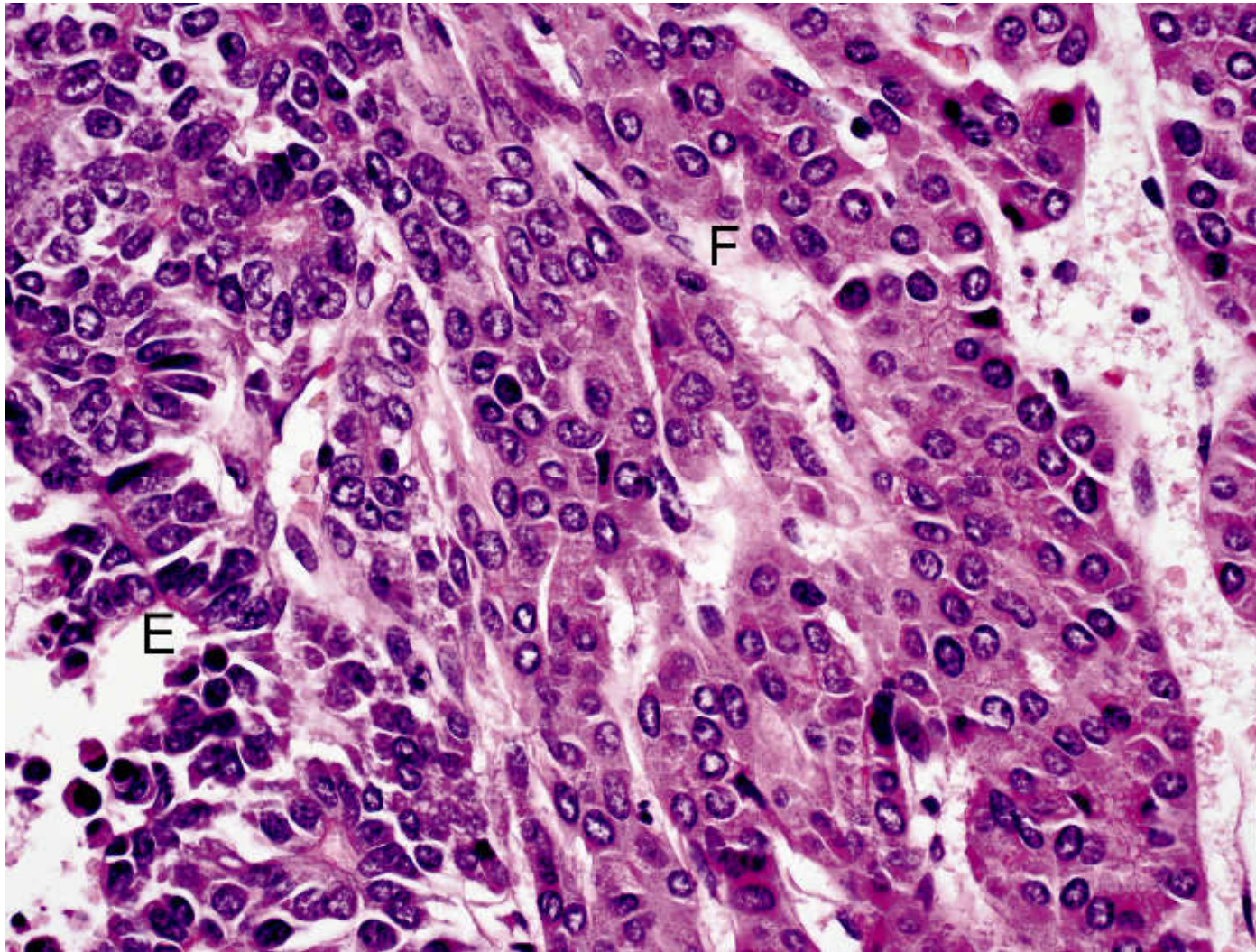
sensitizes for sorafenibin *vitro*^(1,2)

Liver characteristic miRNA

●	miR-122	Regulates fat metabolism, necessary to normal hepatocyte function Decreased cellular levels contribute to fibrosis, steatohepatitis and HCC
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Reference

1. Yang et al. 2013.
2. Bai et al. 2009.
3. Murakami et al. 2006.

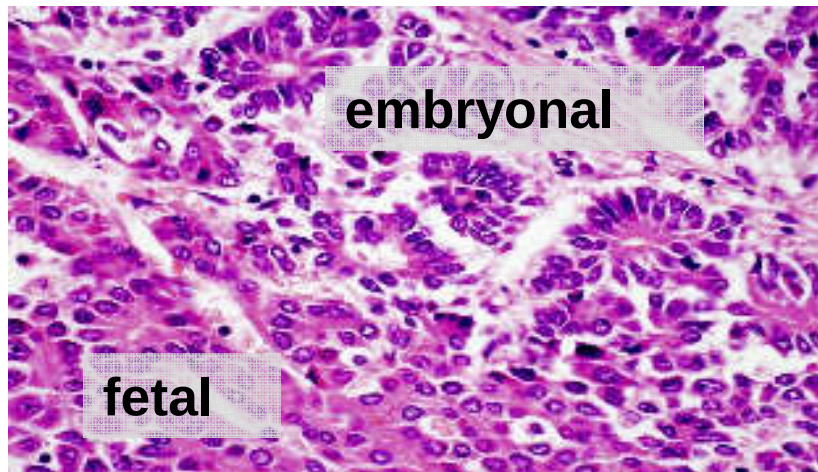


*„microRNA expression might predict prognosis of epithelial **hepatoblastoma**”*

Monika Gyugos¹, Gábor Lendvai¹, István Kenessey¹, Krisztina Schlachter¹, Judit Halász¹, Péter Nagy², Miklós Garami³, Zsuzsa Jakab³, Zsuzsa Schaff¹, András Kiss^{1#}, Virchows Archive, 2014

Clinical data

- ♦ 21 human epithelial hepatoblastoma (average: 45.89 months , 11/10 M/F ratio)
- ♦ Pure fetal: 12 cases, embrional/fetal: 9 cases. Overall considering more or less than 5 % fetal compartment 16 fetal and 9 embryonal cases were analysed.
- ♦ 16 non-tumorous surrounding liver.

