Ready to use miRNA Probes

- Hsa-miR-1
- Hsa-miR-21
- Hsa-miR-146a
- Hsa-miR-150
- Hsa-miR-155
- Hsa-miR-222
- Hsa-miR-328
- Scramble
- U6
- Hsa-Let-7a
- Hsa-miR-10b
- Has-miR-125b
- Hsa-miR-17
- Has-miR-144
- Hsa-miR-145
- Hsa-miR-196a
- Hsa-miR-200a
- Hsa-miR-200b
- Hsa-miR-216a
- Hsa-miR-204
- Hsa-miR-205
- Hsa-miR-221
- Hsa-Let-7c
- Hsa-miR-7e
- Hsa-miR-9
- Hsa-miR-21-3p
- Hsa-miR-27a
- Hsa-miR-96 B37
- Hsa-miR-106a
- Hsa-miR-126
- Hsa-miR-1285
- Hsa-miR-141
- Hsa-miR-143
- Hsa-miR-147b
- Hsa-miR-151a-3p
- Hsa-miR-152
- Hsa-miR-199a
- Hsa-miR-203a
- Hsa-miR-222
- Hsa-miR-335
- Hsa-miR-375
- Hsa-miR-378
- Hsa-miR-423-3P
- Hsa-miR-622
- Hsa-miR-641

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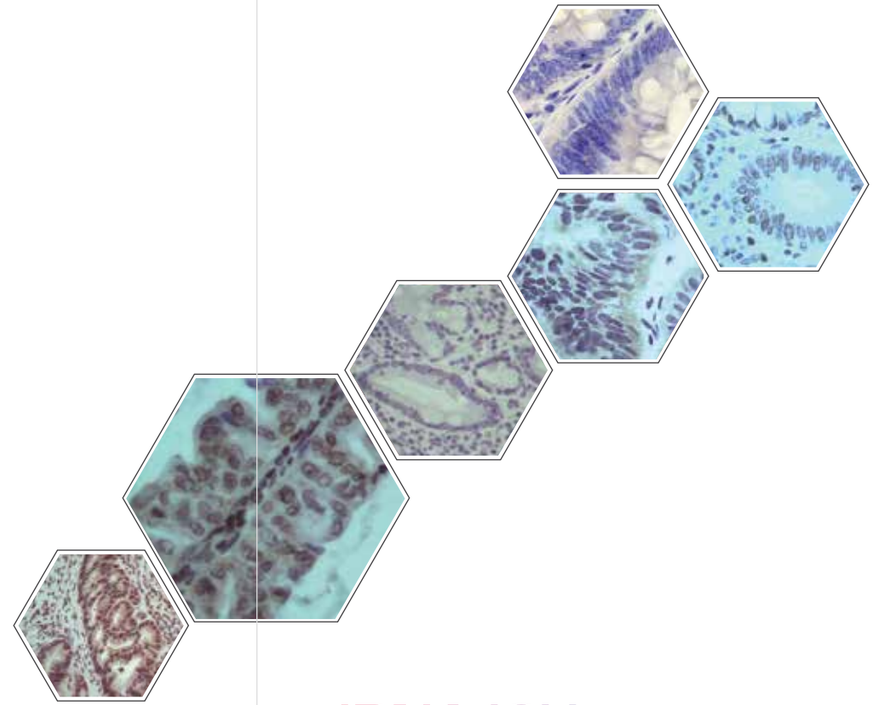

miRNA ISH characterization of Cancer of Unknown Primary (CUP) in FFPE

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[265] miRNA Expression Pattern in Predicting BRCA Mutation Status in Invasive Breast Carcinoma

Sambit K Mohanty, Georgia Liles, Suresh Thakur, Snigdha S Sahu, Krishan Kalra, Mahul B Amin, Raju K Pillai, Farnaz Dadmanesh. Cedars-Sinai Medical Center, Los Angeles, CA; BioGenex Laboratories, Fremont, CA

Background:

MicroRNAs (miRNAs) are short, non-coding RNAs involved in post-transcriptional regulation of gene expression by affecting the stability and translation of mRNAs. It has been shown that miRNAs are aberrantly expressed in breast cancers (BC). Three miRNAs have been associated with breast tumorigenesis: miR21, let-7a and miR17. Although there is limited data for the utility of immunohistochemical (IHC) markers for predicting BRCA mutation status in BC, there is no data available for in situ expression of miRNA within FFPE tissue of BRCA-related BC. Thus, we sought to correlate in situ expression of miR21, let-7a and miR17 with BRCA mutation status in invasive BC.

