©RSNA, 2016 10.1148/radiol.2016160024

Appendix E1

Cell Culture

The MatLyLu cell line was kindly provided by John Isaacs, PhD (Johns Hopkins University, Baltimore, Md), and was maintained in RPMI 1640 medium with 10% fetal bovine serum, 2 mmol/L of L-glutamine, 100 U/mL of penicillin, 100 U/mL of streptomycin, and 250 nmol/L of dexamethasone (Sigma 2915, St Louis, Mo) (1). The cells were found to be negative for rodent pathogens (Impact V rat panel, Idexx Bioresearch, Columbia, Mo).

Model System

We sought to overcome two limiting features of existing mouse models of circulating miRNA biomarkers (2): *(a)* low available blood volume, which restricts the number of collections possible, and *(b)* blood collection via a tail vein or submandibular bleeds, which may contaminate samples with skin cells. Therefore, we chose to use a rat model system with surgically implanted jugular vein polyurethane catheters (Charles River Laboratories, Wilmington, Mass). (Of note, we observed that polyurethane catheters remained more patent and showed more resistance to blockage relative to other materials available from the vendor.) This increased the available blood volume by approximately tenfold and enabled serial puncture-free blood collection (thus avoiding contamination by skin tissue, etc). Cannulas were flushed per the vendor protocol by using taurolidine citrate (Access Technologies, Skokie, Ill) as a lock solution to avoid downstream PCR inhibition by heparin. The MatLyLu derivative of the Dunning rat prostate cancer model was selected because of its rapid growth of syngeneic tumors, which prevents the expiration of cannula patency and enables the use of immunocompetent rats (1).

Passive Cavitation Detection and Signal Processing

A miniature flat passive cavitation detector was positioned at the side of the transducer and aligned to detect broadband emissions from inertially collapsing bubbles in the focal area during each focused US pulse. The passive cavitation detector was 3 mm in aperture, with the frequency band of 6.3–14.2 MHz at a 6-dB level (Panametrics XMS-310; Olympus, Waltham, Mass). The signals received by the passive cavitation detector were amplified by 20 dB (Panametrics PR5072; Olympus) and recorded by using a digital oscilloscope.

RNA Isolation

Lysates were thawed on ice, followed by thorough homogenization at room temperature (3). A mixture of three synthetic *C. elegans* miRNA oligoribonucleotides (4) and MS/2 carrier RNA (5) (10165948001; Roche, Basel, Switzerland) formulated in Qiazol (Qiagen, Hilden, Germany) was then added to the samples, and the solution was rehomogenized. Total RNA was isolated from these samples and Qiazol lysates of the MatLyLu cell line by using the miRNeasy kit (Qiagen) with minor modifications as described previously (3) (J.R.C.).

miRNA Profiling and Identification of Candidate miRNA Biomarkers

RNA derived from four samples of untreated rat plasma and the MatLyLu cell line were used for discovery of candidate biomarkers (J.R.C., M.D.G.). Samples were profiled for the relative abundance of 375 miRNAs by using microRNA ready-to-use PCR, human panel I, V2.M RTqPCR arrays (Exiqon, Vedbaek, Denmark). Thirteen microliters of each sample were reverse transcribed with the miRCURY LNA Universal RT microRNA PCR kit (Exiqon), as directed. Reverse transcription products were combined with SYBR Green master mix and loaded into the 384-well RT-qPCR arrays. Quantitative PCR was performed on a 7900HT instrument (Applied Biosystems, Foster City, Calif). In addition, each RNA sample was separately assayed for the spike-in oligonucleotide *cel*-miR-39 by TaqMan RT-qPCR (Applied Biosystems), as described previously (4). Data from all miRNA RT-qPCR arrays were imported into SDS Enterprise software (V2.2.2; Applied Biosystems), and cycle threshold values were calculated by using automated, assay-specific baseline and threshold settings. The difference between the mean plasma cycle threshold and cell line cycle threshold was calculated for each miRNA, and five of the top 10 miRNAs that showed the greatest difference in cycle threshold values were selected as candidate biomarkers: miR-34c, miR-100, miR-129–5p, miR-196a, and miR-9 (Fig 5). These biomarkers were undetectable or had low abundance in untreated rat plasma and high abundance in the cell line. To select among the top 10 miRNAs, those with previously reported high expression in any blood cell type were excluded (6), and those for which in-house assays were available were given preference. In our laboratory, we have observed that miR-502–5p and miR-582–5p are present in whole blood, neutrophils, and monocytes (6) (data available on request). In the same study, we observed that miR-196b is present in whole blood and neutrophils. A miR-9* assay was not readily available in-house at the time of analysis. We initially sought to include the analysis of miR-129–3p, but preliminary evaluation of the assay for this miRNA showed inconsistent results. Because of this technical concern and the reasonable performance of the assays for the other miRNAs, we chose not to pursue miR-129–3p further.

Individual RT-qPCR Assays

TaqMan assays (Applied Biosystems) for human miRNAs (identical to the rat sequences) *hsa*miR-16, *hsa*-miR-34c, *hsa*-miR-100, *hsa*-miR-129–5p, and *hsa*-miR-196a, in addition to *C. elegans* miRNA *cel*-miR-39, were obtained from Applied Biosystems. Oligoribonucleotides that corresponded to the mature sequence of each miRNA were synthesized (Integrated DNA Technologies) and serially diluted for standard curves (3). Individual miRNAs were detected by using RT-qPCR, as described previously (4), on a ViiA 7 instrument (Applied Biosystems). Cycle threshold values were calculated by the ViiA 7 signal-processing algorithm (v1.0; Applied Biosystems) to automatically call baseline and threshold with ROX (carboxy-x-rhodamine passive reference dye; Applied Biosystems) normalization. Undetermined cycle thresholds were arbitrarily set to 40 as an estimate of the maximum possible abundance of target. The concentration of analyte was calculated by comparing the experimental cycle threshold to that of the standard curve, and results were presented as the mean of the PCR duplicates. *Cel*-miR-39 normalization was used to correct for variations in RNA recovery during purification, per our standard protocol (4) (J.R.C., M.D.G.).

Statistical Analysis

For the results presented in Figure 6, the data for an individual treatment were compared against those for the mock treatment at the corresponding time point by using one-way analysis of variance (Kruskal-Wallis test), followed by the Dunn multiple-comparisons test. For the results

presented in Figure 7, the data for tumor liquefaction with pulsed focused US at each time point were compared with the pretreatment values by using one-way analysis of variance (Friedman test), followed by the Dunn multiple-comparisons test. Nonparametric tests were chosen because of the relatively small sample sizes and the non-Gaussian distribution of data, in addition to providing conservative estimates of the *P* values. All statistical analysis was performed by using Prism 7.0a software (GraphPad Software, La Jolla, Calif) with criteria for significance given as *P* up to .05, *P* up to .01, or *P* up to .001 (J.R.C., T.D.K.).

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Note.—Numerical data correspond to the graphs displayed in Figure 5. Higher relative abundance is indicated by lower relative cycle threshold values, and lower relative abundance is indicated by higher relative cycle threshold values. miRNAs were ranked according to the difference in cycle threshold values, and then five of the top 10 miRNAs were selected as candidate biomarkers.

† Selected as a candidate biomarker.