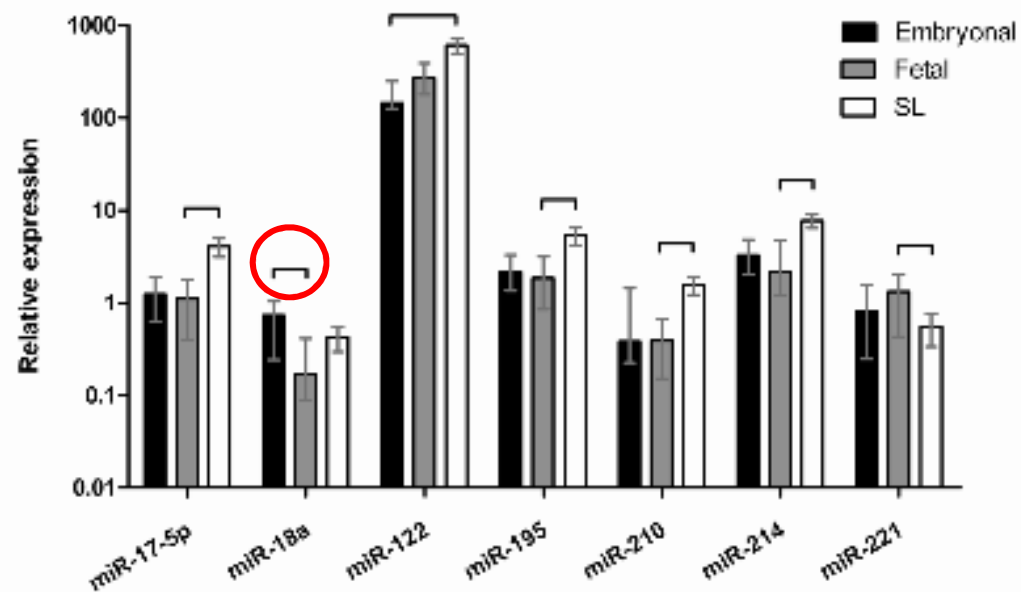
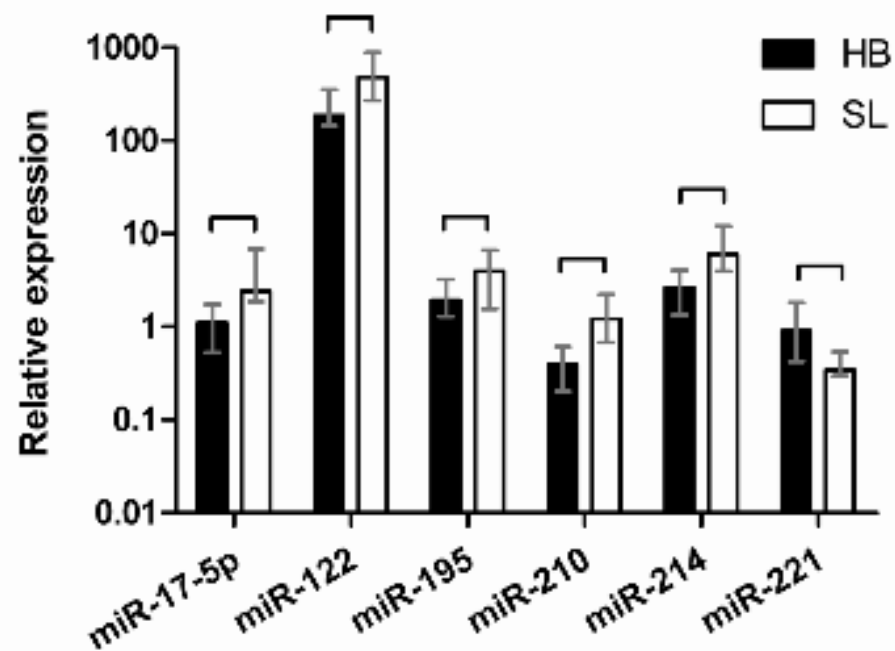


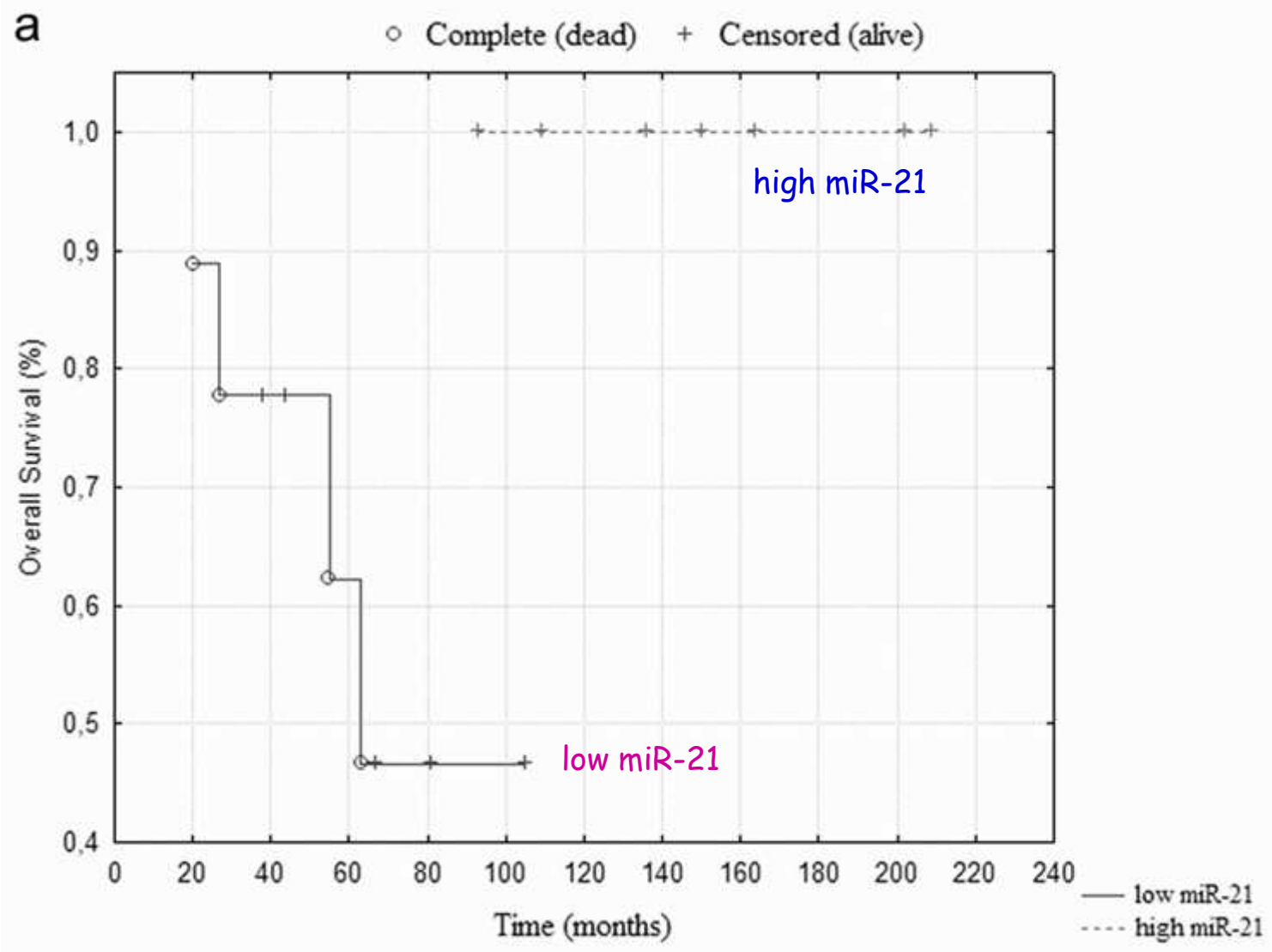
microRNA expression in HB

⊕ Patient's data indicating the available sample types and clinical outcome.