Design:

We selected 13 cases of invasive ductal carcinoma: 6 BRCA and 7 sporadic. In situ hybridization using FAM-labeled miRNA probes (BioGenex) for let-7a, miR21 and miR17 was performed. The staining results were evaluated in the tumor and benign epithelial and myoepithelial nuclei as weak, moderate or strong; percent positivity was estimated as focal (<50%) or diffuse (>50%).

Results:

Tumor expression of miRNA is summarized in Figure 1

Categories	BRCA type	miR-let-7a	miR21	miR17	Grade	Molecular subtype	IMP3	CK8/18	CK14
BRCA (n=6)	BRCA1(5) BRCA2(1)	"3/6 (50%) (Focal & weak=2) Focal & moder-ate=1)"	"1/6 (17%) (Focal & moder-ate)"	"1/6(17%) (Focal & weak)"	"I=1 II=2 III=3"	Basal=1 Luminal=5	2/6 (30%)	3/6 (50%)	2/6 (30%)
"Sporadic (n=7)"	Mutation Negative	"7/7 (100%) (Diffuse & strong=5 Focal & strong=2)"	"7/7 (100%) (Diffuse & strong)"	"7/7 (100%) (Focal & weak=3 Diffuse and strong=4)"	"II=4 III=3"	Basal=2 Luminal=5	1/7 (14%)	7/7 (100%)	3/7 (43%)

In the sporadic group, the expression of miR21, miR17, and let-7a in normal epithelium and myoepithelium is strong and uniform, whereas the expression is focal and weak in the BRCA group.

Conclusions:

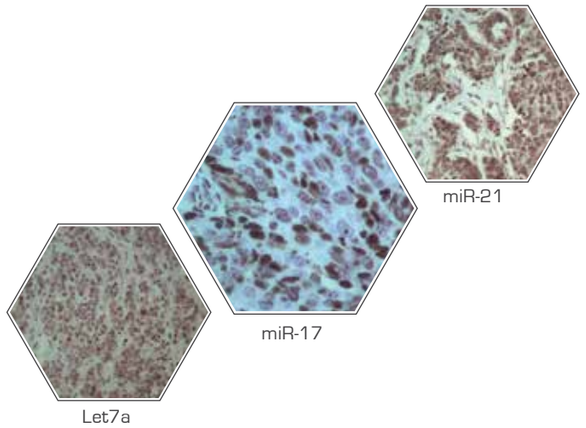
In contrast to microarray-based miRNA studies, we evaluate in situ expression of miRNA within FFPE BC tissue, where histologic features are well-maintained. Compared to sporadic BC, expression of let-7a, miR21 and miR17 is downregulated in BRCA-related BC. Of note, both of the miR21 and let-7a + cases in the BRCA group are Luminal A, suggesting an estrogen receptor linkage. Underexpression of these miRNA markers may favor a BRCA-mutated phenotype in BC and support an alternative pathway of oncogenesis in BRCA-related BC. Ongoing studies in a larger cohort are underway to fully assess the potential of these miRNAs in predicting BRCA mutation status. The ability to interpret miRNA expression patterns may help more accurately determine patients who require BRCA genetic testing, which is both costly and time consuming.

