INTRODUCTION

Multiple studies have revealed that the expression profiles of miRNAs in cancer samples correlate with prognosis, cancer type, and genetic abnormality (Cain 2002, Cain 2004, Takamizawa 2004, Yanaihara 2005). Because of their small size and inherent stability in clinical samples, miRNAs could be ideal biomarkers for diagnostic assays. These small RNAs can provide patient information that can not be determined by standard pathology, including patient prognosis and response to therapy. Analyses are possible using available surgical samples, FFPE blocks, or readily accessible blood, urine, or saliva samples.

MATERIALS AND METHODS

RNA from frozen tissue samples was isolated using the mirVana™ PARIS™ RNA isolation kit (Ambion). RNA from FFPE samples was isolated using the RecoverAll™ isolation kit (Ambion). RNA from blood was isolated using a novel glass fiber filter protocol for extracting small amounts of RNA from large volume samples.

The relative abundance of miRNAs in frozen and FFPE tissue samples was measured using mirVana BioArray. Microarray data was verified by qRT-PCR using TaqMan assays (ABI) or Asuragen technology as noted. The abundance of miRNAs in blood RNA samples was measured by qRT-PCR in the same manner.

RESULTS

Microarrays were used to compare normal, chronic pancreatitis, and carcinoma. These small RNAs can provide patient information that cannot be determined by standard pathology, including patient prognosis and response to therapy. Analyses are possible using available surgical samples, FFPE blocks, or readily accessible blood, urine, or saliva samples.

CONCLUSION

We have used a collection of technologies to isolate and quantify miRNAs from frozen tissues, FFPE samples, serum, plasma, urine, and saliva. The observation that miRNAs are abundant, relatively stable, and easy to recover from patient samples that are readily available in clinical settings suggests that small RNAs might ultimately support diagnostic applications. Combined with the observation that the expression of miRNAs correlates with clinically important factors like prognosis, disease type, and genetic aberration, we believe that miRNAs will ultimately prove to be an ideal analyte for cancer diagnostic assays.

References