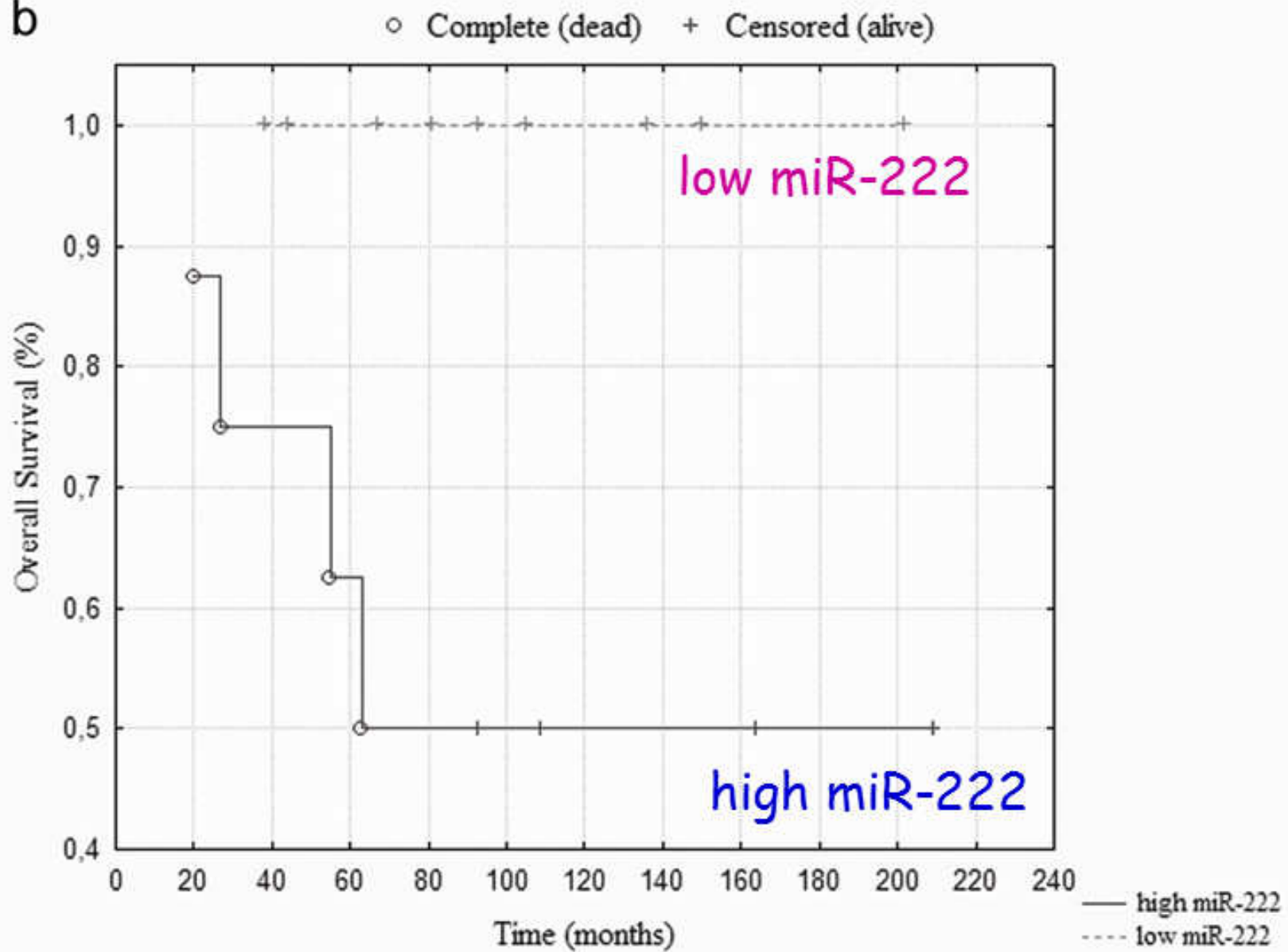
Cases	Gender	Age (year)	Tumor compartment n=23		Surrounding Liver	Sample/patient	Metastasis	Recidive	Death
1	male	0.36	F			1		Yes	Yes
2	female	1.44		E	SL	2			
3	male	10.14	F		SL	2		Yes	
4	male	5.14	F		SL	2	Lung	Yes	Yes
5	female	5.44	F		SL	2			
6	female	0.30	F		SL	2			
7	male	6.45	F		SL	2			
8	female	2.16	F	E		2			
9	male	3.12	F		SL	2			
10	male	2.40		E		1			
11	male	0.76	F		SL	2			
12	male	0.98	F		SL	2	Lung	Yes	
13	female	1.13	F	E		2			
14	male	7.66	F		SL	2			
15	female	4.76		E		1	Lung	Yes	Yes
16	female	15.82	F		SL	2	Lung	Yes	Yes
17	female	1.19		E	SL	2			
18	female	1.54	F		SL	2	Lung		
19	female	0.98		E	SL	2			
20	male	2.16	F	E	SL	3	Lung	Yes	Yes
Total:			15	8	15	38	6	7	5