Category: Breast Pathology

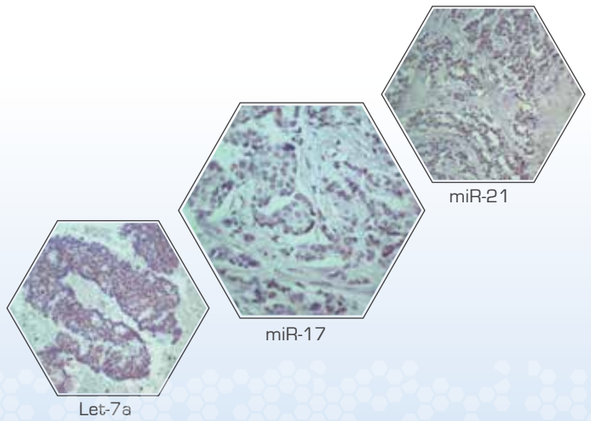
Tuesday, March 4, 2014 9:30 AM
Poster Session III # 11, Tuesday Morning
USCAP 2014

Sporadic Breast Cancer vs. BRCA Mutated Breast Cancer

Sporadic Breast Cancer



BRCA Mutated Breast Cancer



[1852] Differential Expression of miR-196a and miR-216a in Cholangiocarcinoma and Pancreatic Ductal Adenocarcinoma

Jinping Lai, Brent K Larson, Suresh Thakur, Snigdha S Sahu, Sunil Agarwal, Maha Guindi, Krishan Kalra, Deepti Dhall, Raju K Pillai. Cedars-Sinai Medical Center, Los Angeles, CA; BioGenex Inc, Fremont, CA

Background:

Cholangiocarcinomas (CC) and pancreatic ductal adenocarcinomas (PDAC) are virtually indistinguishable histologically and have overlapping immunohistochemical profiles. MicroRNAs (miRNAs) are short non-coding RNAs involved in post-transcriptional regulation of gene expression. Dysregulation of miRNAs and their cognate targets are increasingly implicated in many cancers. Use of microRNA in diagnostic applications has been limited by inability to determine expression patterns in situ on a cellular level, as profiling-based strategies using tissue homogenates may not adequately resolve expression differences in tumor microenvironment.

Design:

13 cases of CCs (12 intrahepatic and 1 extrahepatic) and 18 cases of PDACs were used in the study. Cases were subjected to in situ hybridization (ISH) using FAM-labeled miRNA probes (BioGenex) for miR-21, miR-10b, miR-196a and miR-216a followed by super sensitive ISH Detection Kit (BioGenex, DF400-YAX). Nuclear staining was evaluated semi-quantitatively by intensity (low, no or weak stain; high, moderate to intense stain). Statistical analysis was performed by using Fisher's exact two-tailed test.

Results:

High level expression of both nuclear miR-196a and miR-216a expression was seen in 85% (11/13) of CC. PDAC cases showed high level expression of nuclear miR-196a and miR-216a expression in 22% (4/18) and 28% (5/18) cases, respectively, which was significantly different from CC ($p<0.01$). No significant difference in the expression of miR-21 and miR-10b was identified between the CCs and PDACs (both $P>0.05$).

Conclusions:

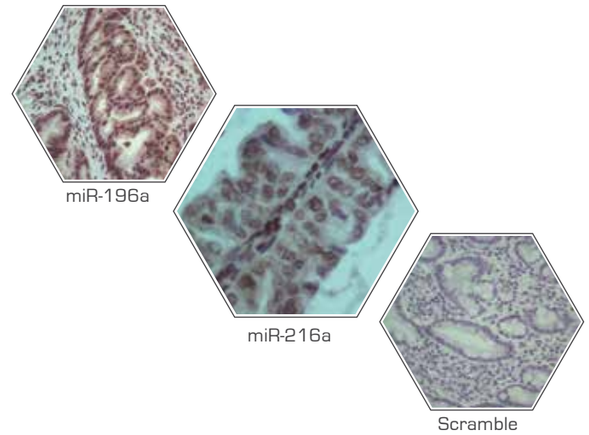
miR-196a and miR-216a expression were upregulated in CC compared to PDAC. This study demonstrates feasibility of an "in situ" evaluation in FFPE where morphologic control of cells of interest and differentiating cancer and benign cell expression is retained. Ongoing studies in a larger cohort are underway to fully assess the potential of these markers in differentiating CC from PDAC.

Category: Pancreas and Biliary Tree

Tuesday, March 4, 2014 1:00 PM
Poster Session IV # 152, Tuesday Afternoon
USCAP 2014

Cholangiocarcinoma (CC) vs. Pancreatic ductal adenocarcinoma (PDAC)

Cholangiocarcinoma (CC)



Pancreatic ductal adenocarcinoma (PDAC)