F: fetal, E: embryonal, SL: surrounding liver

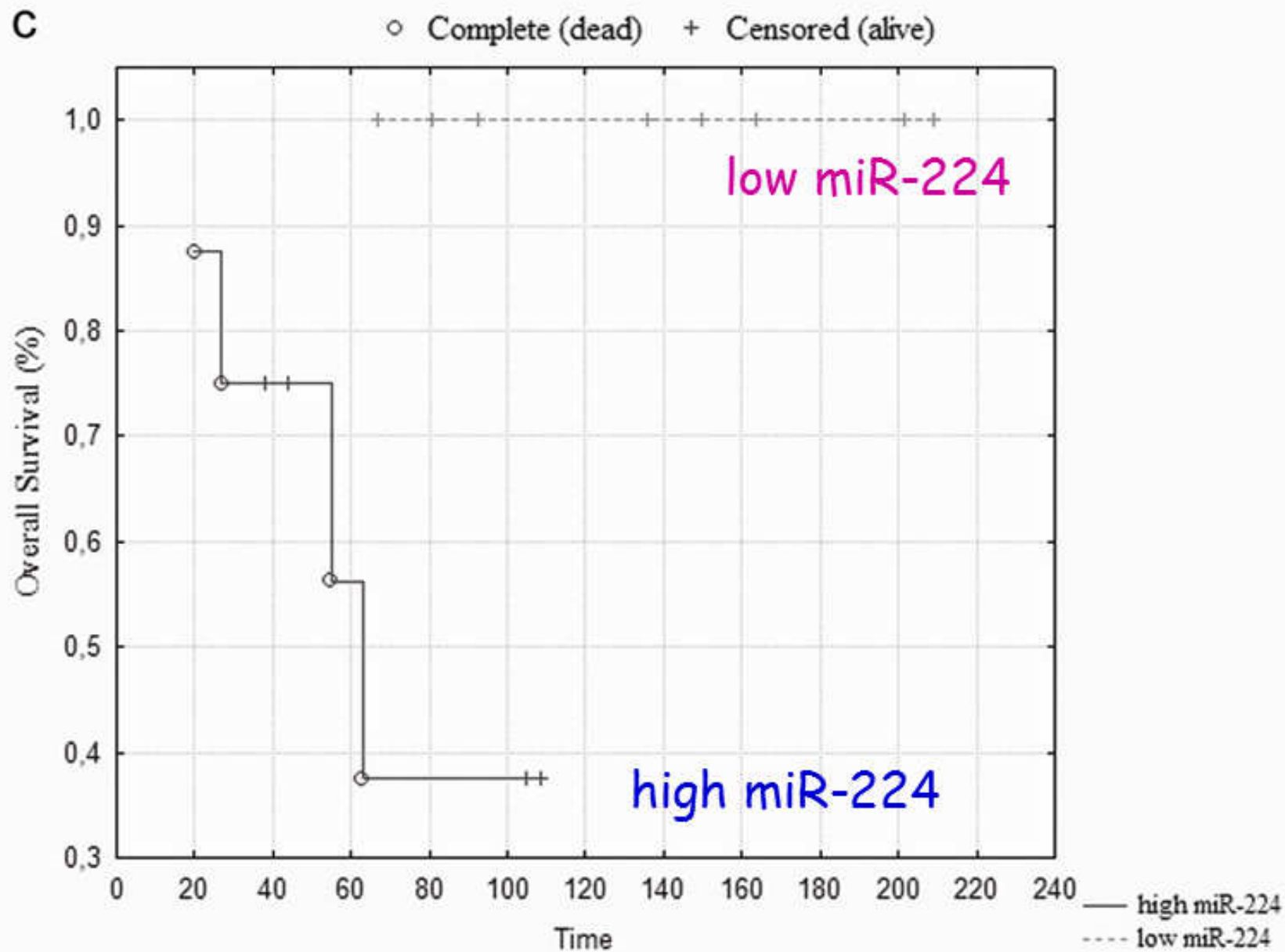


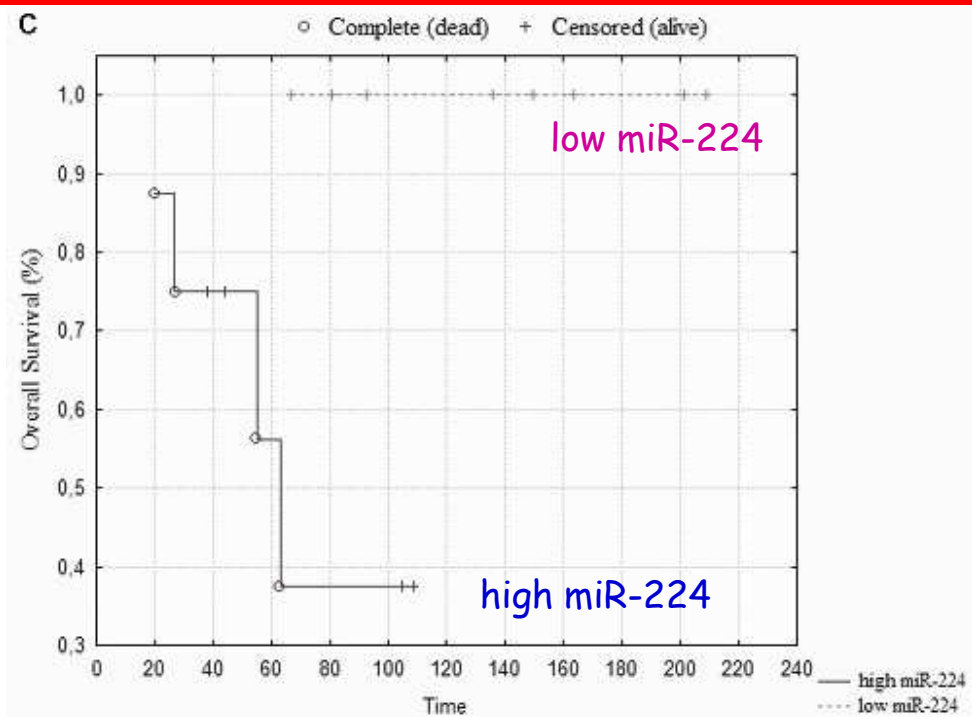
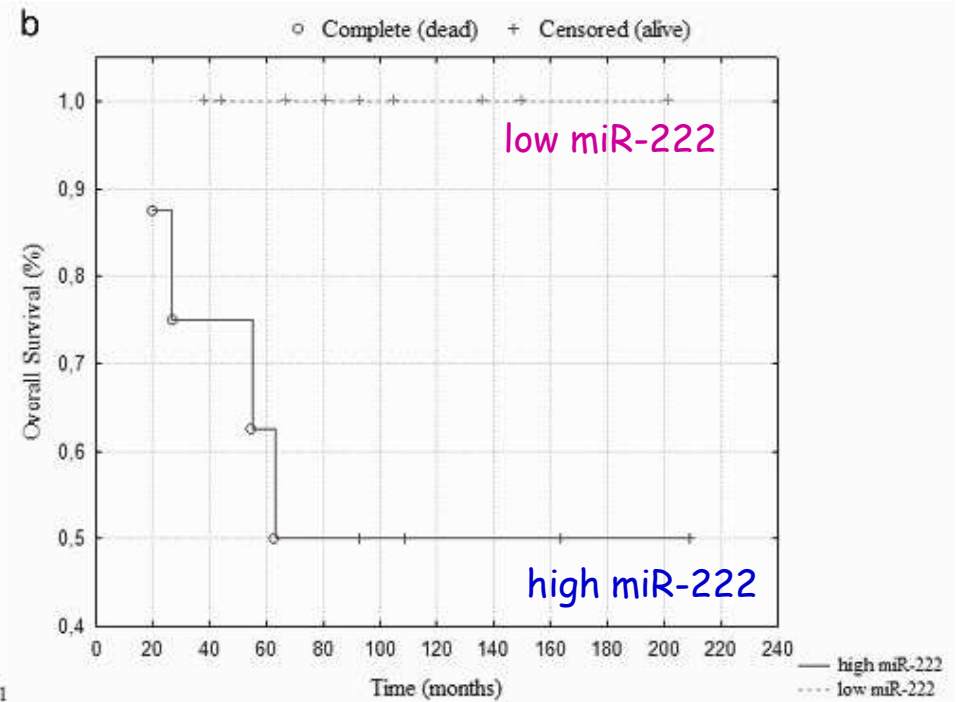
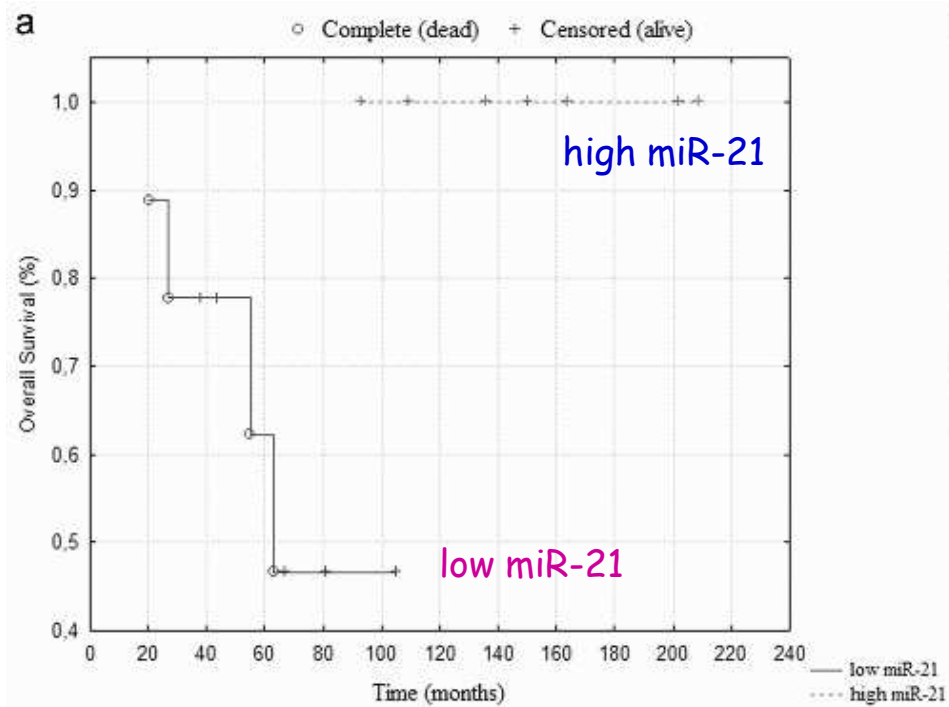


b



C





microRNA expression in HB

- Histological subtypes of HB did not show correlation with survival.
- Higher expression of miR-18a was detected in the embryonal than in the fetal HB component. Further, lower expression of miR-17-5p, miR-122, miR-195, miR-210 and miR-214 and higher expression of miR-221 was found in epithelial components of HB than in SL.
- Furthermore, **high miR-21** and **low miR-222 and miR-224 levels** were associated with increased OS of SIOPEL-treated HB patients.
- These results suggest that miRNA profiling is of potential use as a diagnostic and predictive tool in HB.

„microRNA expression might predict prognosis of epithelial hepatoblastoma”

Monika Gyugos¹, Gábor Lendvai¹, István Kenessey¹, Krisztina Schlachter¹, Judit Halász¹, Péter Nagy², Miklós Garami³, Zsuzsa Jakab³, Zsuzsa Schaff¹, András Kiss^{1#}, Virchows Archive, 2014

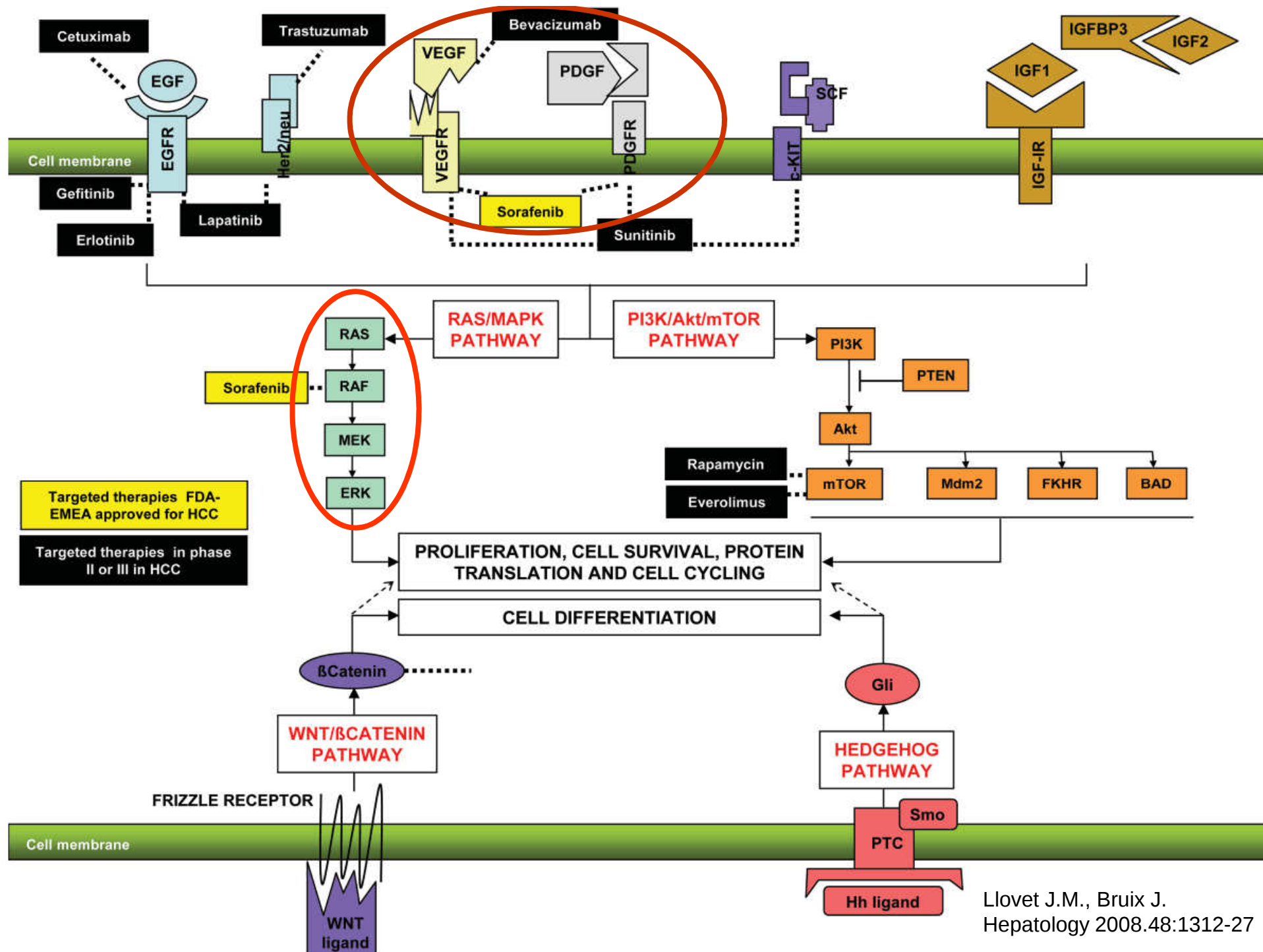
HCC and sorafenib

- Sorafenib (Nexavar®)

- Multikinase inhibitor (cRaf, bRaf, VEGFR-2, VEGFR-3, PDGFR- β , c-kit, Flt3)
- Irresectable cases and in case of recurrence
- „In patients with advanced HCC, median survival and the time to radiologic progression were nearly **3 months longer** for patients treated with sorafenib than for those given placebo.”
(SHARP trial 2008)

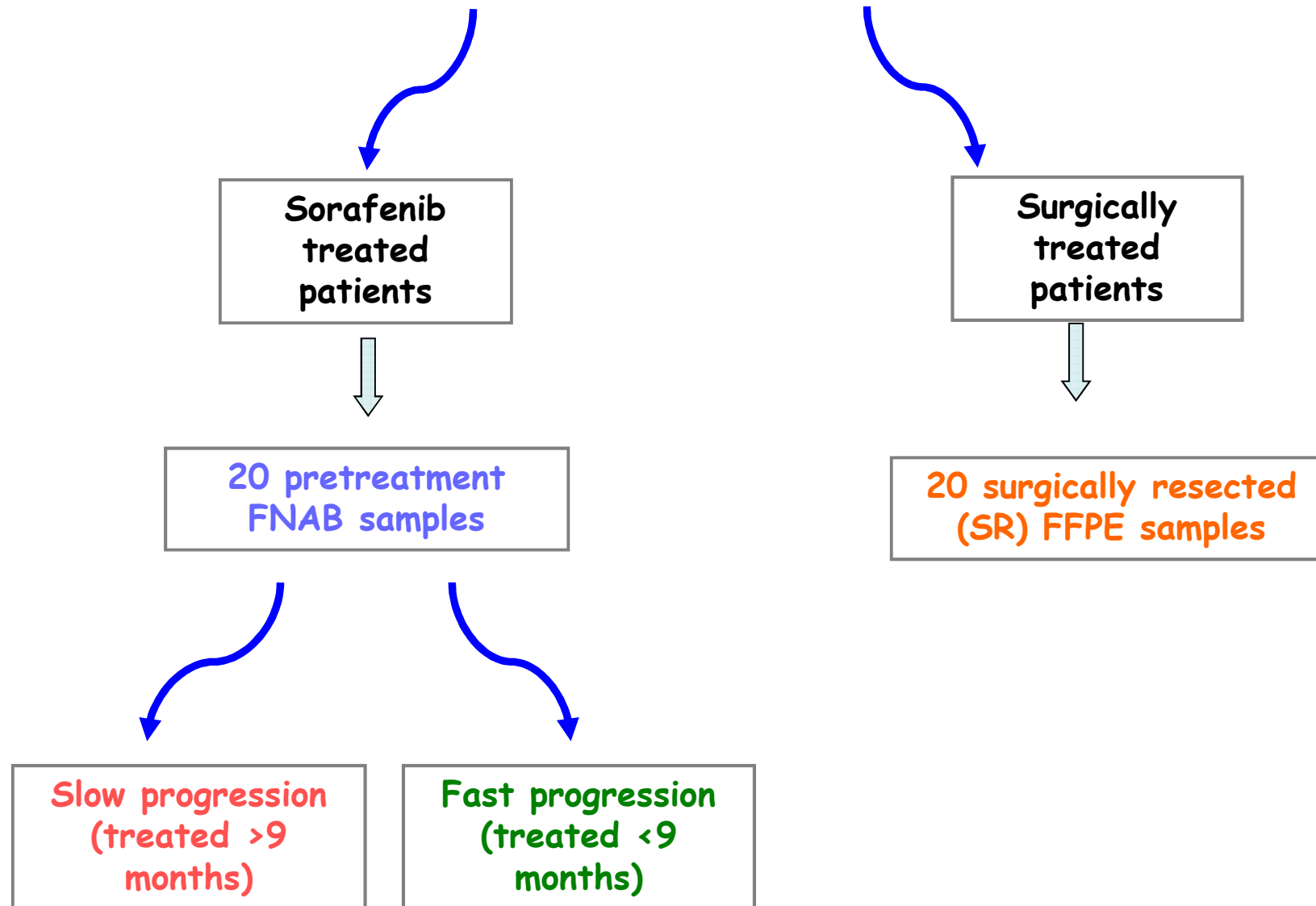
Disease-control rate: 43%

$$\text{DCR} = \text{SD} + \text{PR} + \text{CR}$$



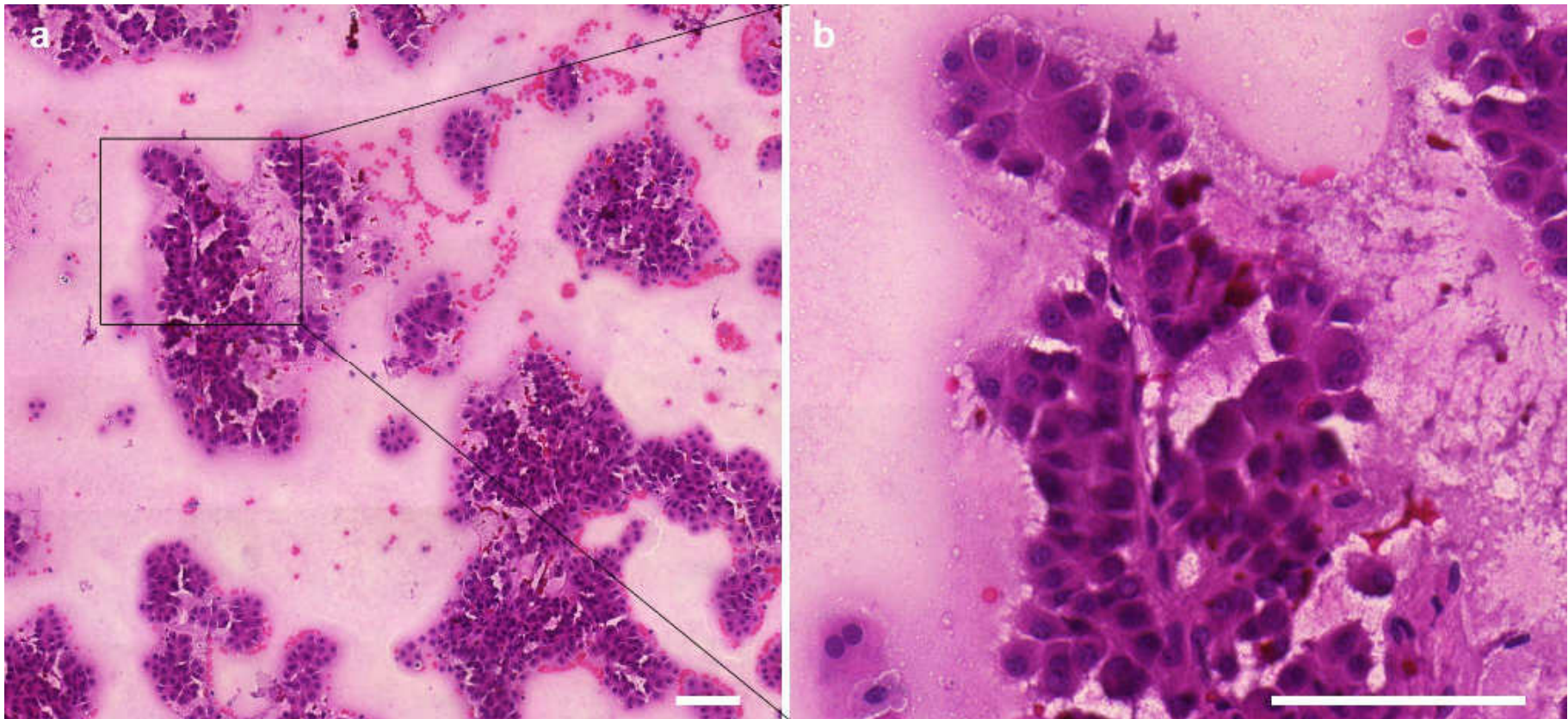
Llovet J.M., Bruix J.
Hepatology 2008.48:1312-27

Patients and material



Sorafenib treated HCC patients and FNAB samples

Twenty sorafenib treated HCC patients (Szt. Istvan - Szt. László Hospital, Oncology Department) pretreatment FNAB samples at 2. Dept. of Pathology



Representative image of a hepatocellular carcinoma sample obtained by fine needle aspiration. Irregularly shaped tumor aggregates with transgressing endothelium can be seen. Scale bars 100 mm.

miRNS expression and clinicopathological parameters

Patients were divided into „high ” and „low miR expression” groups according to medián values of relative expression.

<i>Fisher exact teszt $p = 0,003$</i>		miR-17-5p	
		high	low
ECOG	0	10	3
	1	0	7

Increased miR-17-5p expression showed correlation with better ECOG performace status

<i>Fisher exact teszt $p = 0,023$</i>		miR-214	
		high	low
Tumor méret	>5 cm	2	8
	≤5 cm	8	2

Increased miR-214 expression revealed correlation with smaller tumor size.

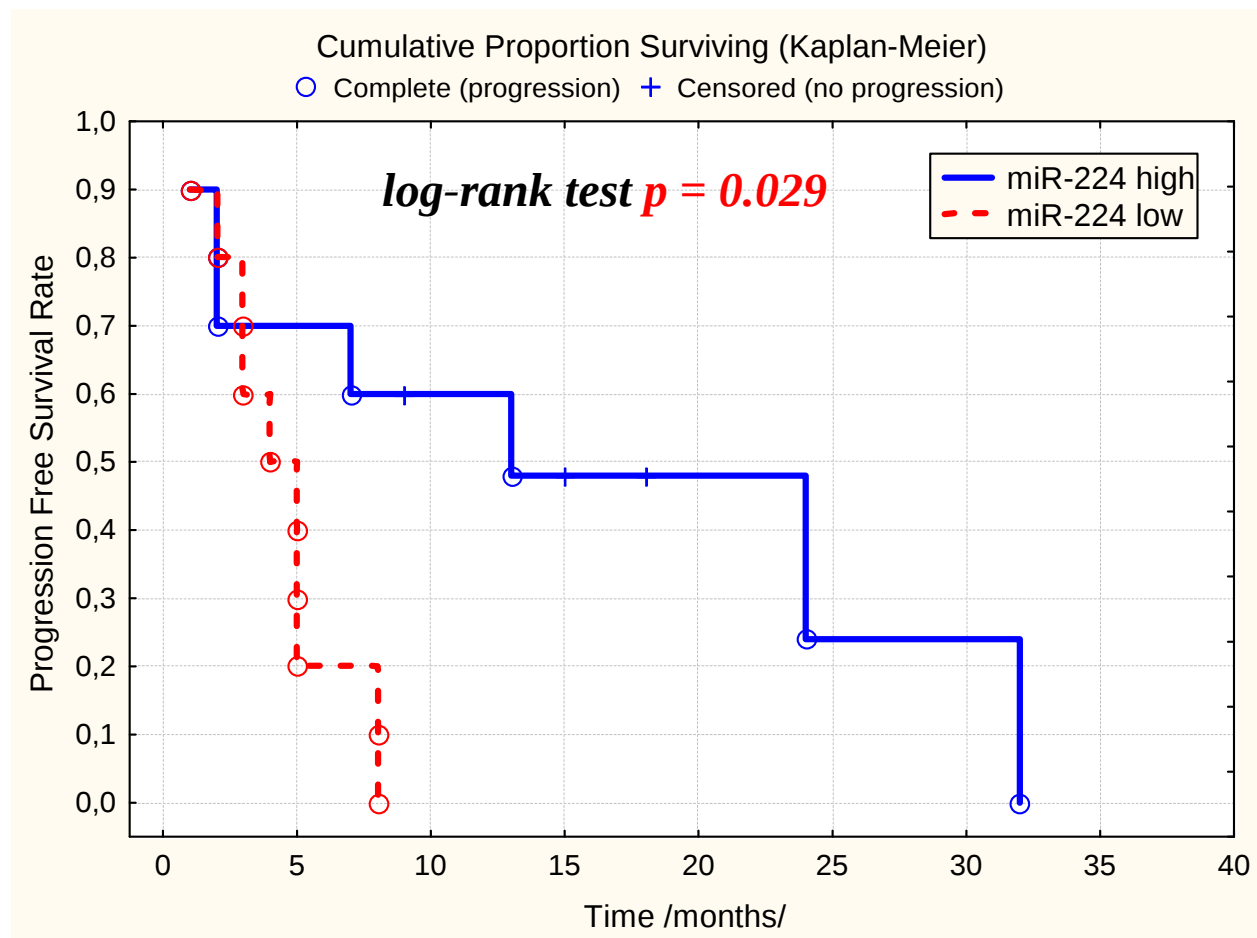
→ in corcordance with the literature:
miR-214 is a know tumor suppressor, whic inhibits the growth of HCC cells *in vitro*⁽¹⁾.

Reference

1. Wang et al. 2012. Biochem Biophys Res Commun . 428: 525-31.

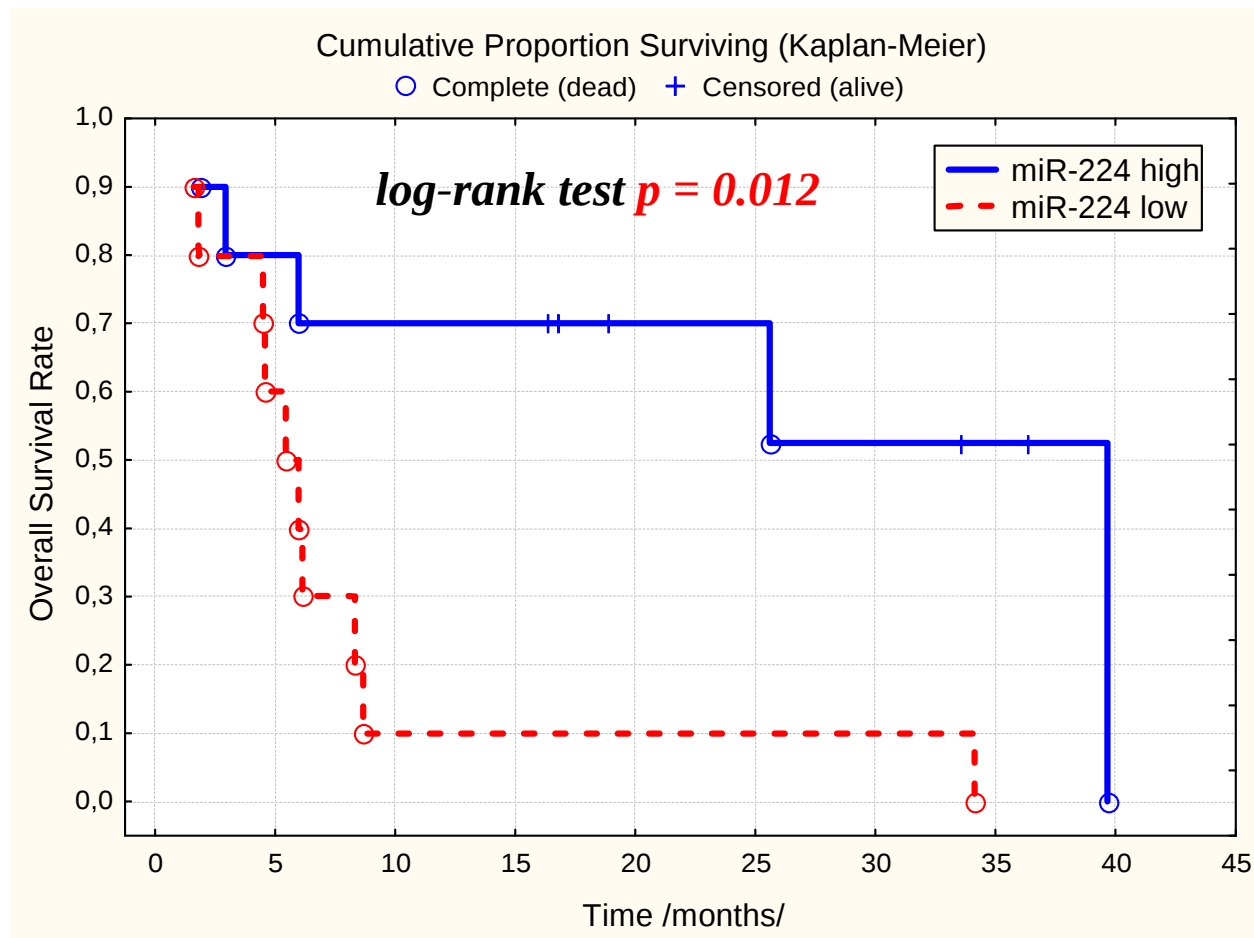
Pretreatment **miR-224 expression** and **disease outcome**

Progression-free survival



Pretreatment **miR-224 expression** and **disease outcome**

Overall survival



Validated and potential targets of miR-224

- API5; Bcl2; MAPK1; SMAD4

→ miR-224 **regulates apoptosis in** HCC cells

- miR-224 is one of the most frequently overexpressed oncomiR in HCC
- Increased miR-224 expression is associated with worse prognosis HCC patients with resected tumor as well as in cervix carcinoma and glioma

→ Putative miR-224 targets are : PDGFR- α and - β (Dweep et al. 2011, Murakami et al., 2006)

- PDGFR- β → **known target of sorafenib**

→ Chu et al. 2013. JECRC 32:16

* biopsy material of 93 HCC patients (65 sorafenib treated)

* increased **PDGFR- β expression is associated with poor prognosis**



Expression and prognostic value of VEGFR-2, PDGFR- β , and c-Met in advanced hepatocellular carcinoma

De Meng Zhu^{1,2}, Li-Li Liu^{1,2}, Bo Zhang¹, Wei Wang¹, Min-Jie Cheng¹, Li-Jian Liu¹, Chang-Li Chen^{1,2}, Li-Li Liu¹, Xian-Xian Liu^{1,2}, Li-Li Liu^{1,2}, Jun Wang¹, Jie-Jie Chen¹ and Jian-Wei Xie^{1*}

Abstract

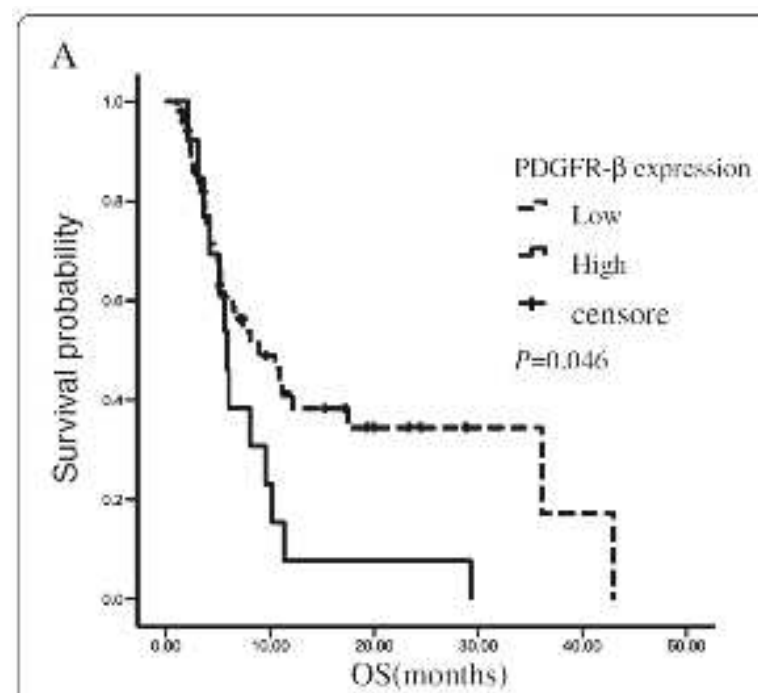
Background: We explore the clinical and prognostic significance of expression of vascular endothelial growth factor receptor (VEGFR-2), platelet-derived growth factor receptor (PDGFR- β), and c-Met in patients with hepatocellular carcinoma (HCC).

Methods: The expression of VEGFR-2, PDGFR- β , and c-Met was determined by immunohistochemical examination of the tissues of 141 HCC patients. The relationships of these markers with clinicopathological factors and prognosis were then analyzed.

Results: High expression of VEGFR-2, PDGFR- β , and c-Met was found in 103 (73%), 103 (73%), and 103 (73%) patients, respectively. Expression of VEGFR-2 correlated with gender ($P = 0.001$), tumor size ($P = 0.001$), tumor stage ($P = 0.001$), degree of tumor differentiation ($P = 0.001$), and tumor grade ($P = 0.001$). Expression of PDGFR- β correlated with a pathological level ($P = 0.001$), tumor size ($P = 0.001$), and hepatic metastasis ($P = 0.001$). No significant correlation was identified between expression of c-Met and clinicopathological factors. Expression of VEGFR-2 correlated with overall survival ($P = 0.001$) and expression of c-Met correlated with progression-free survival ($P = 0.001$).

Conclusions: We found that in patients with HCC, high expression of VEGFR-2 correlated with tumor size and hepatic metastasis. High expression of PDGFR- β was associated with tumor grade. High expression of c-Met was associated with tumor size and tumor grade.

Keywords: Hepatocellular carcinoma, VEGFR-2, PDGFR- β , c-Met, survival analysis, prognosis



RESEARCH ARTICLE

Open Access



Functional microRNA high throughput screening reveals miR-9 as a central regulator of liver oncogenesis by affecting the PPARA-CDH1 pathway

Alexandra Drakaki^{1,2}, Maria Hatzia Apostolou³, Christos Polytarchou³, Christina Vorvis³, George A. Poultsides⁴, John Souglakos², Vassilis Georgoulas² and Dimitrios Iliopoulos^{3*}

Abstract

Background: Hepatocellular carcinoma (HCC) is the second leading cause of cancer-related deaths, reflecting the aggressiveness of this type of cancer and the absence of effective therapeutic regimens. MicroRNAs have been involved in the pathogenesis of different types of cancers, including liver cancer. Our aim was to identify microRNAs that have both functional and clinical relevance in HCC and examine their downstream signaling effectors.

Methods: MicroRNA and gene expression levels were measured by quantitative real-time PCR in HCC tumors and controls. A TargetScan algorithm was used to identify miR-9 downstream direct targets.

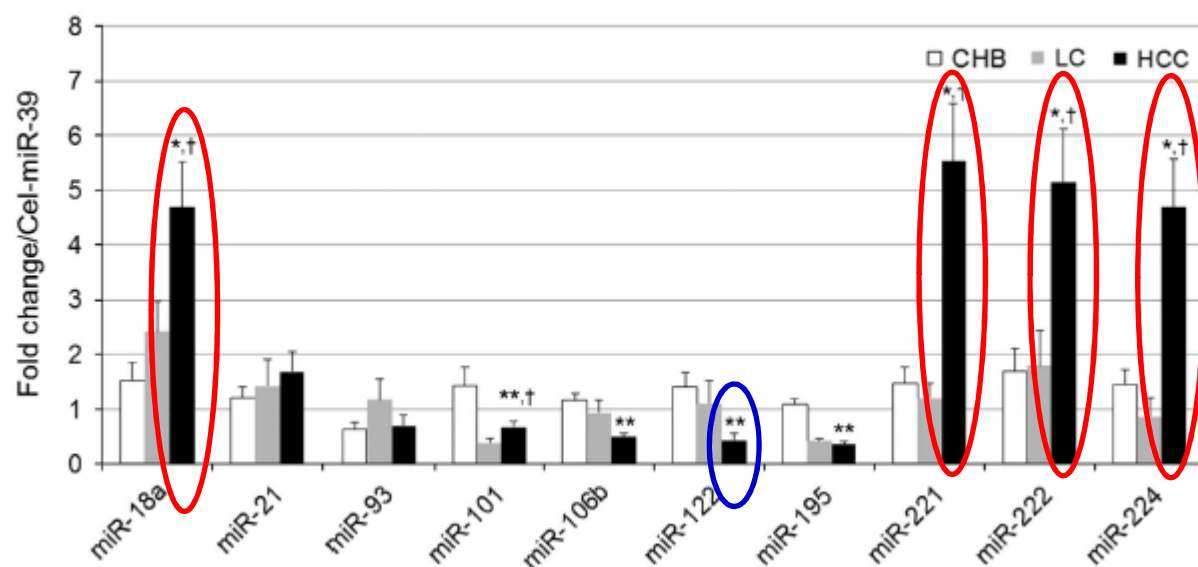
Results: A high-throughput screen of the human microRNAome revealed 28 microRNAs as regulators of liver cancer cell invasiveness. MiR-9, miR-21 and miR-224 were the top inducers of HCC invasiveness and also their expression was increased in HCC relative to control liver tissues. Integration of the microRNA screen and expression data revealed miR-9 as the top microRNA, having both functional and clinical significance. MiR-9 levels correlated with HCC tumor stage and miR-9 overexpression induced SNU-449 and HepG2 cell growth, invasiveness and their ability to form colonies in soft agar. Bioinformatics and 3'UTR luciferase analyses identified E-cadherin (CDH1) and peroxisome proliferator-activated receptor alpha (PPARA) as direct downstream effectors of miR-9 activity. Inhibition

Serum exosomal microRNAs as novel biomarkers for hepatocellular carcinoma

Won Sohn^{1,4}, Jonghwa Kim^{1,4}, So Hee Kang¹, Se Ra Yang¹, Ju-Yeon Cho¹, Hyun Chin Cho², Sang Guon Shim² and Yong-Han Paik^{1,3}

Recent studies have shown that circulating microRNAs are a potential biomarker in various types of malignancies. The aim of this study was to investigate the feasibility of using serum exosomal microRNAs as novel serological biomarkers for hepatocellular carcinoma (HCC) in patients with chronic hepatitis B (CHB). We measured the serum exosomal microRNAs and serum circulating microRNAs in patients with CHB ($n=20$), liver cirrhosis (LC) ($n=20$) and HCC ($n=20$). Serum exosomal microRNA was extracted from 500 μ l of serum using an Exosome RNA Isolation kit. The expression levels of microRNAs were quantified by real-time PCR. The expression levels of selected microRNAs were normalized to *Caenorhabditis elegans* microRNA (Cel-miR-39). The serum levels of exosomal miR-18a, miR-221, miR-222 and miR-224 were significantly higher in patients with HCC than those with CHB or LC ($P<0.05$). Further, the serum levels of exosomal miR-101, miR-106b, miR-122 and miR-195 were lower in patients with HCC than in patients with CHB ($P=0.014$, $P<0.001$, $P<0.001$ and $P<0.001$, respectively). There was no significant difference in the levels of miR-21 and miR-93 among the three groups. Additionally, the serum levels of circulating microRNAs showed a smaller difference between HCC and either CHB or LC. This study suggests that serum exosomal microRNAs may be used as novel serological biomarkers for HCC.

Experimental & Molecular Medicine (2015) 47, e184; doi:10.1038/emmm.2015.68; published online 18 September 2015



Conclusions

- microRNAs could be investigated in archive FNAB cytology samples
- microRNAs are potential predictive factors
- Pretreatment miR-224 level might bear with predictive value regarding to therapeutic response in HCC patients treated with sorafenib.



**Thank you
attention !**



for your



Thank you for your attention !

Prof. Dr. Zsuzsa Schaff

- Dr. Gyöngyösi Benedek
- Dr. Krisztina Schlachter
- Dr. Gábor Lendvai
- Monika Gyugos
- Dr. Balázs Járay
- Dr. István Kenessey
- Dr. Eszter Székely



- Prof. Dr. László Harsányi
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- Dr. Attila Szijártó
- Prof. Dr. György Bodoky
- Dr. Éva Végh
- Dr. Miklós Garami
- Dr. Zsuzsa Jakab

